



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 194203

TO: Sheela Huff
Location: rem/3A15/3C18
Art Unit: 1643
Friday, June 30, 2006
Case Serial Number: 10/671054

From: Willis McCumber
Location: Biotech-Chem Library
REM-1A75
Phone: (571)272-2697

willis.mccumber@uspto.gov

Search Notes

Examiner Huff,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services.

Willis McCumber
ASRC Aerospace Corporation
Library Technician
STIC Biotech/Chem Library
(571)272-2697

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71973

194203

my

STIC-Biotech/ChemLib

From: Huff, Sheela
Sent: Tuesday, June 27, 2006 5:27 PM
To: STIC-Biotech/ChemLib
Subject: 10671054--search request

Please search and interference search SEQ ID No. 1-2 of the above.

Thanks-

Sheela Huff
Art Unit 1643
571-272-0834
Remsen 3A15
mailbox Remsen 3C18

FOR
SCANNING
ONLY

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

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Query Match	81.4%	Score 2993	DB 2	Length 674
Beet Local Similarity	82.9%	Pred. No. 3.6e-202		
Matches 558	Conservative 40	Mismatches 71	Indels 4	Gaps 3
7	PGF-AALRRAPQILLILIAACALALALPAREATOFLRPRORARQVPEEAKOGHLEREC	65		
5	PGPTALALGTA--LILILILASSSHTVLLIRAREEAFLLRPRORARQVPEEAKOGHLEREC	62		
66	VEELCSREAREAREVENDPETDYFPRYADCTINKTSGPYTKKSGFATCVONLDPDOCTPNC	125		
63	VEEVCSKEAREAREVENDPETDYFPRYOCMKRYGRPEIKONENFATCVONLDPDOCTPNC	122		
126	DRKGTAACODLMGNFPLCLCKAGWGRLCDKOVNCSOENGGLQICHNRGSPHSCSHG	185		
123	DKRGTAACODLMGNFPLCLCKAGWGRLCDKOVNCSOENGGLQICHNRGSPHSCSHG	182		
186	FELSDGRTCODIDECADSEACGEARCKNLPGSYCLDEGFAYSOEKACRDVDECTOG	245		
183	FSLQSDWKSQODIDECTSDTCDPARCKNLPGSYCLDKGTYTSKEXTCDVDCEQOD	242		
246	RCQOVCVNRSYSTCHCDGRGGLKLSQMDTCEDILPCYPPEVAASVKSLLYGRMSSGP	305		
243	RCQOVCVNRSYSTCHCDGRGGLKLSQMDTCEDILPCYPPEVAASVKSLLYGRMSSGP	302		

Query Match 80.4%; Score 2955.5; DB 2; Length 673; Beel Local Similarity 81.6%; Pred. No. 1.6e-199; Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY 306 VILRLFRKRLDPTRLVAEFDRPTDPBEGILLFAGHODSTIVLALAGRIELRLNGVG 365
DB 303 VIRLFRKRLDPTRLVAEFDRPTDPBEGVLFPAGRSSTWIVGLRGRLEQLRNGVG 362
QY 366 RVTSAGGVINHGMMQTSVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLNLTVGG 425
DB 363 RITSGGTITNHGMQITISVELDRNLVIKNRDAVMKIAVAGGLFQLERGLYHLNLTVGG 422
QY 426 IPEHEKDLVDPINRDLDCGRSWNMLNGEDTTIQEYKVNTRQCSVYTERGSPYRSGF 485
DB 423 IPEHEKDLVDPINRDLDCGRSWNMLNGEDTTIQEYKVNTRQCSVYTERGSPYRSGF 482
QY 486 AFPSLDLMRTPLDVGESTVEVEVAHIRPAADPTGVFALMAPDLRAVPEVSLVLDVHST 545
DB 483 AFPSLDLMRTPLDVGESTVEVEVAHIRPAADPTGVFALMAPDLRAVPEVSLVLDVHST 541
QY 546 KKLKKQLVLAVENTALALMEIKVCDQGEHVVTVSLRDGEATLEVDGTRGQSEVSAALQ 605
DB 542 KKLKKQLVLAVENTALALMEIKVCDQGEHVVTVSLRDGEATLEVDGTRGQSEVSAALQ 601
QY 606 ERLAVLERHLRSPVLTAGGLPDVPTSAVTAIFYRCMTLENNRRLDLDEAAYRHSDI 665
DB 602 ERLDLKTRLGSLVLTAVGGPLPDVQVSTEVTAIFYRCMTLENNRRLDLDEAAYRHSDI 661
QY 666 TASHCPVPEPAA 678
DB 662 TASHCPVPEHVT 674

RESULT 3
A48089
growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C:Accession: A48089; S37437
R:Manfioletti, G.; Avanzini, C.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: UNIPROT:Q61592; UNIPARC:UPI000004A5B8; GB:X59846; NID:9407060; PIDN
A:Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F.38-89/Domain: Gla domain homology #status atypical <Gla>
F.117-150/Domain: EGF homology <EG1>
F.157-192/Domain: EGF homology <EG2>
F.196-233/Domain: EGF homology <EG3>
F.239-274/Domain: EGF homology <EG4>
F.308-666/Domain: sex hormone-binding globulin homology <SHB>
F.318-470/Domain: laminin G repeat homology <LGR>

QY 7 PGPAALRAAPOLLILLIAECALALLPAREATOLRPRORARAFQVEEAKOGLRECV 66
DB 5 PGPAALRAAPOLLILLIAECALALLPAREATOLRPRORARAFQVEEAKOGLRECV 63
QY 67 EELCSREARAEVFENDEPTDFYFRYLDCLINKYSGPYTKNSGFATCYQNLPDQCTPNPCD 126
DB 64 EELCSREARAEVFENDEPTDFYFRYLDCLINKYSGPYTKNSGFATCYQNLPDQCTPNPCD 123
QY 127 RKGQVACODLMGNFFCCKAGWGRCLCDKDVNCEQSNNGCLQICHHKPGSFHCSCSGF 186
DB 124 RKGTHICODLMGNFFCCKAGWGRCLCDKDVNCEQSNNGCLQICHHKPGSFHCSCSGF 183

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QY      187 ELSSDGRTCODIDECADSEAGSEARCKNLPGSYSLCDEGFAYSSOEAKACRDVDECIOGR 246
      188 SLASDQGTCDIDBCTDSDTCGDARCKNLPGSYSLCDEGFAYSSOEAKACRDVDECIOGR 243
QY      247 CEYCVNPSGSSYTCCHDGRGGLKLSQDMTCEDTLPCVPSVAVKSVSLYIGRMFSGTPV 306
      244 CEYCVNPSGSSYTCCHDGRGGLKLSQDMTCEDTLPCVPSVAVKSVSLYIGRMFSGTPV 303
QY      307 IRLRFKXLOPTRLVAEPDFPTEDEGILLPFGCHQDSTWIVLALRRLRLQLRNVNVR 366
      304 IRLRFKXLOPTRLVAEPDFPTEDEGILLPFGCHQDSTWIVLALRRLRLQLRNVNVR 363
QY      367 VTSSGPVINGMMQTTISVEELARLVIKVRDAVMKIAVAGDLFQPERGLYHLNLTVGGI 426
      364 ITSSGPTINGMMQTTISVEELARLVIKVRDAVMKIAVAGDLFQPERGLYHLNLTVGGI 423
QY      427 PFHEKDLVQPINPLDGCMSRWMLNGEDTTIOETKVNTRMOCFSVTERGSEFYPSGGA 486
      424 PFHEKDLVQPINPLDGCMSRWMLNGEDTTIOETKVNTRMOCFSVTERGSEFYPSGGA 483
QY      487 FYSLDVWRPTLDVGTSETEVEVAHTRPADGCVLFALMAPDLRAVPLSVLAVDYHSTK 546
      484 TYRLNTRISLDVGTETWEVKVARIKPAITDGVLLALVGD--DVVISVALVDYHSTK 541
QY      547 KLRKQVLVAVENTALALMEIKVDCQGEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 606
      542 KLRKQVLVAVENTALALMEIKVDCQGEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 601
QY      607 RLAVLRHRLSPVLTPAGGLPDVPTVSAPVATFYRGCMTELVNRLLDDEAAVYKSHDIT 666
      602 RLDTLFTLHQSGVHTVYVGLPEVSVISAPVATFYRGCMTELVNKGKILDLTPASVYKSHDIT 661
QY      667 AHSCEPVEPA 676
      662 SHSCPEVEPA 671
Db

```

RESULT 4
KXHU
N/A: alternate names: vitamin K-dependent protein S
C: species: Homo sapiens (man)
C: date: 21-Sep-1990 #sequence: revision 26-Jan-1996 #text change 09-Jul-2004
R: accession: A35610; A35611; A26157; A25891; A35612; A60903; S02424; S09519
R: Schmidt, D.K.; Tatro, A.V.; Phelp, L.G.; Tomczak, J.A.; Long, G.L.
Biochemistry 29, 7845-7852, 1990
A: title: Organization of the human protein S gene.
A: reference number: A35610; PMID:91084444; PMID:2148110
A: accession: A35610
A: molecule type: DNA
A: residues: 1-676 <SCH>
A: cross-references: UNIPARC:UPI000013238; GB:M57853; NID:g190547; PIDN:
A: note: the authors translated the codon TTT for residue 26 as Leu
R: Ploos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Bertina, R.M.
Biochemistry 29, 7853-7861, 1990
A: title: Intron-exon organization of the active human protein S gene Psalpa and its pse
A: reference number: A35611; PMID:91084445; PMID:2148111
A: accession: A35611
A: molecule type: DNA
A: residues: 1-25 <PL3>
A: cross-references: UNIPARC:UPI0000173343; GB:J02918
R: Hoskins, J.; Norman, D.K.; Beckmann, R.J.; Long, G.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987
A: title: Cloning and characterization of human liver cDNA encoding a protein S precursor
A: reference number: A26157; PMID:87092407; PMID:3467362
A: accession: A26157
A: molecule type: mRNA
A: residues: 1-10; 'P', 12-25; 'L', 27-676 <HOS>
A: cross-references: UNIPARC:UPI000014279B; GB:M15036; NID:g190288; PIDN:AAA6479.1; PID:
R: Lundwall, A.; Dackowski, W.; Cohen, E.; Shaffer, M.; Mahr, A.; Dahlback, B.; Stenflo,
Proc. Natl. Acad. Sci. U.S.A. 83, 6716-6720, 1986
A: title: Isolation and sequence of the cDNA for human protein S, a regulator of blood co

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A: reference number: A25891; PMID:86313649; PMID:2944113
A: accession: A25891
A: molecule type: mRNA
A: residues: 27-220; 'L', 222-262; 'H', 264-344; 'Y', 346-676 <LUN>
A: cross-references: UNIPARC:UPI0000070664; GB:M14338; NID:g190448; PIDN:AAA60181.1; PID:
A: note: part of this sequence, including the amino end of the mature protein, was deter
R: Edenbrandt, C.M.; Lundwall, A.; Wydro, R.; Stenflo, J.
Biochemistry 29, 7861-7868, 1990
A: title: Molecular analysis of the gene for vitamin K dependent protein S and its pseud
A: reference number: A35612; PMID:91084446; PMID:2148112
A: accession: A35612
A: status: not compared with conceptual translation
A: molecule type: DNA
A: residues: 284-676 <EDS>
A: cross-references: UNIPARC:UPI0000173344; GB:J02919
R: Ploos van Amstel, J.K.; van der Zanden, A.L.; Bakker, E.; Reitsma, P.H.; Bertina, R.M.
Thromb. Haemost. 58, 982-987, 1987
A: title: Two genes homologous with human protein S cDNA are located on chromosome 3.
A: reference number: A60903; PMID:88178564; PMID:2895503
A: accession: A60903
A: molecule type: mRNA
A: residues: 351-676 <PLO>
A: cross-references: UNIPARC:UPI0000173345
R: Ploos van Amstel, H.K.; van der Zanden, A.L.; Reitsma, P.H.; Bertina, R.M.
FEBS Lett. 222, 186-190, 1987
A: title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the
A: reference number: S02424; PMID:88005138; PMID:2820795
A: accession: S02424
A: molecule type: mRNA
A: residues: 1-676 <PL2>
A: cross-references: UNIPARC:UPI000013238; EMBL:Y00692; NID:g36578; PIDN:CAA6687.1; PI
C: gene: GDB:PROS1; PROS
A: map position: 3p11.1-3q11.2
A: introns: 26/1; 78/3; 87/1; 116/1; 157/1; 201/1; 243/1; 283/3; 322/2; 385/3; 441/3; 491
C: complex: in plasma forms a complex with C4b binding protein
C: function:
A: description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage des
C: superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat ho
C: keywords: beta-hydroxyaspartic acid; beta-hydroxyaspartic acid; blood coagulation; carbo
F: 1-24/Domain: signal sequence #status predicted <SIG>
F: 25-41/Domain: propeptide #status predicted <PRO>
F: 26-85/Domain: Gla domain homology <GLA>
F: 2-676/Product: plasma protein S #status predicted <MAT>
F: 121-154/Domain: EGF homology <EG1>
F: 161-199/Domain: EGF homology <EG2>
F: 205-241/Domain: EGF homology <EG3>
F: 247-282/Domain: EGF homology <EG4>
F: 315-667/Domain: sex hormone-binding globulin homology <SHB>
F: 325-478/Domain: laminin G repeat homology <LGR>
F: 47-48, 55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #sta
F: 58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241,
F: 111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F: 137/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F: 177, 219, 258/Modified site: erythro-beta-hydroxyaspartic acid (Asn) #status predicted
F: 99, 509, 530/Binding site: carboxylate (Asn) (covalent) #status predicted

```

Query Match 42.0%; Score 1543; DB 1; Length 676;
Best local Similarity 44.4%; Pred. No. 2e-100;
Matches 298; Conservative 127; Mismatches 218; Indels 28; Gaps 14;

```

QY      18 LLLLLLAECALAAALPPAREQFLRPRORAFQVEEAKQGLHEECYVEUCSREARE 77
      19 LLLLLLAECALAAALPPAREQFLRPRORAFQVEEAKQGLHEECYVEUCSREARE 77
Db      12 LACLLLVLPVSBANFLSKOASQVL-VRGRANSLLEETKQNLRECEIEEENKKEARE 70
QY      78 VFENDPETYFYPRYIDCINKY-----GSPTKNS--GFATCVQLPPQCTPNPCDRG 129
      79 VFENDPETYFYPRYIDCINKY-----GSPTKNS--GFATCVQLPPQCTPNPCDRG 129
Db      71 VFENDPETYFYPRYIDCINKY-----GSPTKNS--GFATCVQLPPQCTPNPCDRG 130
QY      130 TQACODLMGNFCLCKAGNGRLCDKDVNEC---SQENGCLQIQCHNKGSPHSGCHSGF 186
      131 TQACODLMGNFCLCKAGNGRLCDKDVNEC---SQENGCLQIQCHNKGSPHSGCHSGF 186
Db      131 YMSCDGRKASFTCTCKPGWGEKEFDINECKDPSNINCGSQICDNTGSHGSCKNCF 190

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QY 187 ELSNGRTQDDIDECA-DSBAGEARCKN.PGSVSCICDEBFAVSSQKACRDVDCIOG 245
 DB 191 VMLSKKKDCKDVDECSLKRSICGTAVCNKLPGDECECPBSEYRNKLKSKSCDDIDECSEN 250
 QY 246 RCEQVCNVPSPGYSYTCQCDGRGGLKLSQDMDTCEBILPCVPFSPVAKSVSLYLGRFSGTP 305
 DB 251 MCAOLCVNYPGGTCTYCDGKKGFKLANQDKSCSEVVSCLPLNLDTKYLTLVLAEPAGV- 309
 QY 306 VIRLPRKLIQPTRLVAEPDFRTPDPGILLPAGGHODSTWLVLAQRLEIQLRNYGVG 365
 DB 310 VLYLKFRLPEISRFSAEPFRFTYDEGVIILYAESIDHSAMILLALRGKXIEVOLNENHS 369
 QY 366 RYTSGGPVTNHGWMQOITISVELARNLVYKKNRDVYMKIYAVAGDLPQPERGLYHMLTVGG 425
 DB 370 KITAGDVVNNNGIMNNVSVBELHSHSISIKAKEAVMDINKRGPKLPENGLLETYVRFNG 429
 QY 426 IPFH-EKDLVQPIPNRLDGCGRSMNWLNGEDTTIOETVKVNTRMQCFSTVERSGSPYPSG 484
 DB 430 PPRKVESELIKPIPNRLDGCIRSMNMLKQGSIGKEIIQEQNKHCLVTVKESGYPPSG 489
 QY 485 PAFYSLDYNRKTPLDVGTSTSEWEVYVAHIRPADTGVLPALMAPRLRAVPLSVALVDYHS 544
 DB 490 IAFQFHIDYN---NVSSAEGMHVAVTLNIRSTGTGWLALVSGN-NTVPPFAVSLVD--S 542
 QY 545 TKKLKKOLVLAVERHAL-ALMEIKVC-DGGEHVVTSLRQGEALTEVDGTGQSEVSA 602
 DB 543 TSE-KSDILTSVENVTYVYIQLSLCSDQSH--LEFRVNRNMLELSTPKIETISHE 598
 QY 603 QLOERLAVLERHLSRPSYLPFAGGLPDVYVTSAPYATAFYRGCCMTLEVNRRLLDDEAYKH 662
 DB 599 DLQRLQAVLDKMKAKAVATYLGGLPDVPSATPNAPFNGCMEVINGQLDLDEALSRH 658
 QY 663 SDITAHSCPPV 673
 DB 659 NDIRAHSCPSV 669

 RESULT 5
 S53434
 Plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment)
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
 C/Accession: S53434
 Biochem. J. 305: 397-403, 1995
 A/Title: Identification of candidate residues for interaction of protein S with C4b binding protein
 A/Reference number: S53433; MUID:95134217; PMID:7832752
 A/Accession: S53434
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-642 <GRE>
 A/Cross-References: UNIPARC:UPI0000176513; EMBL:L31380
 A/Experimental source: tissue type liver
 A/Note: the source is designated as rhesus monkey
 C/Genetics:
 A/Genes: PROS
 C/Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat homology
 F:1-51/Domain: Gla domain homology (fragment) <Gla>
 F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
 F:8-642/Product: plasma protein S #status predicted <MAT>
 F:87-120/Domain: EGF homology <EG1>
 F:127-165/Domain: EGF homology <EG2>
 F:171-207/Domain: EGF homology <EG3>
 F:213-246/Domain: EGF homology <EG4>
 F:281-633/Domain: sex hormone-binding globulin homology <SHB>
 F:291-444/Domain: laminin G repeat homology <LGR>

 Query Match 41.2%; Score 1512.5; DB 2; Length 642;
 Best Local Similarity 44.2%; Pred. No. 2,6e-98;
 Matches 287; Conservative 122; Mismatches 202; Indels 39; Gaps 13;

 45 RRRARQVFEARQGHLERECVEELCSREAREVENDPETDYFPRVYLDICINKGSPYT 104

[illegible]

RESULT 6
KXBOS
plasma protein S precursor - bovine
N:Alternate names: vitamin K-dependent protein S
C:Species: Bos primigenius taurus (cattle)
C:Date: 08-Aug-1987 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C:Accession: A24759; A23888
R:Dahlback, B.; Lundwall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4159-4203, 1986
A:Title: Primary structure of bovine vitamin K-dependent protein S.
A:Reference number: A24759; PMID:86233400; PMID:2940598
A:Accession: A24759
A:Molecule type: mRNA
A:Residues: 1-675 <DAH>
A:Cross-references: UNIPROT:P07224; UNIPARC:UPI00001332E7; GB:M13044; NID:g163697; PIDN
A>Note: Parts of this sequence, including the amino end of the mature protein, were det
R:Dahlback, B.; Lundwall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986
A:Title: Localisation of thrombin cleavage sites in the amino-terminal region of bovine
A:Reference number: A23888; PMID:86168236; PMID:2937785
A:Accession: A23888
A:Molecule type: protein
A:Residues: 42-141 <DA2>
A:Cross-references: UNIPARC:UPI0000173346
C:Complex: In plasma forms a complex with C4b binding protein
C:Function:
A:Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage des
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C:Keywords: beta-hydroxyaspartagine; beta-hydroxyaspartic acid; blood coagulation; carbo-

F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-41/Domain: propeptide #status predicted <PRO>
 F:26-85/Domain: Gla domain homology <Gla>
 F:42-675/Product: plasma protein S #status experimental <MAT>
 F:121-154/Domain: EGF homology <EG1>
 F:161-199/Domain: EGF homology <EG2>
 F:205-241/Domain: EGF homology <EG3>
 F:247-282/Domain: EGF homology <EG4>
 F:315-666/Domain: sex hormone-binding globulin homology <SHB>
 F:325-478/Domain: laminin G repeat homology <LGR>
 F:47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F:58-63,88-113,121-124,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
 F:93-94/Cleavage site: Arg-14a (thrombin) #status experimental
 F:111-112/Cleavage site: Arg-Ser (thrombin) #status experimental
 F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:288-567,449-475,638-666/Disulfide bonds: #status experimental
 F:499/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.2%; Score 1479; DB 1; Length 675;

Best Local Similarity 41.6%; Pred. No. 6,2e-96;

Matches 280; Conservative 132; Mismatches 225; Indels 36; Gaps 13;

22 LLAECALALPAREATOPLRP-----RORRAFOVFEBAKOGHLEECVEELCSREE 74
 11 LLA---CLALVLPVLEANPLSRHAGVLLRRRAANTLLETCKGNLEECIEELCKKEE 67
 75 AREVFENDPTDYFPPRYLDLCINKYSGPYRKNSGFAT-----CYQNLPDQCTPNPCD 126
 68 ARRIFFENNPETEFYFPYKLCLOCSFRAGLFTPAALSTNAPYDLRSCTNAISDQCNPLPCN 127
 127 RKSTQACODMGNFPCCKAGMGRLCDKDVNECSQE---NGGLOIICHNKPSSFHSC 183
 128 EDFMTCKDQATFTCTCKSGMOGCKESDINECKDPVNINNGSSQICENTPSSHSC 187
 184 SGFELSDGRTCODIDBCA-DSEACGARKNLPGSYCLDEGFAVSSEKACRDVDEC 242
 188 NGFVMLSNKKDCQDVDECVALKPSICGTAVCNKIPGDEPCGABGYKKNPVSCKSDVDEC 247
 243 LQGRCEQVNCNSFGSYTCHCDGRGKLTSDMDTCEDILPCVPPSVAKSVKSYLYLGMFS 302
 248 AENLCAQOLCVNPGVSGSYCYCDGKKGFPLADOKSCCAVPCVCLPDLDKNELLYLAEOFV 307
 303 GTVIRLRFKRLDPTLRVAFEDPTPDPEGILLFAGGHODSTWIVALARGRLELQRYN 362
 308 GV-VLYLKRPETTFPSAFDFRTYDSBGVILYAESSDHSAMFLALARGKLEIQKNE 366
 363 GVGRTVSSGPIVNHGMQOTISVEELANLVIKVNRDAVMKIAVAGDLFQPERGLYHLNLT 422
 367 KTKKMTTGKVINIDGLMHVSVBELBGSISVKIAKEAVNMINKPSLFFKTNFLETKVY 426
 423 VGGIPRH-EKDLVQPINPRLDGCKRSMNWNINGEDTTIOETVKNTRMOCFSYTERGSFYP 481
 427 FAVVPKRMENALRPIINPRLDGCIKGMNLMNOSTGSKKEIIORKNHGLVANEKSYYP 486
 482 GSGFAFYSLDYMKTPLDVGTSTWVEVVAHIRPADTVGLFALMAPDLRAVPLSVALVD 541
 487 GTGVAQFSINRYK---NESNPEAMQVINSLINRPSGTGMLALVSDN--TVFPALSLVD 540
 542 YHSTKLKQQLVLAVEHTALME-IKVCDQGEHVTVSLRDEATLEVDGTRGSGSEVS 600
 541 -SATEKL--QDILVESVSWIGRIEALISLCSDDQ--TFLEIRVNRNMLELSTQLRKDSFH 595
 601 AAOQLRLAVLEHLRSPLYTEAGGILPDVPTSAVPTAFYRGCTLEEVNRRLLDLEAVY 660
 596 SEDFOGFAILDRAKMGVTVTYGLDVPFSAATPVNAFYOGCEMVNINGVQVLDLEAYS 655
 661 KHSIDITAFHSCPPV 673
 656 KKNIDIRAHSCPSV 668

RESULT 7

SS3433

Plasma protein S precursor, vitamin K dependent - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 01-Aug-1995 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

C/Accession: S53433

R/Greenberg, J.S.; Fernandez, J.A.; Radtke, K.F.; Griffin, J.H.

Biochem J. 305, 397-403, 1995

A/Title: Identification of candidate residues for interaction of protein S with C4b bin

A/Reference number: S53433; MUID:95134217; PMID:7832752

A/Accession: S53433

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-642 <GRE>

A/Cross-references: UNIPROT:Q20994; UNIPARC:UPI0000176515; EMBL:L31379

A/Experimental source: tissue type liver

C/Genetics:

C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat ho

F:1-51/Domain: Gla domain homology (fragment) <Gla>

F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>

F:8-642/Product: plasma protein S #status predicted <MAT>

F:87-120/Domain: EGF homology <EG1>

F:127-165/Domain: EGF homology <EG2>

F:171-207/Domain: EGF homology <EG3>

F:213-248/Domain: EGF homology <EG4>

F:261-633/Domain: sex hormone-binding globulin homology <SHB>

F:231-444/Domain: laminin G repeat homology <LGR>

Query Match 40.2%; Score 1477.5; DB 2; Length 642;

Best Local Similarity 43.5%; Pred. No. 7,4e-96;

Matches 280; Conservative 125; Mismatches 213; Indels 25; Gaps 11;

45 RORRAFOVFEBAKOGHLEECVEELCSREEFAVFENDPTDYFPPRYLDLCINKYSGPYT 104
 4 RKRANSMLERKOGHLEECIEELCSKEARAEVFENDPTDYFPPRYLACLSFRAGLF 63
 105 KNSGFAT-----CYQNLPDQCTPNPCDCKKQTOACODLMSNPFCLCKAGMGRLLDDK 156
 64 TAARLSTNAPYDLRSCTNAIPDQCNPLPCNEDDPMTCKDQAMFTCTCKSGWEGKEELD 123
 157 VNECSQE---NGGLOIICHNKPSSFHSCSGFELSDDGRTCODIDBCA-DSEACGARC 212
 124 INECKPBNINNGCSQICENTPSSHSCSGFIMLSNKDCQDVDECYKPSICDTAVC 183
 213 KNLPSYSCLDEGFAVSSQEKACRDVDECLOGRCEQVNCNSFGSYTCHCDGRGKLTLSQ 272
 184 KNIPGDFECGCEPGRYNPTLKSCEBDVDECSNMCAQLCVNPGVSGSYCYCDGKRGFLLAQ 243
 273 DMDTCEDILPCVPPSVAKSVKSYLYLGMFSGTIVILRFRKLDQPTRLVAEFDRTDPEG 332
 244 DQSCCAVPCVCLPDLDKNELLYLAEOFVGV-VLYLKRPETTFPSAFDFRTYDSBG 302
 333 ILTFAGGHODSTWIVALARGRLELQRYNNGVGRVTVSSGPIVNHGMQOTISVEELANLV 392
 303 VILYAESSDHSAMFLALARGKLEIQKNEHTTKITGGKRVINDGLMHVSVBELBGSIS 362
 393 IKVNRDAVMKIAVAGDLFQPERGLYHLNLTVGGIPIH-EKDLVQPINPRLDGCKRSMNWL 451
 363 VKIAKEAVNMINKPSLFFKTNFLETKVYFAGLPKVENALIKPINPRLDGCIKGMNLM 422
 452 NGEEDTIOETVKNTRMOCFSYTERGSFYPGSGFAFYSLDYMKTPLDVGTSTWVEVVA 511
 423 NQASGVKEIIDEIIONKHCLVTVKESYYPGSGVAQFSDYK---NVSAGAMQVNVSL 478
 512 HIRPADTVGLFALMAPDLRAVPLSVALVDYHSTKLKQQLVLAVEHTALA-LMEIKYC 570
 479 NIRPSAGTGMALVSGN-NTVPFALSLVD-SATEKL--QDILVESVSWIGRIEALISLCS 534
 571 DQGEHVTVSLRDEATLEVDGTRGSGSEVSAOQLRLAVLEHLRSPLYTEAGGILPDVP 630
 535 SSO--LSLLEMEVSVNSLELTLTOFEKRRISSEEDYOGFAILDRAKMGVTVTYGLDVP 592

```
Oy      631 VTSAPTAIFYRCMTLEVNRRLLDDEAAKYKSDITAHSCPPV 673
       ::||| |||:::||| |::|||
Db      593 FSATPVNAFYNGCMDVIINGVPFLDDEAIKAHNDIRAHSCPVS 635
```

RESULT 8

Plasma protein S - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 18-Feb-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S38819; S37238
R:He, X.; Dahlbaeck, B.
Eur. J. Biochem. 217, 857-865, 1993
A:Title: Molecular cloning, expression and functional characterization of rabbit anticomplement factor C3b inactivator
#:Reference number: S38819; MUID:94039141; PMID:8223642

F;296-449/Domain: laminin G repeat homology <LGR>

Query Match	39.7%	Score 1460.5	DB 2	Length 646
Best Local Similarity	42.7%	Pred. No. 1.2e-94		
Matches 277	Conservative 117	Mismatches 230	Indels 25	Gaps 11
OY	38 ATGFLRPRQBARAFCVFEERAKOGHLEBCEVEELCSREERAREVENDPETDYFPRYLDDCIN 97			
Db	3 ASQVLA-VKRRRANSMLEETKGNLEBECTBELCNBEAREVENDPETDYFPPKYLGLG 61			
OY	98 KYGSPY---TKNSG-----FATCVONLPRDOCTPNPCDBKQTAQCCODLNGNFELCKAGWG 149			
Db	62 SFRALFLPATRRSANGYEPDLRCVNAIIPDQCNPLRCSEBGLYNGCDGQATFICIKPQWQ 121			
OY	150 GRLCDKDVNECSQE---NGGLQICHNKPGSFHSCSGFELSDGRTCODIDBCA-DSE 205			
Db	122 GEKCEIDINECKDPTNINOGCSQICDNTAGSYHSCSKGFWLANEKKCKDKMDECSVPRS 181			
OY	206 AGGARCNLPBSYSCLEDEGFAYSSQEKACPDUNELQGRQEOVCNWSRGSYTHCHQGR 265			
Db	182 VCGTAVCKNTPDPEFCESBEGRYNPRFASCEBIDECSNMQAOLCVNPGGASYCYCGK 241			
OY	266 GGLKXISOMDTEGDLIPCVPFSAVSKSLYYGRMFSGPVIRLRFKRLQPLRLVLAEPDF 325			
Db	242 KGFKLQADKKSCSEANVPCLPLDLDKNYQLLYLAQEPVGA-VLYLFLHLPETIRFSAEPDF 300			
OY	326 RTFDEGILLFPAQHODSTFWILVALRAGRLBQLRLNGVGRVTSGGPVINHGMQOTISYE 385			
Db	301 RLYDEGVALYLAESLDHSTFWPLIALRQKIEIQFNVDYAQAQITTTGGQVINDGLMNVSYE 360			
OY	386 ELARNLVTKVNDAYWKIYVAGDLFOPERGLYHLNLTVGGIIPFH-EKDLVQIPINRLDGC 444			
Db	361 ELEHSVSIKIAQEPVNNINKPGLSLEFKPTNGFLETKVYFAGLRPRKYENALIRPINRLDGC 420			
OY	445 MESSAMNLNEDDTTIQETVKNVTRMOCFSYTERGESFPFGSGFAFYSLDVAWRTLDVGTEST 504			
Db	421 MEGANMLKQAGAGVKEIITQOKKQKDLVTVEKGSYYSPGGIAQPHFDN---NLISYED 476			

[illegible]

RESULT 9

plasma protein S precursor - mouse
 N/Alternate names: vitamin K-dependent glycoprotein S
 C/Species: Mus musculus (house mouse)
 C/Date: 13-Jan-1995 #sequence revision 26-Jan-1996 #text change 09-Jul-2004
 C/Accession: S43504; 159616; S35962
 R/Chu, M.D.; Sun, J.; Bird, P.
 Biochim. Biophys. Acta 1217, 325-328, 1994
 A/Title: Cloning and sequencing of a cDNA encoding the murine vitamin K-dependent protein S
 A/Reference number: S43504; MUID:94198297; PMID:8148380
 A/Accession: S43504

A.Molecular type: [UniProt](#) [P00876](#); [EMBL](#):Z25469; [NID](#):G396426; [PIL](#):
 A.Residues: 1-675 <CHD>
 A.Cross-references: UNIPROT:008761; UNIPARC:UPI000002204D; EMBL:Z25469; NID:G396426; PIL:
 R.Liu, D.; Schmidt, D.K.; Long, G.L.
 Thromb. Res. 74, 135-142, 1994
 A.Title: Structure of mouse protein S as determined by PCR amplification and DNA sequencing
 A.Reference number: 159616; MUID:94302659; PMID:8029814
 A.Accession: 159616
 A.Status: preliminary; translated from GB/EMBL/DBD
 A.Molecule type: mRNA
 A.Residues: 33-492; 'L', 494-675 <RES>
 A.Cross-references: UNIPARC:UPI000016CFD2; GB:L27439; NID:G487866; PID:AAA40006.1; PID
 C.Complex: in plasma forms a complex with C4b binding protein
 C.Function:
 C.Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage des-
 A.Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homology;
 C.Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carboxy-
 F.1-24/Domain: signal sequence #status predicted <SIG>
 F.25-41/Domain: propeptide #status predicted <PRO>
 F.26-85/Domain: Gla domain homology <GLA>
 F.42-675/Product: plasma protein S #status predicted <MAT>
 F.121-154/Domain: EGF homology <EG1>
 F.161-199/Domain: EGF homology <EG2>
 F.205-241/Domain: EGF homology <EG3>
 F.247-282/Domain: EGF homology <EG4>
 F.315-666/Domain: sex hormone-binding globulin homology <SHB>
 F.325-478/Domain: laminin G repeat homology <LGR>
 F.447, 48-55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #eta
 F.158-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241,
 F.111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
 F.153/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F.177, 219, 228/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F.499, 509/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]

Db 126 CNEGYSLACDQGAFTCCFKPGMGQDRQCYDVNECKDPSNVNGSGSQICDNTPGSYHCS 185
 QY 182 CHSGFELSDGRTCODIDECA-DSEACGEARCKNLPQSYGLCDEGFAYSSQEKACRDVD 240
 Db 186 CKRFPALPNKCKDCKDECLAKPSVCGTAVCKNIPGDFECCPDGRIYDSSSKCDVD 245
 QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSAKSVKSLYLGRM 300
 Db 246 ECEENMCAQLCVNPPGYSYCYCDGKGFKAQDQKSGEGIPVCLSLDLKNYELLYLAQ 305
 QY 301 FSGTPYRLRPFKRLQFRLVAEFPRTFDEPGILLFPGGHODSTWYLAAPGLLEQLR 360
 Db 306 FAGV-VLYLKFRLPDITRFSAEFPRTYDEGILLVAESLDHSMNLLIALFDGKIEVOFK 364
 QY 361 YNGVGRYSSGPTVNHGMQGTISVEELARLVKVRDAVMKIAVAGDLPOPERGLHYN 420
 Db 365 NEFSTQITTTGGVNVNNGIMMWSVEEELDDSVSIKIAKEAVMNKLSGLFEPDGFIDTK 424
 QY 421 LTVGGIPIFH-EKDLVOPINRLDGCMSNMWLNGETTIQETVKVNTMOCFSVTERGSF 479
 Db 425 IYFAGLPKRVESALIKRINPRLDGICRGMNLMKGALGAKELIEGKQNKICFLNVEKGSY 484
 QY 480 YPSSGFAPFSLDMKRPFLDVGTSTWEVEVVAHIRPAADTGVLPALMAPDLRAVPSVAL 539
 Db 485 YPSSGIAQFSIDYN---NVTNAEGMQMNTLNIRPSTGTGVMALVSGD--TVFPALSL 538
 QY 540 VDHSTFKKLKKOLVLAVEHTALALME-IKVCGSGEHVTVVSL-RDEGATLEVDGTRGOS 597
 Db 539 VDSRSG---TSQDILVFEVNSVVARLEVASLCSDDQSQOLCNVRNG--LELMTPIRKD 592
 QY 598 EVSAAQLQERLAVLERHLSPVLTFAAGLDPDVPTASAPVAFYRGCTLEVNRLDLDE 657
 Db 593 VVYSKDLQRLAILDKTMKRTVATYLGIPDISFSAFPVNAFYSGCMENVAINGVQDLDE 652
 QY 658 AAYKHSDDITHASCPV 673
 Db 653 AISKNDIRAHSCPSV 668
 RESULT 10
 KRTS
 Plasma protein S precursor - rat
 C/Spectrum: Rattus norvegicus (Norway rat)
 C/Date: 04-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
 C/Accession: J04180
 R.Yasuda, F.; Hayaishi, T.; Tanitame, K.; Nishioka, J.; Suzuki, K.
 J. Biochem. 117, 374-383, 1995
 A/Title: Molecular cloning and functional characterization of rat plasma protein S.
 A/Reference number: J04180; MUID:95332263; PMID:7608128
 A/Accession: J04180
 A/Molecule type: mRNA
 A/Residues: 1-675 <YAS>
 A/Cross-references: UNIPROT:P53813; UNIPARC:UPI00001333EB; GB:S78744; NID:G1041903; PIDN
 C/Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an anticoag
 activation of coagulation factors Va and VIII. This protein also binds to factor Va and
 C/Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
 C/Keywords: beta-hydroxyaspartate; beta-hydroxyaspartic acid; blood coagulation; carbox
 F.1-24/Domain: signal sequence #status predicted <Sig>
 F.1-25-41/Domain: propeptide #status predicted <PRO>
 F.1-26-85/Domain: Gla domain homology <Gla>
 F.1-82-675/Product: plasma protein S #status predicted <MAT>
 F.1-88-116/Domain: thrombin-sensitive #status predicted <THS>
 F.1-161-199/Domain: EGF homology <EG1>
 F.1-205-241/Domain: EGF homology <EG2>
 F.1-247-282/Domain: EGF homology <EG3>
 F.1-315-666/Domain: sex hormone-binding globulin homology <SHB>
 F.1-325-478/Domain: laminin G repeat homology <LGR>
 F.1-325-478-57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F.1-58-63,88-113,121-134,126-143,145-154,161-175,177-184,186-199,205-217,212-226,228-241,2
 F.1-111-112/Cleave site: Arg-Ser (thrombin) #status predicted
 F.1-136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F.1-177,219,258/Modified site: erythro-beta-hydroxyaspartate (Asn) #status predicted

F.499,509/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 39.4%; Score 1448; DB 1; Length 675;
 Best Local Similarity 42.8%; Pred. No. 9,36-94;
 Matches 289; Conservative 124; Mismatches 223; Indels 40; Gaps 15;
 QY 21 LLLAAECALALLPAREATQFLRP-----RORARFOVEEAKOGHLECEVEELCSR 72
 Db 10 VLLA---CLALVLPNSE-TNFLSKERASQVLYRRKRANTLLLEETKGNLERCEIEELCNK 65
 QY 73 EEARVEVNDPEFDYFPYRLDCINKY-----GSPYTKNS--GFATCVNLPDQCTPNP 124
 Db 66 EEARVEVNDPEFDYFPYRLDCINKY-----GSPYTKNS--GFATCVNLPDQCTPNP 125
 QY 125 CDKRGTAQCDLNGNPFCLCKAGMGRCLCKDVNEC---SQENGGCLQICHNKGSGFHC 181
 Db 126 CNEGYSLACDQGAFTCCFKPGMGQDRQCYDVNECKDPSNVNGSGSQICDNTPGSYHCS 185
 QY 182 CHSGFELSDGRTCODIDECA-DSEACGEARCKNLPQSYGLCDEGFAYSSQEKACRDVD 240
 Db 186 CKRFPALPNKCKDCKDECLAKPSVCGTAVCKNIPGDFECCPDGRIYDSSSKCDVD 245
 QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSAKSVKSLYLGRM 300
 Db 246 ECEENMCAQLCVNPPGYSYCYCDGKGFKAQDQKSGEGIPVCLSLDLKNYELLYLAQ 305
 QY 301 FSGTPYRLRPFKRLQFRLVAEFPRTFDEPGILLFPGGHODSTWYLAAPGLLEQLR 360
 Db 306 FAGV-VLYLKFRLPDITRFSAEFPRTYDEGILLVAESLDHSMNLLIALFDGKIEVOFK 364
 QY 361 YNGVGRYSSGPTVNHGMQGTISVEELARLVKVRDAVMKIAVAGDLPOPERGLHYN 420
 Db 365 NEFSTQITTTGGVNVNNGIMMWSVEEELDDSVSIKIAKEAVMNKLSGLFEPDGFIDTK 424
 QY 421 LTVGGIPIFH-EKDLVOPINRLDGCMSNMWLNGETTIQETVKVNTMOCFSVTERGSF 479
 Db 425 IYFAGLPKRVESALIKRINPRLDGICRGMNLMKGALGAKELIEGKQNKICFLNVEKGSY 484
 QY 480 YPSSGFAPFSLDMKRPFLDVGTSTWEVEVVAHIRPAADTGVLPALMAPDLRAVPSVAL 539
 Db 485 YPSSGIAQFSIDYN---NVTNAEGMQMNTLNIRPSTGTGVMALVSGD--TVFPALSL 538
 QY 540 VDHSTFKKLKKOLVLAVEHTALALME-IKVCGSGEHVTVVSL-RDEGATLEVDGTRGOS 597
 Db 539 VDSRSG---TSQDILVFEVNSVVARLEVASLCSDDQSQOLCNVRNG--LELMTPIRKD 592
 QY 598 EVSAAQLQERLAVLERHLSPVLTFAAGLDPDVPTASAPVAFYRGCTLEVNRLDLDE 657
 Db 593 VVYSKDLQRLAILDKTMKRTVATYLGIPDISFSAFPVNAFYSGCMENVAINGVQDLDE 652
 QY 658 AAYKHSDDITHASCPV 673
 Db 653 AISKNDIRAHSCPSV 668
 RESULT 11
 protein S - rat (fragment)
 C/Spectrum: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I59618
 R.Jamison, C.S.; McDowell, S.A.; Marlar, R.A.; Degen, S.J.F.
 Thromb. Res. 78, 407-419, 1995
 A/Title: Developmental expression of protein C and protein S in the rat.
 A/Reference number: I59618; MUID:95389408; PMID:7660357
 A/Accession: I59618
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-346 <RES>
 A/Cross-references: UNIPROT:Q62628; UNIPARC:UPI000006E601; EMBL:U06230; NID:G497116; PIF
 C/Superfamily: Plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
 F.1-337/Domain: sex hormone-binding globulin homology <SHB>
 F.1-149/Domain: laminin G repeat homology (fragment) <LGR>

Query Match 16.3%; Score 600; DB 2; Length 346;
Best Local Similarity 37.5%; Pred. No. 1.3e-34;
Matches 133; Conservative 71; Mismatches 129; Indels 22; Gaps 8;

QY 322 EEDFPTPEEGILTFAGGHQDSTWIVLALRAGRLLEQLRYNGVGRVTSQGVPIHNGMQOT 381
DB 4 ETSCHGFSESL-----DHGNMILLALREKIEVQFNGEFTSTQTTGGVNIINGNIWM 56

QY 382 ISVEELARNLVTKNRDAMKIAVAGDLFQPERGLYHMLTVGGIPFH-EKLVQPINR 440
DB 57 VSVEELDSVSIIKAKEAVNMINKSLFKPPTDGLDTIYAGAPRKVESALIKRINR 116

QY 441 LDGCRSMWMLNGEDDTTQETKVNTRMOCFSVTERGSPYPSGAFYSIDWRPTLDG 500
DB 117 LDGCTRGMMLKQAGLGAKEIVEGKONKCFLTVEKSTYPSGILKQESIDN---NT 172

QY 501 TESTEVEVAHIRPADTGVLPALWAPDLRAVPLSVALVDYHSTKRLKKQLVLAVENT 560
DB 173 NAEWDQINTLNIRPPTGTGVMALVSGD--TVPFALSLVDSGSG---TSQDILVEVENS 227

QY 561 ALALME-IVCGCGEHVTVSL-RDGEATLEVDGTRGQSEVSAALQOEKLAVERHLRSP 618
DB 228 VAAHLEATILCEGSPQSLKCNINRNG---LEIMTPVRKQVIYSKDLQRLALIDKTMKT 284

QY 619 VLTGAGLPDVPVTSAPVAFYRGCGWTELEVRRLDLDAAVYKSHDITFASCPV 673
DB 285 VAVYLGVDIPISFATPVNAFISGCEVINGVQLDDEAISKANDIRAHSCPSV 339

RESULT 12
S78040
fibulin, splice form C precursor - mouse
M.Alternate names: Basement-membrane protein BM-90
C.Species: Mus musculus (house mouse)
C.Date: 24-Jul-1998 #sequence revision 24-Jul-1998 #text_change 09-Jul-2004
C.Accession: S78040; S78560; S36440
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A.Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A.Reference number: S34968; MUID:93358897; PMID:8354280
A.Accession: S78040
A.Molecule type: mRNA
A.Residues: 1-685 <PAM>
A.Cross-references: UNIPROT:Q08879; UNIPARC:UPI0000176527; EMBL:X70854
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Submitted to the EMBL Data Library, January 1993
A.Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A.Reference number: S36440
A.Accession: S78560
A.Molecule type: mRNA
A.Residues: 1-39, 'P', '41-685 <CHU>
A.Cross-references: UNIPARC:UPI000002A96F; EMBL:X70854
C.Genetic: 568/3
A.Introns: 568/3
C.Superfamily: fibulin-1; EGF homology
C.Keywords: alternative splicing; basement membrane; calcium binding; extracellular matr
F1-29/Domain: signal sequence #status predicted <Sig>
F1-30-685/Product: fibulin, splice form C #status predicted <Mat>
F1-98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 362; DB 2; Length 685;
Best Local Similarity 38.2%; Pred. No. 1.5e-17;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 95 CINKGSPYTKNSGFATCYQNLP-----DOCTP--NPDCKGTOAQO 134
DB 327 CINTGSS-----YTQGNVNCGRGYHLNEBGRVCVDVDECAPAPFCG-KG-HNCL 376

QY 135 DLMGNFPLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKGSFHSCSHSGFELS 189
DB 377 NSPGSRFCCKAGFYPDGISRTC-VDINCCQRYPRGLCHKCKENTPGSHSCSAGFRLS 435

QY 190 SDGRTQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 246
DB 436 VDRSCEDVNECLNPGSQE--CANVGSYCCYCRGQVQLSDVDGTCEDIDECALPTGG 493

QY 247 --CEQVCNVSFGSYTCHCDGRGGLKLSQDMTCEDILFV 284
DB 494 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 532

RESULT 13
S34968
fibulin, splice form D precursor - mouse
M.Alternate names: Basement-membrane protein BM-90; calcium-binding protein BM-90
C.Species: Mus musculus (house mouse)
C.Date: 10-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C.Accession: S34968; S36441; S13814
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A.Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A.Reference number: S34968; MUID:93358897; PMID:8354280
A.Accession: S34968
A.Molecule type: mRNA
A.Residues: 1-705 <PAM>
A.Cross-references: UNIPROT:Q08879; UNIPARC:UPI000017651E
R.Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Submitted to the EMBL Data Library, January 1993
A.Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A.Reference number: S36440
A.Accession: S36441
A.Molecule type: mRNA
A.Residues: 1-39, 'P', '41-705 <PAM>
A.Cross-references: UNIPARC:UPI0000028FD1; EMBL:X70854; NID:9396820; PIDN:CAA50207.1; PI
A.Experimental source: cell-line F9 teratocarcinoma
R.Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur. J. Biochem. 193, 651-659, 1990
A.Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared
A.Reference number: S13814; MUID:91065369; PMID:2249686
A.Accession: S13814
A.Molecule type: protein
A.Residues: 28,31-49, 'X', '51-53; 'XX', '110-117;231-240, 'X', '242-243;339-362, 'S', '364-387;434-
A.Cross-references: UNIPARC:UPI000011EBB0; UNIPARC:UPI000017651F; UNIPARC:UPI0000176520,
525; UNIPARC:UPI0000176526
C.Superfamily: fibulin-1; EGF homology
C.Keywords: alternative splicing; basement membrane; calcium binding; extracellular matr
F1-29/Domain: signal sequence #status predicted <Sig>
F1-30-705/Product: fibulin, splice form D #status predicted <Mat>
F1-98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.9%; Score 362; DB 2; Length 705;
Best Local Similarity 38.2%; Pred. No. 1.5e-17;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 95 CINKGSPYTKNSGFATCYQNLP-----DOCTP--NPDCKGTOAQO 134
DB 327 CINTGSS-----YTQGNVNCGRGYHLNEBGRVCVDVDECAPAPFCG-KG-HNCL 376

QY 135 DLMGNFPLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKGSFHSCSHSGFELS 189
DB 377 NSPGSRFCCKAGFYPDGISRTC-VDINCCQRYPRGLCHKCKENTPGSHSCSAGFRLS 435

QY 190 SDGRTQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 246
DB 436 VDRSCEDVNECLNPGSQE--CANVGSYCCYCRGQVQLSDVDGTCEDIDECALPTGG 493

QY 247 --CEQVCNVSFGSYTCHCDGRGGLKLSQDMTCEDILFV 284
DB 494 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 532

RESULT 14
A47221
fibillin 1 precursor - human (fragment)
C.Species: Homo sapiens (man)

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:07:36 ; Search time 303 Seconds
(without alignments)
2094.260 Million cell updates/sec

Title: US-10-671-054-1
Perfect score: 3675
Sequence: 1 MAPSLSPGPAALRRAPQLLL.....AHSCPYEPAADYKDDDDK 686

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3628	98.7	678	2	061MN1_HUMAN
2	3596.5	97.9	721	1	GAS6_HUMAN
3	2993	81.4	674	1	GAS6_RAT
4	2989	81.3	674	2	061RL1_RAT
5	2965	80.7	674	1	GAS6_MOUSE
6	2322	63.2	671	2	02MJP6_NOTYI
7	2293.5	62.4	669	2	06DPA5_XENLA
8	2286	62.2	668	2	06PAE0_XENLA
9	1802	49.0	626	2	04SHY2_TETNG
10	1755	47.8	648	2	07TH4_BRARE
11	1543	42.0	676	1	PROS_HUMAN
12	1516	41.3	649	1	PROS_MACMU
13	1516	41.3	650	2	016519_HUMAN
14	1514	41.2	650	2	09NSD0_HUMAN
15	1479	40.2	675	1	PROS_BOVIN
16	1470.5	40.0	648	2	029094_PIG
17	1457.5	39.7	646	1	PROS_RABIT
18	1452	39.5	675	1	PROS_MOUSE
19	1452	39.5	675	2	03TR66_MOUSE
20	1448	39.4	675	1	PROS_RAT
21	891	24.2	729	2	04SHY3_TETNG
22	634.5	17.3	129	2	06SL2_HUMAN
23	600	16.3	346	2	062628_RAT
24	376	10.2	907	2	068EF9_MOUSE
25	374.5	10.2	2884	2	04SHN1_TETNG
26	366.5	10.0	941	2	05AYP0_DICTI
27	366	10.0	1277	2	07PPC0_ANOCA
28	363	9.9	705	1	FBNL1_MOUSE
29	363	9.9	705	1	FBNL1_MOUSE
30	359	9.8	1577	2	03TWK8_MOUSE
31	358.5	9.8	992	2	09V889_DROME
					08C9Q4_MOUSE

32	358.5	9.8	997	2	09JTS0_MOUSE	09JTS0_MOUSE
33	358	9.7	1018	2	06NZL8_MOUSE	06NZL8_MOUSE
34	357.5	9.7	961	2	09BOC6_MOUSE	09BOC6_MOUSE
35	357	9.7	708	2	P87363_CHICK	P87363_CHICK
36	356.5	9.7	477	2	05XJ74_BRARE	05XJ74_BRARE
37	356.5	9.7	1021	2	03UGU1_MOUSE	03UGU1_MOUSE
38	356.5	9.7	1666	1	LTPP4_MOUSE	LTPP4_MOUSE
39	356	9.7	469	2	05BLE3_BRARE	05BLE3_BRARE
40	354.5	9.6	1587	2	000508_HUMAN	000508_HUMAN
41	353.5	9.6	509	2	04SUJ7_TETNG	04SUJ7_TETNG
42	353.5	9.6	1557	2	075412_HUMAN	075412_HUMAN
43	353.5	9.6	1624	2	075413_HUMAN	075413_HUMAN
44	353	9.6	3857	2	088840_MOUSE	088840_MOUSE
45	352	9.6	1365	2	075N88_HUMAN	075N88_HUMAN

ALIGNMENTS

RESULT 1
ID 061MN1_HUMAN PRELIMINARY; PRT; 678 AA.
AC 061MN1;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-MAR-2006, entry version 10.
DE Growth arrest-specific 6.
GN Name=GAS6; ORFNames=RP11-199F6.6-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15108283; DOI=10.1002/humu.20025;
RA Munoz X., Sumoy L., Ramirez-Lorca R., Villar J., de Frutos P.G.,
RA Sala N.;
RT "Human vitamin K-dependent GAS6: gene structure, allelic variation,
RT and association with stroke.";
RL Hum. Mutat. 23:506-512(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC -!- EMBL/GenBank/DBJ third party annotation (TPA) entry.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
EMBL: BK001240; DA001155.1; -; Genomic DNA.
EMBL: BX072579; CAH71174.1; -; Genomic DNA.
SRR; 061MN1; 261-678.
DR Ensembl: ENSG00000183087; Homo sapiens.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR013120; ConA_like_subgrp.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR001881; EGF_3.
DR InterPro: IPR013091; EGF_Ca_bd.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR013032; EGF-like_reg.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR01791; Laminin-G.
DR InterPro: IPR012680; Laminin-G_2.
DR InterPro: IPR000294; Vitk_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF07645; EGF_CA; 2.
DR Pfam: PF00594; GLA; 1.
DR Pfam: PF02210; Laminin_G_2; 2.

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE OF 1-85.
 RA Mearse A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;
 RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP RECEPTOR INTERACTION.
 RX PubMed=7854420; DOI=10.1038/373623a0;
 RA Varnum B.C., Young C., Elliott G., Garcia A., Bartley T.D.,
 RA Fridegh Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,
 RA Yanagihara D., Bennett L., Sylber M., Merewether L.A., Tseng A.,
 RA Escobar E., Liu E.T., Yamane H.K.;
 RT "X1 receptor tyrosine kinase stimulated by the vitamin K-dependent
 RT protein encoded by growth-arrest-specific gene 6.";
 RL Nature 373:623-626(1995).
 [7]
 RP RECEPTOR INTERACTION.
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;
 RA Selt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,
 RA Mattsson K., Fisher J., Gies D.R., Jones P.F., Maslakowski P.,
 RA Ryan T.E., Tobkes N.J., Chen D.H., Disefano P.S., Long G.L.,
 RA Basilio C., Goldfarb M.P., Lemke G., Gless D.J., Yancopoulos G.D.;
 RT "The anticosagulation factor protein S and its relative, Gas6, are
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";
 RL Cell 80:661-670(1995).
 [8]
 RP ALTERNATIVE SPLICING (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;
 RA Marcandalli P., Goettsa M., Varnum B., Goruppi S., Schneider C.;
 RT "Identification and tissue expression of a splice variant for the
 RT growth arrest-specific gene gas6.";
 RL FEBS Lett. 415:56-58(1997).
 [9]
 RP RECEPTOR INTERACTION.
 RX PubMed=9839948; DOI=10.1074/jbc.271.47.30022;
 RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
 RA Mizuno K.;
 RT "Identification of the product of growth arrest-specific gene 6 as a
 RT common ligand for Axl, Sky, and Met receptor tyrosine kinases.";
 RL J. Biol. Chem. 271:30022-30027(1996).
 [10]
 RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND PROCESSING.
 RX PubMed=9326369; DOI=10.1016/S0014-5793(97)01093-4;
 RA Goruppi S., Yamane H., Marcandalli P., Garcia A., Clogston C.,
 RA Goettsa M., Varnum B., Schneider C.;
 RT "The product of a gas6 splice variant allows the release of the domain
 RT responsible for Axl tyrosine kinase receptor activation.";
 RL FEBS Lett. 415:59-63(1997).
 [11]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 261-721 (ISOFORM 2), AND
 RP MUTAGENESIS OF PHE-530; LEU-663 AND TYR-703.
 RX PubMed=8621659; DOI=10.1074/jbc.271.16.9785;
 RA Mark W.R., Chen J., Hammonds R.G., Sadtick M., Godowski P.J.;
 RT "Characterization of Gas6, a member of the superfamily of G domain-
 RT containing proteins, as a ligand for Rea and Axl.";
 RL J. Biol. Chem. 271:9785-9789(1996).
 [12]
 RP FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
 CC and MER whose signaling is implicated in cell growth and survival,
 CC cell adhesion and cell migration. Plays a role in thrombosis by
 CC amplifying platelet aggregation and secretion in response to known
 CC agonists (By similarity).
 CC -1- SUBUNIT: Monomer (Probable).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1; Synonyms=gas6SV;
 CC Name=1; Synonyms=gas6SV;

CC IsoId=Q14393-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q14393-2; Sequence=VSP_010494;
 CC Name=3;
 CC IsoId=Q14393-3; Sequence=VSP_010492, VSP_010493, VSP_010494;
 CC Note=No experimental confirmation available;
 CC TISSUE SPECIFICITY: Plasma. Isoform 1 and isoform 2 are widely
 CC expressed. Isoform 1 is the predominant form in spleen.
 CC -1- PTM: Isoform 1 is proteolytically processed after secretion to
 CC yield a N-terminal 36 kDa protein and a C-terminal 50 kDa protein
 CC including the laminin G-like domains which activates AXL.
 CC -1- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
 CC dependent carboxylation. These residues are essential for the
 CC binding of calcium (By similarity).
 CC -1- SIMILARITY: Contains 4 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 Gia (gamma-carboxy-glutamate) domain.
 CC -1- SIMILARITY: Contains 2 laminin G-like domains.
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 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC -----
 DR EMBL: U13720; AAA58494.1; -; mRNA.
 DR EMBL: AY256843; AA084057.1; -; Genomic DNA.
 DR EMBL: AY256830; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256831; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256832; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256833; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256834; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256835; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256836; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256837; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256838; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256839; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256840; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256841; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256842; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AY256843; AA084057.1; JOINED; Genomic DNA.
 DR EMBL: AK126533; BAC06580.1; -; mRNA.
 DR EMBL: BC038984; AA084057.1; -; mRNA.
 DR EMBL: AY170372; AA041859.1; -; Genomic DNA.
 DR PIR: B48089; B48089.
 DR PDB: 1H30; X-ray; A=322-721.
 DR GO: GO:0008283; P:cell proliferation; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR013320; Cons_1ike_subgrp.
 DR InterPro: IPR013320; Cons_1ike_subgrp.
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 Best Local Similarity 94.0%; Pred. No. 6,2e-248;
 Matches 678; Conservative 0; Mismatches 0; Indels 43; Gaps 1;
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 DB 1 MAPSPSPGPAALRRAPQULLLLLAACALALIPAREALQFLRPRRRARFOVFEKKGKH 60
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 DB 61 LRECEVEELCSREAREVENDEPETYFYPRIYDCINTKGSPTTKNSGFATCVQNLPDQC 120
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 DB 121 TNPDCRKQTQAQODIMGNFCLCKAGWGRGLCDKDVNCSQENGGCLQICHKKPSFHC 180
 QY 181 SCHSGFEISSDRTQDIDECADSEACGEARCKNIPGYSCLCDSEFAVSSQEKACRDVD 240
 DB 181 SCHSGFEISSDRTQDIDECADSEACGEARCKNIPGYSCLCDSEFAVSSQEKACRDVD 240
 QY 241 ECIQRCQEOVCVNSPQSYTCHCDGRGGLKLSQDMDTCE----- 278

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Db      301  GAQGRSEGHIPDRRGPRPMQDILPCVPVSAKSVKSYLYLGMFSGSTPIRLRPFKRLQPT 360
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QY      318  RLVASFDFPTDPEGILFPAGGHODSTWVLALRGRLELQRYNGVGVTSSTGPIYNG 377
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Db      361  RLVASFDFPTDPEGILFPAGGHODSTWVLALRGRLELQRYNGVGVTSSTGPIYNG 420
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QY      378  NMQGISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNLTVGGIIPFEKDLVQPI 437
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Db      421  NMQGISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNLTVGGIIPFEKDLVQPI 480
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QY      438  NPLRDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSEFYSGAFYSIDYKRTPL 497
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Db      481  NPLRDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSEFYSGAFYSIDYKRTPL 540
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QY      498  DVGSTSTVEVVAHVRPAADGVLPALMAPDLRAVPLSVLVYHSTKTKKOLVVLAV 557
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Db      541  DVGSTSTVEVVAHVRPAADGVLPALMAPDLRAVPLSVLVYHSTKTKKOLVVLAV 600
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QY      558  EHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVSAQLQERLAVLERHLS 617
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Db      601  EHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVSAQLQERLAVLERHLS 660
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QY      618  PVLTRAGLIPDVPTSAPYATYRGCMTLEVNRRLLDLDEAAVKHSDITAHSCPPVEPA 677
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Db      661  PVLTRAGLIPDVPTSAPYATYRGCMTLEVNRRLLDLDEAAVKHSDITAHSCPPVEPA 720
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QY      678  A 678
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Db      721  A 721
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RESULT 3
GAS6_RAT STANDARD; PRT; 674 AA.
ID GAS6_RAT
AC Q63772;
DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 46.
DE Growth-arrest-specific protein 6 precursor (GAS-6) (Growth-
DE potentiating factor) (GPF).
GN Name=Gas6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=95197586; PubMed=7890695; DOI=10.1074/jbc.270.11.5702;
RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura K., Fujita H.,
RA Ohara O., Arita H.;
RT "Vascular smooth muscle cell-derived, Glu-containing growth-
RT potentiating factor for Ca(2+)-mobilizing growth factors.";
RT J. Biol. Chem. 270:5702-5705(1995).
RN [2]
RN RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=7559388; DOI=10.1074/jbc.270.39.22681;
RA Ohashi K., Nagata K., Toshima J., Nakano T., Arita H., Tsuda H.,
RA Suzuki K., Mizuno K.;
RT "Stimulation of sky receptor tyrosine kinase by the product of growth
RT arrest-specific gene 6.";
RT J. Biol. Chem. 270:22681-22684(1995).
RN [3]
RN RECEPTOR INTERACTION.
RX PubMed=6939948; DOI=10.1074/jbc.271.47.30022;
RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
RA Mizuno K.;
RT "Identification of the product of growth arrest-specific gene 6 as a

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RT common ligand for Axl, Sky, and Mer receptor tyrosine kinases.";
RL J. Biol. Chem. 271:30022-30027(1996).
RN [4]
RN GAMMA-CARBOXYGLUTAMIC ACIDS.
RX PubMed=9163328;
RA Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.;
RT "Requirement of gamma-carboxyglutamic acid residues for the biological
RT activity of Gas6: contribution of endogenous Gas6 to the proliferation
RT of vascular smooth muscle cells.";
RL Biochem. J. 323:387-392(1997).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
CC and MER whose signaling is implicated in cell growth and survival,
CC cell adhesion and cell migration. Plays a role in thrombosis by
CC amplifying platelet aggregation and secretion in response to known
CC agonists (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
CC dependent carboxylation. These residues are essential for the
CC binding of calcium (Probable).
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC -----
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CC -----
DR EMBL: D42148; BAA07719.1; -; mRNA.
DR PIR: I55476; I55476.
DR HSSP: P00740; ICFH.
DR SMR: O63772; 258-674.
DR Ensembl: ENSRNOG0000018233; Rattus norvegicus.
DR RGD: 61913; Gas6.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR013320; Cona_like_subgrp.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR010811; EGF_Ca_bd.
DR InterPro: IPR013091; EGF_Ca_bd_2.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR012680; Laminin_G_2.
DR InterPro: IPR000294; VICK_dep_GLA.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF07645; EGF_CA_2.
DR Pfam: PF00594; Gla_1.
DR Pfam: PF02210; Laminin_G_2; 2.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_4.
DR SMART: SM00179; EGF_CA_3.
DR SMART: SM00069; Gla_1.
DR SMART: SM00282; LamG_2.
DR PROSITE: PS00010; ASX_HYDROXYL; 4.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS00026; EGF_3; 4.
DR PROSITE: PS01187; EGF_CA_3.
DR PROSITE: PS00011; GLA_1; 1.
DR PROSITE: PS50998; GLA_2; 1.
DR PROSITE: PS50025; IAM_G_DOMAIN; 2.
KW Calcium; EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein;
KW growth regulation; Metal-binding; Repeat; Signal.
FT SIGNAL 1 27
FT CHAIN 28 674
FT FT
FT DOMAIN 50 91
FT FT
FT DOMAIN 113 151
FT FT
FT DOMAIN 153 193
FT FT
FT DOMAIN 194 234
FT FT
FT DOMAIN 235 275

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FT DOMAIN 295 467 Laminin G-like 1.
FT DOMAIN 474 666 Laminin G-like 2.
FT METAL 326 326 Calcium (By similarity).
FT METAL 328 328 Calcium (via carbonyl oxygen) (By
FT METAL 437 437 similarity).
FT METAL 437 437 Calcium (via carbonyl oxygen) (By
FT METAL 652 652 similarity).
FT CARBOHYD 189 189 Calcium (By similarity).
FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
FT DISULFID 62 67 By similarity.
FT DISULFID 117 130 By similarity.
FT DISULFID 122 139 By similarity.
FT DISULFID 141 150 By similarity.
FT DISULFID 157 168 By similarity.
FT DISULFID 164 177 By similarity.
FT DISULFID 179 192 By similarity.
FT DISULFID 198 209 By similarity.
FT DISULFID 204 218 By similarity.
FT DISULFID 220 233 By similarity.
FT DISULFID 239 248 By similarity.
FT DISULFID 244 257 By similarity.
FT DISULFID 259 274 By similarity.
FT DISULFID 280 280 By similarity.
FT DISULFID 441 467 By similarity.
FT DISULFID 639 666 By similarity.
SQ SEQUENCE 674 AA; 74638 MW; FBF86B864d6F2E CRC64;

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Query Match 81.4%; Score 2993; DB 1; Length 674;
Best Local Similarity 82.9%; Pred. No. 7.3e-205;
Matches 558; Conservative 40; Mismatches 71; Indels 4; Gaps 3;

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QY 7 PGR-AALRRAPOLLLLLLAEALALPPREATOFRRPQRRAPQVFEBAKQGHLEREC 65
DB 5 PGRPALGTA--LILLILLASSSHHTVLLRAREAAQFRPRQRRAPQVFEBAKQGHLEREC 62
QY 66 VEEELCSREAREVENDPETDYFYPRYLDCINKYGSYTNNSGPAITVOMLPDQCTPNPC 125
DB 63 VEEVCSKEAREVENDPETDYFYPRYQECRRKTKGRBEDKNPFAITVKNLPDQCTPNPC 122
QY 126 DRKGTACODLMNPFCLCRAGNGRLCDQVNECSQENSGCLOICHNKPGSFHSCSHG 185
DB 123 DKKGTLQCLDMGNFCLCKDNGGRLCDQVNECSQENSGCLOICHNKPGSFHSCSHG 182
QY 186 FELSSSGRTQDIDECADSEACGACAKNPGSYSCLCDEGFAYSSOEKACRDVDECLQG 245
DB 183 FSLQSDNKSQDIDECCTSDPTCGDARCKNPGSYSCLCDEGFAYSSOEKACRDVDECLQG 242
QY 246 RCEQVQVNSPGSYTCGDCGRGKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGP 305
DB 243 RCEQTCVNSPGSYTCGDCNGGKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGP 302
QY 306 VIRLRKRLQPTRLVAEPFRTPDPGILLFAGGHODSTWIVALRAGRLQLRYNGV 365
DB 303 VIRLRKRLQPTRLVAEPFRTPDPGVLFFAGGRSDTWIVGLRAGRLQLRYNGV 362
QY 366 RYTSSEPVNKGWQITISVEELARNVIKNRDAVKNIAAGDLFQPERGLHYLNTVGG 425
DB 363 RYTSSEPVNKGWQITISVEELARNVIKNRDAVKNIAAGDLFQPERGLHYLNTVGG 422
QY 426 IFPHEKDLVQPINRPLDGCGRSNMNLNGEDPTTIOETVKNVTRNQCSTYERGSFFYGSG 485
DB 423 IFPHEKDLVQPINRPLDGCGRSNMNLNGEDPTTIOETVKNVTRNQCSTYERGSFFYGSG 482
QY 486 AFPSLDYMETPLDVGTESTWEVEVVAIRPADTGVLPALMABDLRAVPLSVLVYHST 545
DB 483 AFPSLYRTSLDVGETTWEVEVVAIRPADTGVLMAL-VEGDKVVLISVALVYHST 541
QY 546 KKLKQLVVLAVENHTALALMEIKVCGQEHVTVVSLRDEGATLEVDGTRGQGSVSAQIQ 605
DB 542 KKLKQLVVLAVENHTALALMEIKVCGQEHVTVVSLRDEGATLEVDGTRGQGSVSAQIQ 601

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QY 606 ERLAVLRHRHSPLYTFAGGLPDVPTASAPATARYCGMTLEVNRLLDDEAAYKISDI 665
DB 602 ERLDLKTRLGSGSVLTIVGGLPDVQVTSPTVATARYCGMTLEVNKTLDTPTASAKISDI 661
QY 666 TASHCPVEPEPAAA 678
DB 662 TASHCPVEPEVHTA 674

RESULT 4
Q6IRL1.RAT PRELIMINARY; PRT; 674 AA.
AC Q6IRL1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Gas6 protein.
GN Name=Gas6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RC TISSUE=Lung.
RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Stransberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Datchenko L., Marnitsina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdil T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywicki M.I., Skalek U., Smilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung.
RA Stransberg R.
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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EMBL: BC070881; AAH70881.1; -; mRNA.
HSSP: P00736; IAPQ.
DR SMR; Q6IRL1; 258-674.
DR Ensembl; ENSRNOG0000018233; Rattus norvegicus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR013320; ConA_like_subgrp.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013991; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR002363; GLA_blood.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR012680; Laminin_G_2.

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RT "The new ortholog of growth arrest-specific 6 (NgGas6) is implicated
RT in stress response during newt forelimb regeneration."
RL Dev. Dyn. 0:0-0(2006).

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CC

DR EMBL: DQ324381; ABC55062.1; -; mRNA.
DR SEQUENCE 671 AA; 74727 MW; 9D860B80336AD64 CRC64;

Query Match 63.2%; Score 2322; DB 2; Length 671;
Best Local Similarity 64.0%; Pred. No. 6.2e-157;
Matches 427; Conservative 89; Mismatches 147; Indels 4; Gaps 4;

QY 10 AALRRAPOLLILLALAEALAL-LPAPRATQFLSPRRARQVPEEAKOGLERECEE 68
DB 4 AALALGAILFLTLAADPAQGTIVPAKASQFLSRQRRANOIFEEETKQGLERECEE 63
QY 69 LCSREAREVFENDEDETFYPRYLDCINKGSPYTKNGSPATQVONLPDOCTPDCDK 128
DB 64 RCSRREAREVFENDEDETFYPRYLECJLFGSPYARNGLTTCVHNLPNQCSFVPCFXD 123
QY 129 GTQACODLGNFPFCLCKAGMGRLCDQVNECSOENGGLQICHNKPSFHCSCGSEFL 188
DB 124 GSTCEDQKGDYFCHCKLGMICKKCDADKDECFVANNNGCNOICLNKPSYHSCSGYAL 183
QY 189 SSDGRTCODIDECADSEA-CGEARCKNLPGSYCLCDEGPAVSSQEKACRDVDECTQGR 247
DB 184 QANNRICEDIDECKSPRTICGTACQCNHISYSCHCKDKGYKADCVADDECDKPC 243
QY 248 EGVCNVSPSTYCHCDRGGLKLSQMDCEPVPVPSVAKSVSYSLTGMFSGTPY 307
DB 244 EGTCTVNTLGSYCHCDRGGLKLSQMDCEPVPVPSVAKSVSYSLTGMFSGTPY 303
QY 308 RLRFKRLQPTRLVAEPFPTPEGILLFAGGHODSTWIVLALRAGRLTQLRYNGVGRV 367
DB 304 WRFRKQPTRLVAEPFPTPEGILLFAGGHODSTWIVLALRAGRLTQLRYNGVGRV 363
QY 368 TSSGPIVNGWQOTISVEELARNLVTKNRDAVMKTLVAGDLFQPERGLYHLNLYGSLP 427
DB 364 TSSGPIVNGWQOTISVEELARNLVTKNRDAVMKTLVAGDLFQPERGLYHLNLYGSLP 423
QY 428 FHEKDLVQINRLDGCMSNMNLNDEPTTIOETVYVNTRMOCFSTEEGSPGSGFAP 487
DB 424 FKHNEINQINRLDGCMSNMNLNDEPTTIOETVYVNTRMOCFSTEEGSPGSGFAP 483
QY 488 YSLDVKRTPLDVGTESTWEVVAHTRPADTGVLFALNAPDLRAVPLSAVLVDYHSTK 547
DB 484 FNIQITASSGEQADKMTVALTRAPAVDTGVLFALNAPDLRAVPLSAVLVDYHSTK 542
QY 548 LKKQIVLVAVENTALMEIKVCDGQEHVVTYSLRDEATLEVDGTRGQSEVSAALQER 607
DB 543 TQOQILILAKTIVSLEVNVCN-NDHSIALFVNKODIVLTVADGLAGQSEVNMMOLEAS 601
QY 608 LAVLEHNLSPVLTFRGGLPDVAVTSAPTAFRGCTLEVNRLDLDEAKHSDITA 667
DB 602 LKLMHMLRGVYTLGGLPDVAVTSAPTAFRGCTLEVNRLDLDEAKHSDITA 661
QY 668 HSCPEVE 674
DB 662 HSCPEVD 668

RESULT 7
Q6BPAS_XENLA PRELIMINARY; PRT; 669 AA.
AC Q6BPAS; 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DR Gas6-prov protein.
GN Name=Gas6-prov;
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OK NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tashy S., Carinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnatatene P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kertman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman A.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Clifton S.W.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RA Klein S., Gerhards D.S.,
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC

DR EMBL: BC076835; AAH76835.1; -; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR013320; Asx_like_subgrp.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR000742; EGF_3.
DR InterPro: IPR001881; EGF_Ca_bd.
DR InterPro: IPR013091; EGF_Ca_bd_2.
DR InterPro: IPR006209; EGF_like_reg.
DR InterPro: IPR013032; EGF_like_reg.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR01791; laminin_G_2.
DR InterPro: IPR012680; laminin_G_2.
DR InterPro: IPR000294; Vitk_deg_GLA.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF07645; EGF_CA_3.
DR Pfam: PF00594; Gla_1.
DR Pfam: PF02210; laminin_G_2_1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF_4.
DR SMART: SM00179; EGF_CA_3.
DR SMART: SM00069; GLA_1.
DR SMART: SM00282; LamG_2.
DR PROSITE: PS00010; ASX_HYDROXYL_3.
DR PROSITE: PS00022; EGF_1_1.
DR PROSITE: PS01186; EGF_2_3.

DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
 DR PROSITE; PS50998; GLA_2; 1.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
 SQ SEQUENCE 669 AA; 75233 MW; A8BE1E632540F643 CRC64;

Query Match 62.4%; Score 2293.5; DB 2; Length 669;
 Best Local Similarity 61.9%; Pred. No. 676-155;
 Matches 413; Conservative 105; Mismatches 144; Indels 5; Gaps 5;

QY 9 PAIRRAPQQLLLLAECALALLPAREATQFLPRGRAPQVFEAKQGHLEECYEE 68
 DB 4 PSALTATWLVTLIAEPLHSTIILSAWDASQFLRORRANQFEEFKQGHLEECYEE 63
 QY 69 LCSREAREVENDPEVDYFPRYLDCINKGSPYTKNSGATVCQNIPDCTNPPCRK 128
 DB 64 QCSREAREVENDPEVDYFPRYLDCINKGSPYTKNSGATVCQNIPDCTNPPCRK 122
 QY 129 GTQACODLMGNFCLCRAGMGRLCDKDVNCSQENGCLQICHNKPGSFHCSHGPEL 188
 DB 123 GSHCTDLHGFCHCKRPGWTGKCSRDNINCAIENGCNHSICLNKRGTHQCLRSGRRL 182
 QY 189 SSDRTQODIDECDAS-DACGEAPCKNLPGSYCLCDGEFAYSSQEKACRDVDECLQRC 247
 DB 183 HTNNKLCIDIDECASPNICGTAQCKNVLSTYVCLCEDEGYRDESTSKQDIDECXGRG 242
 QY 248 EYCVNNSPGSYCHGCDRGLKLSQDMDCEDILPCVPFSAKSVKSLYGRMSSGPVI 307
 DB 243 EYCVNNSPGSYCHGCDRGLKLSQDMDCEDILPCVPFSAKSVKSLYGRMSSGPVI 302
 QY 308 RLRFKRLQPTRLVAEPFRTFDPFEGILLFAGGHODSTWIVLALBAGLELQLRNGYGRV 367
 DB 303 RLRFKRLQPTRLVAEPFRTFDPFEGILLFAGGHODSTWIVLALBAGLELQLRNGYGRV 362
 QY 368 TSSGPIVNHGMQOTISVEELARNLVIKVNDVAKIIVAGDLFQPERGLYHLNLTVGIP 427
 DB 363 TSSGPIVNHGMQOTISVEELARNLVIKVNDVAKIIVAGDLFQPERGLYHLNLTVGIP 422
 QY 428 FHKEDLVQIPNPLDGMBSMNINLGEDTIOEVKKNITMOCQSVTERGSPFYGSFAF 487
 DB 423 FKSEELIQSINPLDGMBSMNINLGEDTIOEVKKNITMOCQSVTERGSPFYGSFAF 482
 QY 488 YSLDYMTPLDVGTESTWEVEVAHIRPADTGVLPALMAPDLRAVELSVALVDYHSTKK 547
 DB 483 FHLIDY-TYPSKETETAMRWVNAQINPATDTGVLPALVSKDM-VVPLSLALIDYHSSAK 540
 QY 548 LKKQLVLAVENTALAMEIKVCDGOEHVTVSLRDEATLEVDGTRGQSEVSAALOER 607
 DB 541 IKRQFILLSTENIVSRIVEQVCD-SEHIVEISASINDLFLSPFGTLGQKELPESQWRT 599
 QY 608 LALVEHLIRSPVLTFRAGLPDVPTSAFPAFRGCTLEVNRRLLDLDEAIVKHSITA 667
 DB 600 LHLNHLGKGVQTVGGLPDVAVTATPVAFYHGCWTMKIKQKPLDLDAVYKNDITS 659
 QY 668 HSCPYE 674
 DB 660 HSCPYE 666

RESULT 8
 ID 06PAEO XENLA PRELIMINARY; PRT; 668 AA.
 AC 06PAEO.
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE MG668463 protein.
 GN Name=MG668463;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;
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 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RL initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Klein S., Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; BC060355; AAH60355.1; -, mRNA.
 DR HSSP; P00743; 1APO.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR0010152; Axx_hydroxyl_S.
 DR InterPro; IPR013320; ConA_like_subgrp.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR001881; EGF_Ca_bd.
 DR InterPro; IPR013091; EGF_Ca_bd_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR012680; Laminin_G_2.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF07645; EGF_CA; 3.
 DR Pfam; PF00584; GLA_1.
 DR Pfam; PF02210; Laminin_G_2; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 4.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 4.
 DR PROSITE; PS01187; EGF_CA; 2.


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DB 238 QDLRSCRPRLPRISPSLKSKSRSLYLGRMFSGVPMVRLRFRPKRPTGSAFEDRTDPE 297
QY 332 GILLFAGHODSTWIVLALRAGRLEQLRYNGVGRVITSSGPFVNHGMQTTISVEELARNT 391
DB 298 GVVFEPAGHLNMSMIVLAVHHGKLOLQKYSIGRVTSSGPRINDGCMRKISVEGGRSL 357
QY 392 VIKANRDPAVKIAGLRFPERGLYHNLTVGGIIPHEKDLVOPINPRLDGCMRSNWT 451
DB 358 VIKIDREAVMKIIVISNLFTRLRKGVHEINFEVGVPPREDQLVQVNPRLDGCCKEWMKL 417
QY 452 NGEDTTIOETVKNTRNOCFSYTERGSGFYSGFAFSLDYMFRPLDVGEHTEVEVVA 511
DB 418 AGEDTSLQETITRSNDNQCFSADDPGAVYPRGTGALNTSDEIPLVSLPSSQ-NLSVRL 476
QY 512 HIRPADVTGVLPAIMAPDLRAVPLSVLVYHSTFKLKKOLVLAVENTLALMEIKVCD 571
DB 477 SLRPTSAVGLVLLLVHND--RVLPLSLVYHSTGQWRDYIIVTADDAIVASAPAPLCO 534
QY 572 GQEHVTVSLRDEBATELVDTGRGQSEVSAALQERLAVLERHLRSPVLTFAAGLPDPV 631
DB 535 GGSHPVHTVTSIGNQTILLVDGQSGRRDD-----ADVPTELLSGSTYIGGLPDPVL 585
QY 632 TSAPTAFYRCMTLEVNRLDLDEAAVGHSDITANSCP 671
DB 586 ASLTVAFAFSGCMVDVILNQPVLDQAVHKHNDIRSHSCP 625

RESULT 10
QY 07T3H4_BRARE PRELIMINARY; PRT; 648 AA.
DB 07T3H4_BRARE
AC 07T3H4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Growth arrest specific 6.
GN ORFName:zgc:63860.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stacheron M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.D., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;

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RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC
DR EMBL; BC053117; AAH53117.1; -, mRNA.
DR HSSP; Q14393; IH30.
DR ZFIN; ZDB-GENE-030131-7773; zgc:63860.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR002453; Beta tubulin_S.
DR InterPro; IPR013320; Cona_like_subgrp.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like_reg.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001792; Laminin_G.
DR InterPro; IPR012680; Laminin_G_2.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PRF00008; EGF_1.
DR Pfam; PRF0645; EGF_CA_3.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF02210; Laminin_G_2; 2.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SM00181; EGF_4.
DR SMART; SM00179; EGF_CA_2.
DR SMART; SM00069; GLA_1.
DR SMART; SM00282; LamG_2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA_2.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
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SQ SEQUENCE 648 AA; 72625 MW; E2935F42AF21CF64 CRC64;

Query Match 47.8%; Score 1755; DB 2; Length 648;
Best Local Similarity 50.8%; Pred. No. 1.9e-116;
Matches 334; Conservative 103; Mismatches 198; Indels 22; Gaps 9;

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 QY 438 NPRLDGCRSMNMLNGEDDTTIGETVYKVTNMOCSFVTERGFSYFSGFAFSLDYWRTP1 497
 DB 427 NPRLDGCMKDMRWMLTGEPTSIQETIRHNERMOCYAVEDHSAFYPGHGFAYFNHSH----- 481
 QY 488 DVGSTSTVEEVVAHRRPADTGVLPALMAPDLRAVPLSVLAVDVHSTTKKLKKQVLVLA 557
 DB 482 --GDNQTSVHT--LRAASSMGVLPALVRQD--RVFPFSISLSDYHPGTLQMTKHLVLSL 535
 QY 558 EHTALALMEIKVCDQEHVTVSLRDGEATLEVDGTGQSEVSAQOLQERLAVLSRHLS 617
 DB 536 GDNVGVSGPVNLSDDQTHVNTVMTGNSBVLVDQAQME-----MMEGVDSLQ--LTS 588
 QY 618 PVLTFAGGLPDVPTVSAPVATFAYRGCMTEVNRRLDLDEAAVKSDITAHSCPPVE 674
 DB 589 SYSTFEGIPDVSLVSSPVSAFPTGCMQDVAVNGQLLDVDEAQHKNDIRSHSCPLVD 645
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 PROS_HUMAN STANDARD; PRT; 676 AA.
 ID P07225; O15518; Q72715;
 AC 01-APR-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-APR-1988, sequence version 1.
 DT 07-MAR-2006, entry version 86.
 DE Vitamin K-dependent protein S precursor.
 GN Name=PROS1; Synonyms=PROS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87092407; PubMed=3467362;
 RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
 RT "Cloning and characterization of human liver cDNA encoding a protein S
 RT precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88005138; PubMed=2830795; DOI=10.1016/0014-5793(87)80217-X;
 RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
 RT sequences for the post-translational processing.";
 RL FEBS Lett. 222:186-190(1987).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91084444; PubMed=2148110;
 RA Schmidt D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
 RT "Organization of the human protein S genes.";
 RL Biochemistry 29:7845-7852(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=91084445; PubMed=2148111;
 RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
 RT "Intron-exon organization of the active human protein S gene PS alpha
 RT and its pseudogene PS beta: duplication and silencing during primate
 RT evolution.";
 RL Biochemistry 29:7853-7861(1990).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Rieder M.J., Garrington D.P., da Ponte S.H., Hastings N.C.,
 RA Ahearn M.O., Koldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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 RA Klausner R.D., Collins F.S., Wagner N., Shemen C.M., Schuler G.D.,
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 RA Richards S., Worley K.C., Hale T., Garcia A.M., Gay L.J., Hulik S.W.,
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 RA Yahay J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP NUCLEOTIDE SEQUENCE OF 27-676.
 RX MEDLINE=86313649; PubMed=2944113;
 RA Lundwall A., Dackowski W., Cohen E., Shaffer W., Mahr A., Dahlback B.,
 RA Stenflo J., Wydro R.;
 RT "Isolation and sequence of the cDNA for human protein S, a regulator
 RT of blood coagulation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
 RN [8]
 RP CARBOHYDRATE-LINKAGE SITE ASN-530.
 RX PubMed=16335952; DOI=10.1021/pr0502065;
 RA Liu T., Qian W.-T., Griltsenko M.A., Camp D.G. II, Monroe M.E.,
 RA Moore R.J., Smith R.D.;
 RT "Human plasma N-glycoproteome analysis by immunoaffinity subtraction,
 RT hydrazide chemistry, and mass spectrometry.";
 RL J. Proteome Res. 4:2070-2080(2005).
 RN [9]
 RP VARIANT HEERLEN PRO-501.
 RX MEDLINE=90335440; PubMed=2143091;
 RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A., Coenen J.,
 RA Leenhuys M.P., Deutz-Terlow P.P., van der Linden I.K., Reitsma P.H.;
 RT "Heerlen polymorphism of protein S, an immunologic polymorphism due to
 RT dimorphism of residue 460.";
 RL Blood 76:538-548(1990).
 RN [10]
 RP VARIANT PROS1 DEFICIENCY SER-258.
 RA Cooper D.N.;
 RL Unpublished observations (SEP-1993).
 RN [11]
 RP VARIANT PROS1 DEFICIENCY TOKUSHIMA GLU-196.
 RX MEDLINE=94129009; PubMed=8298131;
 RA Hayashi T., Nishio K., Shigekiyo T., Saito S., Suzuki K.;
 RT "Protein S Tokushima: abnormal molecule with a substitution of Glu for
 RT Lys-155 in the second epidermal growth factor-like domain of protein
 RT S.";
 RL Blood 83:663-690(1994).
 RN [12]
 RP VARIANTS PROS1 DEFICIENCY CYS-482; CYS-485 AND GLY-561, AND VARIANTS
 RP PRO-501 AND MET-559.
 RX MEDLINE=99374922; PubMed=10447256;
 RX DOI=10.1002/(SICI)1098-1004(1999)14:1<30::AID-HUMVA3.3.CO;2-O;
 RA Espinosa-Parilla Y., Morell M., Souto J.C., Tirado I.,
 RA Fontcuberta J., Baticelli X., Sala N.;
 RT "Protein S gene analysis reveals the presence of a cosegregating
 RT mutation in most pedigrees with type I but not type III PS
 RT deficiency.";
 RL Hum. Mutat. 14:30-39(1999).
 CC -1- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
 CC activated protein C in the degradation of coagulation factors Va

and *VitA*. It helps to prevent coagulation and stimulating fibrinolysis.

-1- SUBCELLULAR LOCATION: secreted protein.

-1- TISSUE SPECIFICITY: Plasma.

-1- DISEASE: Defects in *PROS1* are the cause of protein S deficiency (PROS1 deficiency) (MIM:176880). It is associated with an increased risk to develop thrombotic disease (thrombophilia).

-1- SIMILARITY: Contains 4 EGF-like domains.

-1- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.

-1- SIMILARITY: Contains 2 laminin G-like domains.

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EMBL, M15036: AAA36479.1; -, mRNA.
EMBL, Y00692: CAA68687.1; -, mRNA.
EMBL, Y00692: CAA68688.1; -, ALT. SEQ. mRNA.
EMBL, M57853: AAA60357.1; -, Genomic DNA.
EMBL, M57840: AAA60357.1; JOINED; Genomic DNA.
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EMBL, M36563: AAA60180.1; JOINED; Genomic DNA.
EMBL, AY308744: AAP45054.1, ALT. SEQ. Genomic DNA.
EMBL, BC015801: AAH15801.1; -, mRNA.
PIR, A35610: KXHS.
PDB, 1Z6C: NMR; A=200-286.
ENSEMBL, ENSG00000184500; Homo sapiens.
H-InvDB, HIX0022087; -.
HGNC, HGNC:9456; PROS1.
MIM, 176880: Gene+phenotype.
Reactome, P07225; -.
LinkHub, P07225; -.
GO, GO:0005576; C:extracellular region; NAS.
GO, GO:0004866; F:endorpeptidase inhibitor activity; TAS.
GO, GO:0007596; P:blood coagulation; TAS.
InterPro, IPR0000152; Asx_hydroxyl_S.
InterPro, IPR013320; ConA_like_subgrp.
InterPro, IPR006210; EGF.
InterPro, IPR000742; EGF_3.
InterPro, IPR001881; EGF_Ca_bd.
InterPro, IPR013091; EGF_Ca_bd_2.
InterPro, IPR006209; EGF_like_reg.
InterPro, IPR013032; EGF_like_reg.
InterPro, IPR003283; GLA_blood.
InterPro, IPR001791; Laminin_G.
InterPro, IPR012679; Laminin_G_1.
InterPro, IPR012680; Laminin_G_2.
InterPro, IPR000294; Vitk_dep_GLA.
Pfam, PF00008; EGF_2.
Pfam, PF07645; EGF_CA_2.
Pfam, PF00594; Gla_1.
Pfam, PF00054; Laminin_G_1; 1.

Query Match	42.0%	Score 1543:	DB 1:	Length 676:
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DB 12 LACILLVLPVEBANFLSKQASQYL-VRKRRAANLLEETQGNLERECIEELCKNEARE 70		:::	:::	:::
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DB 191 VMLSKPKCKKVDCESKLPSICGTAVCKNI PGDEPCECPGGRYNLKSKSCEDIDECSEN 250	:::	:::	:::	:::
QY 246 RCEOVCNVSPGSYCHDGRGCLTSDMDNCEPILTCVPEFSAKSKSLYGRMFGCTP 305	:::	:::	:::	:::
DB 251 MCAQLCVNPFGYCYCDGKKGFPLADQKSCVAVSVCLPLNLTQKYLLEYLAEQFAGV- 309	:::	:::	:::	:::
QY 306 VIRLRFKALQTRLVAEFPETPDPEGILLFAGGHODSTWLVALARGLLEQLRYNGVG 365	:::	:::	:::	:::
DB 310 VLYLKFRLPEISRSASAEFPDPTVDSQVLLYAESIDHSAMULLALRGCKIEVOLKNEHTS 369	:::	:::	:::	:::
QY 366 RVTSSGPVYHGMQTTISVEELANLVYKNNRDAVMKIAGDLPQERGLYHLNLTVVG 425	:::	:::	:::	:::
DB 370 KITGGVGINNGGLNMWVSVEELSHSISIKIAKEAAMDINKPGLFKEPENGILLKTYVFAAG 429	:::	:::	:::	:::
QY 426 IPFH-EKDLVQIPRPRDGCGRSNMYLNGEDDTTOEVKXNTNMQCSYTERGSPFYGSG 484	:::	:::	:::	:::
DB 430 FPRKVESELKFIPIPRLDGCRSNMLMKQASGKIKETIÖKÖNKHCLVYEEKSYTPGSG 489	:::	:::	:::	:::
QY 485 FAFYSLDYMRTPLDVGTESFWEVEVVAHIRPAADTVGLFALMAPDLRAVPLSVALVDYHS 544	:::	:::	:::	:::
DB 490 IAGPHIDYN---NVSSABEGHVVNTLINIRPSTGTGMALVAGN-NTVPEFAVSLVD-S 542	:::	:::	:::	:::
QY 545 TKKLKKQVLVLAHHTL-ALMETKYC-DOGEHVVTYSLDGEATLEVDSTROQSEVSA 602	:::	:::	:::	:::
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QY 663 SDITASHCPVY 673	:::	:::	:::	:::
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RESULT 12				
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AC Q28520;				
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.				
DT 07-MAR-2006, entry version 56.				
DE Vitamin K-dependent protein S precursor (Fragment).				
GN Name=PROS1; Synonyms=PROS.				
OS Macaca mulatta (Rhesus macaque).				
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
OC Cercopithecoidea; Cercopithecinae; Macaca.				
OX NCBI_Taxid=9544;				
RN [1]				

Db 584 MKGKATYLGGLPDVPFSATPVNAFYNGCMENVINGVLDLDEAISKNDIRAHSCPSV 642

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RESULT 13
ID Q16519 HUMAN PRELIMINARY; PRT; 650 AA.
AC Q16519;
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DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Protein S precursor (Fragment).
GN Name=PROS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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OC Homo.
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RX MEDLINE=66313649; PubMed=294413;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
CC -1- FUNCTION: Anticoagulant plasma protein. It is a cofactor to
and vitra. It helps to prevent coagulation and stimulating
fibrinolysis (by similarity).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivative license
CC -----
EMBL: M4338; AAA60181.1; -.
HSSP: P00740; 1CFH.
DR SMR; Q16519; 174-260.
DR Ensembl; ENSG00000184500; Homo sapiens.
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DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR013320; ConA_like_subgrp.
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DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR013091; EGF_Ca_bd_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR002383; GLA_blood.
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DR InterPro; IPR012679; Laminin_G_1.
DR InterPro; IPR012680; Laminin_G_2.
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DR Pfam; PF00008; EGF; 2.
DR Pfam; PF007645; EGF_CA; 1.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00054; Laminin_G_1; 1.
DR Pfam; PF02210; Laminin_G_2; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; Lamg; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS00988; GLA_2; 1.
DR PROSITE; PS00025; Lam_G_DOMAIN; 2.
DR PROSITE; EGF-like domain; Signal.
FT SIGNAL; <1 15 Potential.

```

```

FT CHAIN 16 650 protein S.
FT NON TER 1 1
SQ SEQUENCE 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;
Query Match 41.3%; Score 1516; DB 2; Length 650;
Best Local Similarity 44.4%; Pred. No. 2.2e-99;
Matches 291; Conservative 127; Mismatches 210; Indels 28; Gaps 14;
QY 33 LPAREATQFLPRPRRRAPOVFEKAKOGLERECVEELCSREAREVENDPETYPRY 92
DB 1 LSPKQASQVL-VRRRRANSLLEETKQNLRECEELCNKEAREVENDPETYPRY 59
QY 93 LDCINKY-----GSPYTKNS--GFATCVQNLPGCTPNPCDRGTQACODLMNPFCLC 144
DB 60 LVCLRSQTGLFPAARSTAYPRRLRCVNAIPQCCPLPCNENGYNSCKGKXSFCTTC 119
QY 145 KAGWGRGLCDKDVNEC---SQENGCLOICHNKGSPHSCSGFELSDPRTCODIDEC 201
DB 120 KPGWQGEKCEFDINECKDPNINNGCSQICDNTPGSYHSCGKNGVLMNSKCKDCKVDEC 179
QY 202 A-DSEAGGEARCKRLPGSYSCLDDEGFAYSQEKACDVDECLGRCEQCVNSPGSYTC 260
DB 180 SLRPSICGTAVCKNIIIDFECBCEGGRYVNLKSKSCEDIDECSENMCAQLCVNYPGGHTC 239
QY 261 HCDGRGGLKLSQMDTCEDILPCVPSVSAKSVSLYGNMFSGTPVRLRPFKRLQPTRLV 320
DB 240 YCDGKGFKLADQOKSCVSVCLPLNLTRELYLAEQAGV-VLYLFRLEPSRFS 298
QY 321 AEPDFRTPEEGILLFAGGHQDSTWIVLALRAGRLLEQLRYNGVGRVTSNGPVINHGMQ 380
DB 299 AEPDFRTYDEGVILVASTYHSAMILLARGKIEIQLKNEHTSKITGGDVYINNGLM 358
QY 381 TIVSEELARLVLYKNRDAMKIAVAGDLFQPERGLYHMLTVGCIPIH-EKDLVQPIH 439
DB 359 MVSVEELHSHSISIKIAKAAVMDINKPGPLFKPPNGLETXYVPAEPKYESELIKIPN 418
QY 440 RLDCGKRSWNLNGEDTTIOETVKVNTRMQCFSTVTRSGSPGFAFSLDVMKRPILDV 499
DB 419 RLDCGKRSWNLNGEDTTIOETVKVNTRMQCFSTVTRSGSPGFAFSLDVMKRPILDV 474
QY 500 GTESTVEVEVAHIRPADTGVLALMAPDLRAVPLVALVDYHSTKLLKKQLVLAVER 559
DB 475 SSAEGWHVNTLTNIRSTGTGVMALVSGN-NTPRAVSLVD--STSE-KSQDILLSVEN 530
QY 560 TAL-ALMEIKVC-DGGEHYVTVSLRDEATLEVDTGRGSEVSAALOERLAVLERHRS 617
DB 531 TVYIRIQAALSLCSDQSH--LEFRVNRNMLELSTPLKLETISHEDLQRLAVLDKAMKA 587
QY 618 PVLTFAGGLPDVPVNTAPVTAFFRGCMTELVNRRLLDLDEAAVKHSDITAHSCPV 673
DB 588 KQATYLGGLPDVPFSATPVNAFYNGCMENVINGVLDLDEAISKNDIRAHSCPSV 643

```

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RESULT 14
ID Q9NSD0 HUMAN PRELIMINARY; PRT; 650 AA.
AC Q9NSD0;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Protein S precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
RA Dahlback B.;
RL Submitted (FEB-1992) to the EMBL/Genbank/DDJ databases.
CC -----

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CC EMBL: X12892; CAA31383.1; -, mRNA.
 CC HSSP: P00740; 1CFH.
 DR SMR: Q9NSD0; 174-260.
 DR Ensembl: ENSG00000184500; Homo sapiens.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR013320; Cona_like_subgrp.
 DR InterPro: IPR006210; EGF_3.
 DR InterPro: IPR000742; EGF_3.
 DR InterPro: IPR001881; EGF_Ca_bd.
 DR InterPro: IPR013091; EGF_Ca_bd_2.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR013032; EGF_like_reg.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR012679; Laminin_G_1.
 DR InterPro: IPR012680; Laminin_G_2.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF07645; EGF_CA_1.
 DR Pfam: PF00594; GLA_1.
 DR Pfam: PF00054; Laminin_G_1_1.
 DR Pfam: PF02210; Laminin_G_2_1.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF_4.
 DR SMART: SM00179; EGF_CA_3.
 DR SMART: SM00069; GLA_1.
 DR SMART: SM00282; LamG_2.
 DR PROSITE: PS00010; ASX_HYDROXYL_3.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00186; EGF_2; 3.
 DR PROSITE: PS00026; EGF_3; 4.
 DR PROSITE: PS01187; EGF_CA_2.
 DR PROSITE: PS00011; GLA_1; UNKNOWN_1.
 DR PROSITE: PS00998; GLA_2; 1.
 DR PROSITE: PS00025; Lam_G_DOMAIN; 2.
 DR Signal.
 FT SIGNAL.
 FT CHAIN 1..15 Potential.
 FT CHAIN 16..650 Potential.
 SQ SEQUENCE 650 AA; 72480 MW; C673455CEB645174 CRC64;

Query Match 41.2%; Score 1514; DB 2; Length 650;
 Best Local Similarity 44.4%; Pred. No. 3.1e-99;
 Matches 290; Conservative 127; Mismatches 208; Indels 28; Gaps 14;

QY 36 REATQPLRRORARAFVFEFEAKOCHLERECVELCSREERARVFEENDPEVDYPPRYLDC 95
 DB 4 QQAQSVL-VRKRANSLLEETTKGNLERECIEELCNKEERAEVFEENDPEVDYPPRYLVC 62
 QY 96 INKY-----GSPYTGNS--GFATCVQNLPDQCTPNPDRKGYQACODLMGNFFCLCKAG 147
 DB 63 IASFOGTLTAARQSTNAYPDLRSQVNAIPDQSPPLPCHNEDGTMCKDGAATCTCKCKG 122
 QY 148 WGRGLCDKDVNEC---SOENGGLQI CHNKPSSFHCSCHSGFELSSDGRTQDIDECAD-D 203
 DB 123 WGEKEKEPDI NECKDPSNINGGCSQICDNTPGSYHSCCKNGFVWLINXKCKDVIDECSLK 182
 QY 204 SEACGARCKNLPGSISCLCDEGFAYSSQKACRDVDECIQSGCEQVCVNSPSSYTCND 263
 DB 183 PSICGTAVCNKLIGDEPECECPGEGRYNLKSKSCEDIDECENNCADLCVNYPGSHITCYCD 242
 QY 264 GRGGLTSDMDICEPIILPCVPSVAKSVSLYIGRMFSTPYIRLRFKLOPTRLVAEP 323
 DB 243 GKKGKFLAQOKSCSEVSVCLPLNLTXYLVLIAEPAFV-VLYLKRLPRLPSRPSAEF 301
 QY 324 DFRTPDEGLILPAGGHODSTWTLVALRAGRLLEQLRYNGGRVTSAGPVINHGMOCTIS 383
 DB 302 DFRTYSEGVILVAESLYHSAMLLINLRGKIEVQLKNHTSKITTTGGVDINNGLMMVVS 361

QY 384 VEEIARNILIKVRNDVAKVIAVAGDLFQPERGLYHLNLTVGQIPFH-EKDLVQPIINPRD 442
 DB 362 VEELEHSISIKAKAVAWINDIKPGFLFKPENGLETQKYVFAGFPRKVESELKIPINPRD 421
 QY 443 GOMRSWNLWNGEDDTTQETVKVNTMOCFSTYTERGSPFPGSGFAYSLDYKRTPLDVGE 502
 DB 422 GCISRWNLWKQASGSIKEIIQEKMKCLVTYVEKSYYPGSGIAQFHIDYN---NVSA 477
 QY 503 STWEYEVVAHIRPADTGVFLNMAPDRAVPLSVALVDVYSTKGLKKQLVLAVERHAL 562
 DB 478 EGMHVNVLNLRPSIGTGMALNLSGN-NYVPFANSLVD--STSE-KQDILLSVENTYI 533
 QY 563 -ALMEIKVC-DQGEHVTVSLSDGEATLEVDGTRQOSEVSAALQERLAVLERRHSPYL 620
 DB 534 YRIQALSLCSPDQSH---LEFRVNNNLDELSTPLKERTISHEDLQRLAVLIDKAKAKYA 590
 QY 621 TPAGGLPVYPTSAAYVTFYRCQMTLEVNRRLLDDDEAAVYKSDTATSCPEV 673
 DB 591 TYLGGLPVVPFSATPVNAFYNGCMEVNTINGQLDDEAISKNDIRAHSCPSV 643

RESULT 15
 PROS BOVIN STANDARD; PRT; 675 AA.
 AC P07224;
 DT 01-APR-1988, integrated into UniProtKB/Swiss-Prot.
 DT 01-APR-1988, sequence version 1.
 DT 07-MAR-2006, entry version 70.
 DE Vitamin K-dependent protein S precursor.
 GN Name=PROS1; Synonyms=PROS;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxId=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=86233400; PubMed=2940598;
 RA Dahlback B., Lundwall A., Stenflo J.,
 RT "Primary structure of bovine vitamin K-dependent protein S.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4199-4203 (1986).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Wydro R., Cohen E., Dackowski W., Stenflo J., Lundwall A.,
 RA Dahlback B.;
 RP Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP PROTEIN SEQUENCE OF 42-141, HYDROXYLATION SITES ASP-136; ASN-177;
 RP ASN-219 AND ASN-258, CARBOHYDRATE-LINKAGE SITE ASN-499, AND DISULFIDE
 RP BONDS.
 RX MEDLINE=86168236; PubMed=2937785;
 RA Dahlback B., Lundwall A., Stenflo J.,
 RT "Localization of thrombin cleavage sites in the amino-terminal region
 of bovine protein S.";
 RL J. Biol. Chem. 261:5111-5115 (1986).
 CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
 activated protein C in the degradation of coagulation factors Va
 and VIIIa. It helps to prevent coagulation and stimulating
 fibrinolysis.
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: Contains 4 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 Gla (gamma-carboxy-glutamate) domain.
 CC -!- SIMILARITY: Contains 2 laminin G-like domains.

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CC EMBL: M13044; AAA30757.1; -, mRNA.
 CC EMBL: X12891; CAA31382.1; -, mRNA.
 DR PIR: A24759; KXBOB.
 DR HSSP: P00740; 1CFH.
 DR SMR: P07224; 200-285.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:03:41 ; Search time 198 Seconds
(without alignments)
1584.093 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675
Sequence: 1 MAPSLRGPALRRAPQLLL.....AHSCPVEPAADYKDDDDK 686

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3675	100.0	686	ADM40823	Adm40823 Human Gas
2	3628	98.7	678	AAR99414	Aar99414 Human gas
3	3628	98.7	678	Aaw46463	Aaw46463 Human gro
4	3628	98.7	678	AAY29794	Aay29794 Human gro
5	3628	98.7	678	AAV57383	Aay57383 Amino aci
6	3628	98.7	678	Adl83231	Adl83231 Human PRO
7	3628	98.7	678	ADM40825	Adm40825 Human Gas
8	3628	98.7	678	ADM60275	Adm60275 Human gas
9	3628	98.7	678	ADT91779	Adt91779 Human GAS
10	3628	98.7	678	ADV91450	Adv91450 Human gro
11	3628	98.7	678	AE887023	Aee87023 Human che
12	3628	98.7	679	ADD48757	Add48757 Human pro
13	3146	85.6	624	AD067207	Adg67207 Novel hum
14	2955.5	80.4	673	AAW46462	Aaw46462 Murine gr
15	2955.5	80.4	673	AAV29793	Aay29793 Murine gr
16	2955.5	80.4	673	AAB33459	Aab33459 Human PRO
17	2955.5	80.4	673	AAV57382	Aay57382 Amino aci
18	2955.5	80.4	673	AB884840	Abb884840 Human PRO
19	2955.5	80.4	673	AB895446	Abb895446 Human ang
20	2955.5	80.4	673	ADD10337	Add10337 Human sec
21	2955.5	80.4	673	ADD11297	Add11297 Human sec
22	2955.5	80.4	673	ADD37090	Add37090 Human sec
23	2955.5	80.4	673	ADE41298	Ade41298 Human sec

24	2955.5	80.4	673	8	ADH43481	Adh43481 Human PRO
25	2955.5	80.4	673	8	ADK82826	Adk82826 Human PRO
26	2931	79.8	703	8	ABO84420	AbO84420 Mouse can
27	2622	71.3	518	8	ABO84421	AbO84421 Human can
28	1547.5	42.1	676	8	ADP24054	Adp24054 PRO polyP
29	1547.5	42.1	676	8	ADT91805	Adt91805 Human GAS
30	1547.5	42.1	676	9	ADZ14050	Adz14050 Human pro
31	1543	42.0	676	2	AAW46464	Aaw46464 Human pro
32	1543	42.0	676	2	AAV29795	Aay29795 Human pro
33	1543	42.0	676	3	AAV57384	Aay57384 Amino aci
34	1543	42.0	676	7	ADD46140	Add46140 Human pro
35	1543	42.0	676	7	ADE62065	Ad62065 Human pro
36	1532	41.7	650	8	AD017650	Ad017650 Human sof
37	1516	41.3	650	1	AAP81137	Aap81137 Human pro
38	1516	41.3	650	7	ADD48900	Add48900 Human pro
39	1515.5	41.2	676	1	AAP70083	Aap70083 Human rec
40	1511.5	41.1	635	2	AAR72350	Aar72350 Mature hu
41	1510.5	41.1	635	2	AAR31875	Aar31875 Vitamin K
42	1479	40.2	675	1	AAP81136	Aap81136 Bovine Pr
43	1448	39.4	675	7	ADD48898	Add48898 Rat Prote
44	1437.5	39.1	675	2	AAR70728	Aar70728 Human pro
45	1297	35.3	227	9	ADV91465	Adv91465 Human gro

ALIGNMENTS

RESULT 1
ID ADM40823 standard; protein; 686 AA.
XX
AC ADM40823;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human Gas6 protein with a C-terminal epitope tag SEQ ID NO:1.
XX
KW growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
KW receptor internalisation; cell proliferation; cell apoptosis prevention;
KW signaling molecule; cell marker; human.
XX
OS Homo sapiens.
XX
PN W02004029209-A2.
XX
PD 08-APR-2004.
XX
PF 24-SEP-2003; 2003WO-US030330.
XX
PR 24-SEP-2002; 2002US-0413157P.
XX
(GEN2) CENTOCOR INC.
XX
Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
XX
WPI; 2004-316097/29.
XX
New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
PT manufacturing medicines or for identifying inhibitors of Gas6 and its
PT receptors.
XX
PS Claim 2; SEQ ID NO 1; 28pp; English.
XX
XX The present invention describes an isolated growth arrest specific gene 6
XX (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
XX terminus. The epitope tag comprises a flag sequence of 8 amino acids (SEQ
XX ID NO:2, ADM40824), or a polypeptide sequence. The variant Gas6
XX polypeptide has 75% identity to native human Gas6 protein. Also
XX described: (1) a recombinant DNA molecule encoding the amino acid
XX sequence of the polypeptide described above; (2) a vector comprising the
XX above nucleic acid; (3) a host cell comprising the vector, where the host
XX cell is of mammalian origin; and (4) a composition comprising the

CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic activity. The composition is useful for manufacturing medicines or for identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide may also be used for Gas6-dependent receptor phosphorylation, receptor internalisation, cell proliferation, prevention of cell apoptosis, or induction of signalling molecules or cell markers. The present sequence CC represents the human Gas6 protein with an epitope tag fused at the C-terminus, from the present invention.

CC
XX
SQ Sequence 686 AA;

Query Match 100.0%; Score 3675; DB 8; Length 686;
Best Local Similarity 100.0%; Pred. No. 7,1e-248;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAPSISPGPALRRAPOLLILLILAAECALALLPAREATQFLRPRORAFQVFEAKQKH 60
DB 1 MAPSISPGPALRRAPOLLILLILAAECALALLPAREATQFLRPRORAFQVFEAKQKH 60
QY 61 LERECVEELCSRBEAREVEFENDPETDYFPRYLDCINKYSGPYTKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSRBEAREVEFENDPETDYFPRYLDCINKYSGPYTKNSGFATCVQNLPDQC 120
QY 121 TPNPCDRKQTOACQDLMGNFCLCKAGWGRLCDKDVNCSQENGCLQICHNKPSFHC 180
DB 121 TPNPCDRKQTOACQDLMGNFCLCKAGWGRLCDKDVNCSQENGCLQICHNKPSFHC 180
QY 181 SCHSGFEISSDRTCCDIDECADSEAGBARCNLPGSYCLCDEGFAYSSQEKACRDVD 240
DB 181 SCHSGFEISSDRTCCDIDECADSEAGBARCNLPGSYCLCDEGFAYSSQEKACRDVD 240
QY 241 ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
DB 241 ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFPTDPPEGILLFAGGHODSTWIVLALRAGRLQLQR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFPTDPPEGILLFAGGHODSTWIVLALRAGRLQLQR 360
QY 361 YNGVGRVTVSSGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHLN 420
DB 361 YNGVGRVTVSSGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHLN 420
QY 421 LTVGGIPHEKDLVQPINRLDCMNSMMNLNGEDTTIETVKNTRMOCFSYTERGSFY 480
DB 421 LTVGGIPHEKDLVQPINRLDCMNSMMNLNGEDTTIETVKNTRMOCFSYTERGSFY 480
QY 481 PGSGFAFYSIDYMRTPLDVGTESTWEVEVAHIRPAADTGVLFALWAPDLRAVPLSVALV 540
DB 481 PGSGFAFYSIDYMRTPLDVGTESTWEVEVAHIRPAADTGVLFALWAPDLRAVPLSVALV 540
QY 541 DYHSTKTKLKQVYLAVENTALAMEIKYCDGGEHVTVYSLRGEATLEVDGTRGSEFS 600
DB 541 DYHSTKTKLKQVYLAVENTALAMEIKYCDGGEHVTVYSLRGEATLEVDGTRGSEFS 600
QY 601 AAQLOERLAVLEHRLASPVLTFFAGLBDVPVTSAPVTAFFRGCMTEVNRRLDLEEAY 660
DB 601 AAQLOERLAVLEHRLASPVLTFFAGLBDVPVTSAPVTAFFRGCMTEVNRRLDLEEAY 660
QY 661 KHSIDITAHSCPPVEPAADYKDDDK 686
DB 661 KHSIDITAHSCPPVEPAADYKDDDK 686

```

RESULT 2
AAR99414

ID AAR99414 standard; protein; 678 AA.

XX AAR99414;

XX 04-DEC-1996 (first entry)

XX Human gas6 protein, an S protein homologue and axl receptor ligand.

XX Axl receptor ligand; human protein S homologue; growth factor;
KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;
KW recombinant production.

OS Homo sapiens.

PN US538861-A.

PD 23-JUL-1996.

PF 29-JUL-1994; 94US-00282141.

PR 29-JUL-1994; 94US-00282141.

PA (AMGE-) AMGEN INC.

PI (SCHN/) SCHNEIDER C.

PI Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;

DR MPI: 1996-353825/35.

DR N-PSDB; AAT41544.

PT DNA encoding gas6, the axl receptor ligand - useful to regulate growth of

PT myeloid cells and malignancies.

PS Claim 1; Col 19-22; 36pp; English.

CC AAR99414 is the gas6 protein (from the growth arrest specific gene number 6). The gas6 protein has homology to human protein S which functions as a cofactor in a protease cascade that regulates coagulation. Gas6 expression, as with gas1 and gas2, is associated with cell growth arrest which suggests a possible role of gas6 in the regulation of cell growth. In fact the gas6 protein is an axl receptor (axlr) ligand and a growth factor for any cells expressing axlr e.g. bone marrow, spleen, thymus, CC ovary, heart, intestine and lung cells. The axl receptor is involved in CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate CC growth of such cells

SQ Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAPSISPGPALRRAPOLLILLILAAECALALLPAREATQFLRPRORAFQVFEAKQKH 60
DB 1 MAPSISPGPALRRAPOLLILLILAAECALALLPAREATQFLRPRORAFQVFEAKQKH 60
QY 61 LERECVEELCSRBEAREVEFENDPETDYFPRYLDCINKYSGPYTKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSRBEAREVEFENDPETDYFPRYLDCINKYSGPYTKNSGFATCVQNLPDQC 120
QY 121 TPNPCDRKQTOACQDLMGNFCLCKAGWGRLCDKDVNCSQENGCLQICHNKPSFHC 180
DB 121 TPNPCDRKQTOACQDLMGNFCLCKAGWGRLCDKDVNCSQENGCLQICHNKPSFHC 180
QY 181 SCHSGFEISSDRTCCDIDECADSEAGBARCNLPGSYCLCDEGFAYSSQEKACRDVD 240
DB 181 SCHSGFEISSDRTCCDIDECADSEAGBARCNLPGSYCLCDEGFAYSSQEKACRDVD 240
QY 241 ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
DB 241 ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEFDFPTDPPEGILLFAGGHODSTWIVLALRAGRLQLQR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFPTDPPEGILLFAGGHODSTWIVLALRAGRLQLQR 360
QY 361 YNGVGRVTVSSGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHLN 420
DB 361 YNGVGRVTVSSGPVINGMMQTTISVEELARNLVTKNRDAVMKIAVAGDLFQPERGLYHLN 420

```

QY 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480
 DB 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480
 QY 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVALV 540
 DB 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVALV 540
 QY 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600
 DB 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600
 QY 601 AAQLOERLAVLERHLSRSPVLTFAGGLPDVPTSAFVTAFFRGCMTELVNRRLLDLDEAY 660
 DB 601 AAQLOERLAVLERHLSRSPVLTFAGGLPDVPTSAFVTAFFRGCMTELVNRRLLDLDEAY 660
 QY 661 KHSIDTAHSCPPVEPAAA 678
 DB 661 KHSIDTAHSCPPVEPAAA 678

RESULT 3

AAW46463 ID AAW46463 standard; protein; 678 AA.

AAW46463 AC

DT 15-MAY-1998 (first entry)

DE Human growth arrest specific-gene 6 (gas6) protein.

KM Growth arrest specific-gene 6; gas6; Raa; Axl; receptor; mitogenic agent;

KM receptor tyrosine kinase; regulation; protease cascade; insulin;

KM growth regulation; serum-free culture medium; human; Schwann cell;

KM receptor activator; erbB receptor; heregulin; cAMP level; proliferation;

KM treatment; nervous system injury.

OS Homo sapiens.

XX

FT Key

FT Domain

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PS Disclosure; Fig 2; 51pp; English.
 XX
 CC The present sequence represents a human growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Raa and Axl receptor. Rse is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 SQ Sequence 678 AA:
 Query Match 98.7%; Score 3628; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1,3e-244; Mismatches 0; Gaps 0;
 Matches 678; Conservative 0; Indels 0; Gaps 0;
 QY 1 MAPSLSPGPAALRRAPOLLILLILAECALALPAREATOPLRPRORAPQVFEAKQGH 60
 DB 1 MAPSLSPGPAALRRAPOLLILLILAECALALPAREATOPLRPRORAPQVFEAKQGH 60
 QY 61 LERECVELCSREBARFVFNDEPTDYFYPRIYDICKINRGSPYTKNSGFATCVQNLDPQC 120
 DB 61 LERECVELCSREBARFVFNDEPTDYFYPRIYDICKINRGSPYTKNSGFATCVQNLDPQC 120
 QY 121 TPNPCKKQKQOACODLNGNFCCLCKAGWGRCLDKVNECSQENGGCLQICHNKGSGFHC 180
 DB 121 TPNPCKKQKQOACODLNGNFCCLCKAGWGRCLDKVNECSQENGGCLQICHNKGSGFHC 180
 QY 121 TPAPCDKKGQOACODLNGNFCCLCKAGWGRCLDKVNECSQENGGCLQICHNKGSGFHC 180
 DB 121 TPAPCDKKGQOACODLNGNFCCLCKAGWGRCLDKVNECSQENGGCLQICHNKGSGFHC 180
 QY 181 SCHSGFELSSDGRTCODIDECADSEACGAEKCKNLPSYSCLCEGFAYSQEKACDVPD 240
 DB 181 SCHSGFELSSDGRTCODIDECADSEACGAEKCKNLPSYSCLCEGFAYSQEKACDVPD 240
 QY 241 ECLQGRCEQVCNPSGYSYCHDGRGGLKLSQMDTCEDILLPCVPFSAKSVKSLYGRM 300
 DB 241 ECLQGRCEQVCNPSGYSYCHDGRGGLKLSQMDTCEDILLPCVPFSAKSVKSLYGRM 300
 QY 301 FSGTPVRLRLFKKLOPRRLVAEFPFRFDEBGLILFAGGHQDSWTIVLALRAGRLEQLR 360
 DB 301 FSGTPVRLRLFKKLOPRRLVAEFPFRFDEBGLILFAGGHQDSWTIVLALRAGRLEQLR 360
 QY 361 YNGVGRVTSQGVINHGMMOTISVEELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420
 DB 361 YNGVGRVTSQGVINHGMMOTISVEELARLVKVRDAVMKIAVAGDLFQPERGLYHLN 420
 QY 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480
 DB 421 LTVGIPFHEKDLVOPINRLDGCMSWMNLNGEDTTIOETVKVNTRMQCFSTYERGSFY 480
 QY 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVALV 540
 DB 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVALV 540
 QY 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600
 DB 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVVVSLRDGEATLEVDGTGQSEVS 600
 QY 601 AAQLOERLAVLERHLSRSPVLTFAGGLPDVPTSAFVTAFFRGCMTELVNRRLLDLDEAY 660
 DB 601 AAQLOERLAVLERHLSRSPVLTFAGGLPDVPTSAFVTAFFRGCMTELVNRRLLDLDEAY 660
 QY 661 KHSIDTAHSCPPVEPAAA 678
 DB 661 KHSIDTAHSCPPVEPAAA 678

RESULT 4

FT Domain

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AAV29794
 ID AAV29794 standard; protein; 678 AA.
 XX
 AC AAV29794;
 XX
 DT 15-NOV-1999 (first entry)
 XX
 DE Human growth arrest-specific gene 6 protein.
 XX
 KM Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;
 KM growth arrest-specific gene 6; proliferation; differentiation;
 KM gli1 cell; Schwann cell; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PM US5955420-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 10-MAY-1995; 95US-00438864.
 XX
 PR 10-MAR-1995; 95US-00402253.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
 XX WPI; 1999-539585/45.
 DR
 XX
 XX Activation of the Rse receptor on a cell, useful for promoting cell
 PT proliferation and differentiation.
 XX
 PS Disclosure; Fig 2; 48pp; English.
 XX
 CC A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents human gas6 given in the present invention
 XX
 SQ Sequence 678 AA;
 Query Match 98.7%; Score 3628; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPSLSPGPAALRRAPQILLILAAACALALPAREATQFLPRRQRAQVREAKQGH 60
 DB 1 MAPSLSPGPAALRRAPQILLILAAACALALPAREATQFLPRRQRAQVREAKQGH 60
 QY 61 LERECEVEELCSREAREVEFENDEPETYFYPRYLDCINKKSPYTKNSGFATCVQNLPDQC 120
 DB 61 LERECEVEELCSREAREVEFENDEPETYFYPRYLDCINKKSPYTKNSGFATCVQNLPDQC 120
 QY 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
 DB 121 TPNPCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
 QY 181 SCHSGEELSSDGTCCDIDECADSEACGEARKCNLPFSYCLDEGFAYSSQEKACRDV 240
 DB 181 SCHSGEELSSDGTCCDIDECADSEACGEARKCNLPFSYCLDEGFAYSSQEKACRDV 240
 QY 241 ECLQGCCEQVCNVPSTYCHCGRGGLKLSQDMDCEDLLPCVPSVAKSVSLEYGRM 300
 DB 241 ECLQGCCEQVCNVPSTYCHCGRGGLKLSQDMDCEDLLPCVPSVAKSVSLEYGRM 300
 QY 301 FSGTPYIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSITWVLAIRAGRLLEQLR 360
 DB 301 FSGTPYIRLRFKRLQPTRLVAEPDFRTFDEGILLFAGHQDSITWVLAIRAGRLLEQLR 360
 QY 361 YNGVGVTSSGPIYINNGMOTISVEELARNLVKVRNDAMVKIAVAGDLFQPERGLYHLN 420
 DB 361 YNGVGVTSSGPIYINNGMOTISVEELARNLVKVRNDAMVKIAVAGDLFQPERGLYHLN 420

QY 421 LTVGGIPFHEKDLVQPINRDLGCMRSNMNLNGEDTTIOETVKVNTRMQCFSTVERGSFY 480
 DB 421 LTVGGIPFHEKDLVQPINRDLGCMRSNMNLNGEDTTIOETVKVNTRMQCFSTVERGSFY 480
 QY 481 PGSGFAFYSLDWARTPLDVGETSTWEVEVAHIRPADTGVLPALMAPDLRAVPLSLVA 540
 DB 481 PGSGFAFYSLDWARTPLDVGETSTWEVEVAHIRPADTGVLPALMAPDLRAVPLSLVA 540
 QY 541 DYHSTRKKLKKOLVLAVENTALAMEIKVCDQOEHVTVSLRDGEATLEVDGTRGSEVS 600
 DB 541 DYHSTRKKLKKOLVLAVENTALAMEIKVCDQOEHVTVSLRDGEATLEVDGTRGSEVS 600
 QY 601 AAQLOERLAVLBRHLRSPVLTFRAGGLPDVPTSPAPYATFYRCGMLTEVNRLLDDEAY 660
 DB 601 AAQLOERLAVLBRHLRSPVLTFRAGGLPDVPTSPAPYATFYRCGMLTEVNRLLDDEAY 660
 QY 661 KHSIDITANSCPVEPAAA 678
 DB 661 KHSIDITANSCPVEPAAA 678
 RESULT 5
 ID AAV57383 standard; protein; 678 AA.
 XX
 AC AAV57383;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 XX Amino acid sequence of human gas6 (h gas6) protein.
 DE
 XX Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
 KM central nervous system; peripheral nervous system; injury; trauma;
 KM nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 XX protein S.
 XX
 OS Homo sapiens.
 XX
 PN US6033660-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 10-MAY-1995; 95US-00438862.
 XX
 PR 10-MAY-1995; 95US-00438862.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Mather JP, Chen J, Li R;
 XX
 DR WPI; 2000-246046/21.
 XX
 PT Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.
 XX
 PS Disclosure; Fig 2; 52pp; English.
 XX
 CC The invention relates to a method for treating nervous system injuries in
 CC mammals by administering human Schwann cells (SC) that have been cultured
 CC in serum-free medium. The serum-free medium is a nutrient solution
 CC supplemented with two mitogens, one of which, is a Res/Axl receptor
 CC activator, to increase survival and proliferation of SC. The method is
 CC used to treat (or prevent) central or peripheral nervous system injury,
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
 CC or lesions associated with nutritional deficiencies, systemic disease,
 CC toxins or demyelination. Culturing cells in the specified medium allows
 CC proliferation of adult SC for use in autologous transplants. The present
 CC sequence represents a human gas6 (h gas6) protein, having 44% sequence
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
 CC survival factor for SCs in defined serum-free culture

Sequence 678 AA:
Query Match 98.7%; Score 3628; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPSLSPGPAALRRAPQQLLLLLAECALALPAREATQFLPRORAFQVFEAKQGH 60
DB 1 MAPSLSPGPAALRRAPQQLLLLLAECALALPAREATQFLPRORAFQVFEAKQGH 60
QY 61 LERECVEELCSREAREVEFENDPETYFPRYLDICINKGSPYTKSGFATCVQNLDPQC 120
DB 61 LERECVEELCSREAREVEFENDPETYFPRYLDICINKGSPYTKSGFATCVQNLDPQC 120
QY 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
DB 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
QY 181 SCHSGFELSSDGTCCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240
DB 181 SCHSGFELSSDGTCCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240
QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVSLYGRM 300
DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVSLYGRM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEPDFTFDEGILLFAGGHODSTWIVLALRAGRLQLR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEPDFTFDEGILLFAGGHODSTWIVLALRAGRLQLR 360
QY 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKVRNDAVMKLAIVAGDLFOBERGLYHNL 420
DB 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKVRNDAVMKLAIVAGDLFOBERGLYHNL 420
QY 421 LTVGGIPFHEKDLVQPINPRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480
DB 421 LTVGGIPFHEKDLVQPINPRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480
QY 481 PGGGFAFYSLDVNRTPLDVNTSESTWEVVAHTRPADTGVLPALAMPDLRAVPLSALV 540
DB 481 PGGGFAFYSLDVNRTPLDVNTSESTWEVVAHTRPADTGVLPALAMPDLRAVPLSALV 540
QY 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVTVSLRQGEATLEVDGTRGQSEVS 600
DB 541 DYHSTKKLKKQLVLAVENTALALMEIKVCDGQEHVTVSLRQGEATLEVDGTRGQSEVS 600
QY 601 AAOLOERLAVLEHRLSPVLTPFAGGLPDVPTSAVTAIFYRGCMTELEVNRLDLDEAAY 660
DB 601 AAOLOERLAVLEHRLSPVLTPFAGGLPDVPTSAVTAIFYRGCMTELEVNRLDLDEAAY 660
QY 661 KHSDDTAHSCRPVEPAA 678
DB 661 KHSDDTAHSCRPVEPAA 678
RESULT 6
ADL83231
ID ADL83231 standard; protein; 678 AA.
AC ADL83231;
XX 17-JUN-2004 (first entry)
DE Human PRO12613, SEQ ID 433.
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW Immune-mediated inflammatory disease; human.
OS Homo sapiens.
XX
XX WO2004024097-A2.

XX 25-MAR-2004.
PD 15-SEP-2003; 2003WO-US029097.
XX 16-SEP-2002; 2002US-0411392P.
PR (GENTH) GENENTECH INC.
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,
PI Wu TJ;
XX WPI; 2004-329389/30.
DR N-PSDB; ADL83230.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
PS Claim 10; Fig 433; 695dp; English.
XX
XX The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypereosinophilia, rheumatoid arthritis, autoimmune mediated hemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 678 AA:
Query Match 98.7%; Score 3628; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPSLSPGPAALRRAPQQLLLLLAECALALPAREATQFLPRORAFQVFEAKQGH 60
DB 1 MAPSLSPGPAALRRAPQQLLLLLAECALALPAREATQFLPRORAFQVFEAKQGH 60
QY 61 LERECVEELCSREAREVEFENDPETYFPRYLDICINKGSPYTKSGFATCVQNLDPQC 120
DB 61 LERECVEELCSREAREVEFENDPETYFPRYLDICINKGSPYTKSGFATCVQNLDPQC 120
QY 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
DB 121 TPNPCDRKGTQACODLMGNFPCICKAGMGRLCDKDVNECSQENGGCLQICHNKPSPFHC 180
QY 181 SCHSGFELSSDGTCCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240
DB 181 SCHSGFELSSDGTCCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQEKACRDVD 240
QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVSLYGRM 300
DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVSLYGRM 300
QY 301 FSGTPVIRLRFKRLQPTRLVAEPDFTFDEGILLFAGGHODSTWIVLALRAGRLQLR 360
DB 301 FSGTPVIRLRFKRLQPTRLVAEPDFTFDEGILLFAGGHODSTWIVLALRAGRLQLR 360
QY 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKVRNDAVMKLAIVAGDLFOBERGLYHNL 420
DB 361 YNGVGRVTSGGPIVINGMOTISVEELARNLVIKVRNDAVMKLAIVAGDLFOBERGLYHNL 420
QY 421 LTVGGIPFHEKDLVQPINPRLDGCMSNMWLNGBEDTTIGETVKNVTRMOCFSYTERGSFY 480

DB 421 LTVGGIPFHEKDLVQPINRDLGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480
QY 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540
DB 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540
QY 541 DYHSTKCLKKQVLVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
DB 541 DYHSTKCLKKQVLVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
QY 601 AAQLOERLAVLERHLRSPVLTFAAGLPDVPTVSAPVTAFYRGCMTELVNRLLIDDEAY 660
DB 601 AAQLOERLAVLERHLRSPVLTFAAGLPDVPTVSAPVTAFYRGCMTELVNRLLIDDEAY 660
QY 661 KHSDDITAHSCPVEPEPAA 678
DB 661 KHSDDITAHSCPVEPEPAA 678

RESULT 7

ID ADM40825 standard; protein; 678 AA.

AC ADM40825;

DT 01-JUL-2004 (first entry)

DE Human Gas6 protein SEQ ID NO:3.

KW growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;

KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;

KW receptor internalisation; cell proliferation; cell apoptosis prevention;

KW signaling molecule; cell marker; human.

OS Homo sapiens.

PN WO2004029209-A2.

PD 08-APR-2004.

PF 24-SEP-2003; 2003WO-US030330.

PR 24-SEP-2002; 2002US-0413157P.

PA (CENZ) CENTOCOR INC.

PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;

DR WPI; 2004-316097/29.

PT New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for

PT manufacturing medicines or for identifying inhibitors of Gas6 and its

PT receptors.

PS Disclosure; SEQ ID NO 3; 28pp; English.

XX

XX

CC

CC

CC

CC

CC

CC

XX SQ Sequence 678 AA;
Query Match 98.7%; Score 3628; DB 8; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPSLSPGPAALRRAPOLLILLALLAEACALAAALPAREATQFLRRPRRRAQVFEAKQKH 60
DB 1 MAPSLSPGPAALRRAPOLLILLALLAEACALAAALPAREATQFLRRPRRRAQVFEAKQKH 60
QY 61 IERECVEELCSREAREVFEENDPETDYPRYLDCINKYSGPYTNGSGPATCVQNI.PDOC 120
DB 61 IERECVEELCSREAREVFEENDPETDYPRYLDCINKYSGPYTNGSGPATCVQNI.PDOC 120
QY 121 TPNPCDRRGTOACQOLMGNFCLCKAGNGGRICDDVNECSQENGGCLOICNKGSGPFC 180
DB 121 TPNPCDRRGTOACQOLMGNFCLCKAGNGGRICDDVNECSQENGGCLOICNKGSGPFC 180
QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDBGFAYSQEKACRDVD 240
DB 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDBGFAYSQEKACRDVD 240
QY 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPPSVAKSVKSLYLGM 300
DB 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMOTCEDILPCVPPSVAKSVKSLYLGM 300
QY 301 FSGTPVIRLRFRKLOPTRLVAEFDRTPDPEGILLPAGGHODSTWIVLALRAGRLELQLR 360
DB 301 FSGTPVIRLRFRKLOPTRLVAEFDRTPDPEGILLPAGGHODSTWIVLALRAGRLELQLR 360
QY 361 YNGVGRVTSQSGPVINHGMMQTISVEELANLVIKNRRDAVMKIAVAGDLFOBERGLYHUN 420
DB 361 YNGVGRVTSQSGPVINHGMMQTISVEELANLVIKNRRDAVMKIAVAGDLFOBERGLYHUN 420
QY 421 LTVGGIPFHEKDLVQPINRDLGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480
DB 421 LTVGGIPFHEKDLVQPINRDLGCKRSMWMLNGEDTTIOETVKVNTRMQCFSTERGSPY 480
QY 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540
DB 481 PGSGFAFSLDYMRPLDVGTSTWEEVVAHIRPADTGVLPALMAPDLRAVPLSVLV 540
QY 541 DYHSTKCLKKQVLVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
DB 541 DYHSTKCLKKQVLVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
QY 601 AAQLOERLAVLERHLRSPVLTFAAGLPDVPTVSAPVTAFYRGCMTELVNRLLIDDEAY 660
DB 601 AAQLOERLAVLERHLRSPVLTFAAGLPDVPTVSAPVTAFYRGCMTELVNRLLIDDEAY 660
QY 661 KHSDDITAHSCPVEPEPAA 678
DB 661 KHSDDITAHSCPVEPEPAA 678

RESULT 8

ID ADN60275 standard; protein; 678 AA.

AC ADN60275;

DT 18-NOV-2004 (first entry)

DE Human growth arrest-specific 6 (GAS6) protein.

KW angiogenesis modulator; tumorigenesis modulator; angiogenesis; Ax1;

KW tubulin cofactor D; transglutaminase 2; cytosine deaminase;

KW peptidase M41; paraplegin; CD13 aminopeptidase; PK-1; zip kinase; Gas6;

KW Srm160; non-muscle myosin heavy chain; calmodulin 2; symporter;

KW semaphorin; zinc finger helixcase; plexin-A2; deoxycytidylate deaminase;

KW sugar transporter; tumorigenesis; antiangiogenic; cytoskeletal;

KW cerebroprotective; vasotropic; antiinfectility; cardiac;

KM antibody therapy; antisense therapy; RNA interference therapy;
 XX RNAi therapy; cancer; stroke; infertility; heart disease; human.
 OS Homo sapiens.
 XX
 PN WO2004039955-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 29-OCT-2003; 2003WO-US034281.
 XX
 PR 29-OCT-2002; 2002US-0421989P.
 PR 17-OCT-2003; 2003US-0512251P.
 XX
 PA (RIGE-) RIGEL PHARM INC.
 XX
 PI Lorens JB, Atchison RE, Friera A, Holland S;
 XX
 DR WPI; 2004-376181/35.
 DR N-PSDB; ADN60274.
 XX
 PT Identifying a compound that modulates angiogenesis or tumorigenesis,
 PT useful in diagnosing and treating angiogenesis, cancer, stroke,
 PT infertility and heart disease, comprises contacting the compound with
 PT angiogenesis polypeptide.
 XX
 PS Disclosure; Page 65; 105pp; English.
 XX
 CC The present invention describes a method for identifying a compound that
 CC modulates angiogenesis or tumorigenesis. The method comprises: (a)
 CC contacting the compound with angiogenesis polypeptide, e.g. Ax1, tubulin
 CC cofactor D, transglutaminase 2, cytosine deaminase, peptidase M41
 CC (paraplegin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, Srm160, non-
 CC muscle myosin heavy chain, calmodulin 2, novel symporter, novel
 CC semaphorin, novel zinc finger helixase (FLJ22611), plexin-A2,
 CC deoxycytidylate deaminase or novel sugar transporter; (b) determining the
 CC functional effector of the compound upon the angiogenesis polypeptide or
 CC the physical effect of the compound upon the target polypeptide or its
 CC fragment or inactive variant; and (c) determining the chemical or
 CC phenotypic effect of the compound upon a cell comprising the target
 CC polypeptide or its fragment or inactive variant, thus identifying a
 CC compound that modulates cell cycle arrest. Also described is a method of
 CC modulating angiogenesis in a subject. The angiogenesis or tumorigenesis
 CC modulating compound has antiangiogenic, cytostatic, cerebroprotective,
 CC vasoregic, antifertility and cardiac activities, and can be used in
 CC antibody, antisense and RNA interference (RNAi) therapies. The method is
 CC useful in identifying a compound that modulates angiogenesis. The methods
 CC and compounds or compositions are useful in diagnosing and treating
 CC angiogenesis, cancer, stroke, infertility and heart disease. The present
 CC sequence represents a human growth arrest-specific 6 (GAS6) protein,
 CC which is used in the exemplification of the present invention.
 XX
 XX Sequence 678 AA:
 XX
 Query Match 98.7%; Score 3628; DB 8; Length 678;
 Best Local Similarity 100.0%; Pred. No. 1.3e-244;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 ECLQRCGEYCVNNSPGSYTCHCDGRGGLKLSQDMDCEDLLPCVPFSVAKSVKSLYLGRM 300
 DB 241 ECLQRCGEYCVNNSPGSYTCHCDGRGGLKLSQDMDCEDLLPCVPFSVAKSVKSLYLGRM 300
 QY 301 FSGTPIVRLRFKRLQPTRLVAEFDFTFDEBGLLFAAGHQDSTWIVLALRAGLELQLR 360
 DB 301 FSGTPIVRLRFKRLQPTRLVAEFDFTFDEBGLLFAAGHQDSTWIVLALRAGLELQLR 360
 QY 361 YNGVGRYTSVSGPVYINHGMOQTISVEELARLVLKVRNDAMKIAVAADLFOPEBGLYHLN 420
 DB 361 YNGVGRYTSVSGPVYINHGMOQTISVEELARLVLKVRNDAMKIAVAADLFOPEBGLYHLN 420
 QY 421 LTVGGIPEFHEKDLVQPINPRLDGMRSNNLNGEDTTIOETVKNTMOCPSYTERGSFY 480
 DB 421 LTVGGIPEFHEKDLVQPINPRLDGMRSNNLNGEDTTIOETVKNTMOCPSYTERGSFY 480
 QY 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPAADTVLPALMAPDLRAVPLSVLV 540
 DB 481 PGSGFAFYSLDYKRTPLDVGTSTWEEVVAHIRPAADTVLPALMAPDLRAVPLSVLV 540
 QY 541 DYHSTKKLKKQVLVLAVERHALMEIKVCDGGEHVTVSLRDGEATLEVDTRGQSEVS 600
 DB 541 DYHSTKKLKKQVLVLAVERHALMEIKVCDGGEHVTVSLRDGEATLEVDTRGQSEVS 600
 QY 601 AAQLOERLAVLERHLSPLVTFAGGLPDVPTSAVPVAFYRGCMTLEVNRLLDLDEAAV 660
 DB 601 AAQLOERLAVLERHLSPLVTFAGGLPDVPTSAVPVAFYRGCMTLEVNRLLDLDEAAV 660
 QY 661 KHSIDITAHSCPPVEPAAA 678
 DB 661 KHSIDITAHSCPPVEPAAA 678

RESULT 9
 ID ADT91779
 ID ADT91779 standard; protein; 678 AA.

AC ADT91779;
 DT 13-JAN-2005 (first entry)
 XX
 DE Human GAS6 polypeptide #1.
 XX
 KM Human; GAS6; osteoarthritis; OA; receptor tyrosine kinase; antiarthritic;
 KM osteopathic.
 OS Homo sapiens.
 OS
 PN WO2004092735-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 16-APR-2004; 2004WO-EP004052.
 XX
 PR 18-APR-2003; 2003US-0463935P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PI Daouti S, Kumar CS, Latario BJ;
 XX
 DR WPI; 2004-758393/74.
 DR N-PSDB; ADT91780.
 XX
 PT Identifying a compound for treating osteoarthritis (OA) comprises
 PT contacting a test compound to a reaction mixture that comprises a
 PT polypeptide member of the TYRO3 subfamily of receptor tyrosine kinases
 PT and a ligand to the polypeptide.
 XX
 PS Claim 6; SEQ ID NO 3; 101pp; English.
 PS
 CC The invention relates to a method of identifying a compound for treating

osteoarthritis (OA) comprising contacting a test compound to a reaction mixture that comprises a polypeptide member of the TNF3 subfamily of receptor tyrosine kinases and a ligand to the polypeptide, where the reaction mixture conditions permit binding of the polypeptide to the ligand to form a binding complex, detecting levels of formation of the binding complex in the reaction mixture in the presence of the test compound, and comparing the level of the binding complex formed in the presence of the test compound to the level of binding complex formed in the absence of the test compound, where a decrease in the level of the binding complex formed in the presence of the test compound indicates that the test compound may be used to treat OA. The invention also relates to a method for treating, preventing or ameliorating OA and a method of identifying an individual having OA, comprising detecting a TNF3 polypeptide in a biological sample derived from the individual and comparing the level of the TNF3 polypeptide in the individual to levels of the TNF3 polypeptide in individuals not having OA, where elevated levels of the TNF3 polypeptide in the biological sample derived from the individual indicates that the individual has OA. The method is useful for the development of drugs for treating osteoarthritis. This sequence represents a human Gas6 polypeptide of the invention.

Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 8; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.3e-244; Indels 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60
1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60
61 LERECVEELCSREAREVFNDEPDTYFPRYIDCINKGSPYTKNSGATCQNLPDCC 120
61 LERECVEELCSREAREVFNDEPDTYFPRYIDCINKGSPYTKNSGATCQNLPDCC 120
121 TNPDCDRKGTQACODLMGNFCLCKRAGMGARLCKDVNCSQENGCLOICNNKPSGFC 180
121 TNPDCDRKGTQACODLMGNFCLCKRAGMGARLCKDVNCSQENGCLOICNNKPSGFC 180
181 SCHSGFELSSDRTCODIDECADSEAGGARCKNLPGSYSCLDCBFAVSSQOKACRDV 240
181 SCHSGFELSSDRTCODIDECADSEAGGARCKNLPGSYSCLDCBFAVSSQOKACRDV 240
181 SCHSGFELSSDRTCODIDECADSEAGGARCKNLPGSYSCLDCBFAVSSQOKACRDV 240
241 ECLQRCCEVCNPSSTYCHCDGRGLTSDMDTCBILPCVPSVAKSVSLYLGM 300
241 ECLQRCCEVCNPSSTYCHCDGRGLTSDMDTCBILPCVPSVAKSVSLYLGM 300
241 ECLQRCCEVCNPSSTYCHCDGRGLTSDMDTCBILPCVPSVAKSVSLYLGM 300
301 FSGTPYIRLRFKRLQPTRLVAEFDFTPEGILLFAGGHODSTWIVLALRAGRLQLR 360
301 FSGTPYIRLRFKRLQPTRLVAEFDFTPEGILLFAGGHODSTWIVLALRAGRLQLR 360
301 FSGTPYIRLRFKRLQPTRLVAEFDFTPEGILLFAGGHODSTWIVLALRAGRLQLR 360
361 YNGVGVTSSGPAVINHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGILYHN 420
361 YNGVGVTSSGPAVINHGMQTTISVEELARNLVIKVRDAVMKIAVAGDLFQPERGILYHN 420
421 LTVGGIPRFEKQIVQINPRLDCMSNMNLNEDDTTIOETVNVNRMOCSTERSGF 480
421 LTVGGIPRFEKQIVQINPRLDCMSNMNLNEDDTTIOETVNVNRMOCSTERSGF 480
481 PGSGFAFYSLDVMRTPLDVGTSTWEVVAHTRPADTGVLPALNAPDLRAVPLSVALV 540
481 PGSGFAFYSLDVMRTPLDVGTSTWEVVAHTRPADTGVLPALNAPDLRAVPLSVALV 540
541 DYHSTYKLLKKQVLVAERTALAMEIKVCDGGEHVVTSLRGEATLEVDGTRGSGSEVS 600
541 DYHSTYKLLKKQVLVAERTALAMEIKVCDGGEHVVTSLRGEATLEVDGTRGSGSEVS 600
601 AAOLORLAVLEBHLASPVLTFAAGLPDVVTSAPTAFAFGCMTELVNRLDLDEAAY 660
601 AAOLORLAVLEBHLASPVLTFAAGLPDVVTSAPTAFAFGCMTELVNRLDLDEAAY 660
661 KHSIDTAHSCPVEPAAA 678
661 KHSIDTAHSCPVEPAAA 678

DB 661 KHSIDTAHSCPVEPAAA 678

RESULT 10

ADV91450 standard; protein; 678 AA.

ADV91450;

10-MAR-2005 (first entry)

Human growth arrest specific gene 6 (Gas6) polypeptide.

Growth arrest specific gene 6; Gas6; cardiovascular disease; cancer; atherosclerosis; sepsis; glomerulosclerosis; diabetes; rheumatoid arthritis; HIV infection; osteoarthritis; osteoporosis; multiple sclerosis; cardiovascular-gen.; antineutritic; antiarthritic; anti-HIV; cytostatic; neuroprotective; thrombolytic; cardiac; cerebroprotective; vasotropic; antiarteriosclerotic; antibacterial; immunosuppressive; nephrotropic; antidiabetic; osteopathic; antibody production.

Homo sapiens.

WO2004108748-A2.

16-DEC-2004.

24-SEP-2003; 2003WO-US029909.

24-SEP-2002; 2002US-0413250P.

(CENZ) CENTOCOR INC.

Yang J, Heavner G, Jordan R, Sweet RW;

WPI; 2005-031655/03.

Novel human growth arrest specific polypeptide-6, useful for generating antibodies against growth arrest specific polypeptide-6, and for treating cardiovascular, rheumatoid arthritis, HIV infection, leukemia, multiple sclerosis.

Example 2; SEQ ID NO 1; 107pp; English.

The invention relates to an isolated human growth arrest specific gene 6 (Gas6) polypeptide. The invention also relates to a recombinant DNA molecule encoding the polypeptide, an antibody or antigen binding fragment capable of binding to the polypeptide and a labeled antibody generated against Gas6. The Gas6 polypeptide is useful for generating antibodies against Gas6, which involves immunization with the polypeptide or screening recombinant antibodies with the polypeptide. The antibodies are useful for detecting Gas6 polypeptide in a sample suspected of containing Gas6. Compositions containing the polypeptide are useful for preventing or treating cardiovascular diseases resulting from a dysfunction in a mammal. The compositions are also useful for treating cancer, atherosclerosis, sepsis, glomerulosclerosis, diabetes, rheumatoid arthritis, HIV infection, osteoarthritis, osteoporosis and multiple sclerosis. This sequence represents the human Gas6 polypeptide of the invention.

Sequence 678 AA;

Query Match 98.7%; Score 3628; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.3e-244; Indels 0; Gaps 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60
1 MAPSLSPGPAALRRAPQLLLLLLAECALALLPAREATQFLRPRORRAFOVEEAKQGH 60
61 LERECVEELCSREAREVFNDEPDTYFPRYIDCINKGSPYTKNSGATCQNLPDCC 120
61 LERECVEELCSREAREVFNDEPDTYFPRYIDCINKGSPYTKNSGATCQNLPDCC 120


```

Db      61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120
Qy      121 TPNCDBRKTQACODLMGNFFCLCKAGWGRLCDKDVNECSOENGGCLQICHNRGSPHC 180
Db      121 TPNCDBRKTQACODLMGNFFCLCKAGWGRLCDKDVNECSOENGGCLQICHNRGSPHC 180
Qy      181 SCHSGFELSDGRTCCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVD 240
Db      181 SCHSGFELSDGRTCCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVD 240
Qy      241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYIGRM 300
Db      241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYIGRM 300
Qy      301 FSGTPIRLRFKRLQPTRLVAEPFRTFDEPGILLFAGGHQDSTWIVLALRAGRLQLR 360
Db      301 FSGTPIRLRFKRLQPTRLVAEPFRTFDEPGILLFAGGHQDSTWIVLALRAGRLQLR 360
Qy      361 YNGVGRVTSSGPIVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420
Db      361 YNGVGRVTSSGPIVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420
Qy      421 LTVGGIIPFHEKDLVQPINRPLDGMRSWMNLNGEDTTIOETVKNTRMOCFSYTERGSFY 480
Db      421 LTVGGIIPFHEKDLVQPINRPLDGMRSWMNLNGEDTTIOETVKNTRMOCFSYTERGSFY 480
Qy      481 PGSGFAFYSLDYNRTPLDVGTSTWEVEVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540
Db      481 PGSGFAFYSLDYNRTPLDVGTSTWEVEVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540
Qy      541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600
Db      541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600
Qy      601 AAQLOERLAVLEHRLSPVLTFAAGLPDVVTSAPVTAFTAFRGCMTELVNRRLDLDBAAY 660
Db      601 AAQLOERLAVLEHRLSPVLTFAAGLPDVVTSAPVTAFTAFRGCMTELVNRRLDLDBAAY 660
Qy      661 KHSIDITAHSCPVEPAAA 678
Db      661 KHSIDITAHSCPVEPAAA 678

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RESULT 11

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AEE87023
ID      AEE87023 standard; protein; 678 AA.
XX      AEE87023;
AC      AEE87023;
DT      23-FEB-2006 (first entry)
XX      XX
DE      Human chemotherapy response-related protein Segid107.
KW      Chemotherapy; cancer; cytostatic; gene therapy; pharmaceutical;
        breast tumor; diagnostic; prognosis.
XX      Homo sapiens.
OS      Homo sapiens.
PN      MO2005119260-A2.
XX      XX
PD      15-DEC-2005.
XX      XX
PF      30-MAY-2005; 2005MO-EP005787.
XX      XX
PR      03-JUN-2004; 2004EP-00013107.
XX      XX
PA      (FARB ) BAYER HEALTHCARE AG.
PI      Munnes M;
XX      XX
DR      MPI: 2006-047692/05.
XX      N-PSDB; AEE86958.
XX      XX

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PT      Investigating response to anti-cancer chemotherapy comprises determining
PT      the expression level of gene(s) of interest in a biopsy sample.
XX      XX
PS      Disclosure; SEQ ID NO 107; 248bp; English.
XX      XX
CC      This invention relates to a novel method of investigating response to
CC      anti-cancer chemotherapy. The method comprises determining, in a biopsy
CC      sample taken from a neoplastic lesion after the onset of a chemotherapy
CC      schedule, the expression level of up to 65 genes included in the
CC      specification. The invention may be useful for the development of
CC      compounds with a cytostatic activity whilst the disclosed sequences may
CC      prove useful for gene therapy. The method is useful for investigating
CC      response to anti-cancer chemotherapy. The method, composition, and kit
CC      are useful or predicting, diagnosing, prognosing, preventing, and
CC      treating malignant neoplasia and breast cancer. The present sequence is
CC      that of the protein encoded by a human gene related to the response to
CC      cancer chemotherapy. The gene was claimed for use in the method of the
CC      invention.
XX      XX
SO      Sequence 678 AA:

```

```

Query Match      98.7%; Score 3628; DB 10; Length 678;
Best Local Similarity 100.0%; Pred. No. 1,3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MAPSLSPGPAALRAPOLLLLLAABCALAALLPAREATQFLRRORARQVFEAKQGH 60
Db      1 MAPSLSPGPAALRAPOLLLLLAABCALAALLPAREATQFLRRORARQVFEAKQGH 60
Qy      61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120
Db      61 LERECVELCSREAREVEFENDPETDYFPRYLDCINKSGSPYTKNSGFATCVONLPDQC 120
Qy      121 TPNCDBRKTQACODLMGNFFCLCKAGWGRLCDKDVNECSOENGGCLQICHNRGSPHC 180
Db      121 TPNCDBRKTQACODLMGNFFCLCKAGWGRLCDKDVNECSOENGGCLQICHNRGSPHC 180
Qy      181 SCHSGFELSDGRTCCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVD 240
Db      181 SCHSGFELSDGRTCCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVD 240
Qy      241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYIGRM 300
Db      241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYIGRM 300
Qy      301 FSGTPIRLRFKRLQPTRLVAEPFRTFDEPGILLFAGGHQDSTWIVLALRAGRLQLR 360
Db      301 FSGTPIRLRFKRLQPTRLVAEPFRTFDEPGILLFAGGHQDSTWIVLALRAGRLQLR 360
Qy      361 YNGVGRVTSSGPIVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420
Db      361 YNGVGRVTSSGPIVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHLN 420
Qy      421 LTVGGIIPFHEKDLVQPINRPLDGMRSWMNLNGEDTTIOETVKNTRMOCFSYTERGSFY 480
Db      421 LTVGGIIPFHEKDLVQPINRPLDGMRSWMNLNGEDTTIOETVKNTRMOCFSYTERGSFY 480
Qy      481 PGSGFAFYSLDYNRTPLDVGTSTWEVEVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540
Db      481 PGSGFAFYSLDYNRTPLDVGTSTWEVEVAHIRPAADTGVLPALMAPDLRAVPLSVALV 540
Qy      541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600
Db      541 DYHSTKKLKKQVLVAVEHTALAMEIKVCDGQEHVTVSLRGEATLEVDGTRGQSEVS 600
Qy      601 AAQLOERLAVLEHRLSPVLTFAAGLPDVVTSAPVTAFTAFRGCMTELVNRRLDLDBAAY 660
Db      601 AAQLOERLAVLEHRLSPVLTFAAGLPDVVTSAPVTAFTAFRGCMTELVNRRLDLDBAAY 660
Qy      661 KHSIDITAHSCPVEPAAA 678
Db      661 KHSIDITAHSCPVEPAAA 678

```

RESULT 12

ADD48757 standard; protein; 679 AA.

ADD48757;

02-DEC-2004 (revised)
29-JAN-2004 (first entry)

Human Protein L13720, SEQ ID NO 14467.

Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.Homo sapiens.
Unidentified.

MO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-033347P.

(GENO) GEN HOSPITAL CORP.
(FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; L13720.

New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
Example 1; Page; 1017p; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (described in Table 3
of the specification) which is differentially expressed during pain.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 679 AA;

Query Match 98.7%; Score 3628; DB 7; Length 679;

Best Local Similarity 100.0%; Pred. No. 1,3e-244;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAPSLSPGPAALARRAPOLLILLILAAECALAAALPAREATOPFRRPORAFOVFEKQKH	60
DB	1	MAPSLSPGPAALARRAPOLLILLILAAECALAAALPAREATOPFRRPORAFOVFEKQKH	60
QY	61	LERECVEELCSREAREVFENDPETDYFPRYLDCINKKSGPYTKNSGFATCVNLPDQC	120
DB	61	LERECVEELCSREAREVFENDPETDYFPRYLDCINKKSGPYTKNSGFATCVNLPDQC	120
QY	121	TNPDCRKGTQACQDLMGNFCLCAAGNGRLCDXDVNCSQENGCCLQICNNKSGSFIC	180
DB	121	TNPDCRKGTQACQDLMGNFCLCAAGNGRLCDXDVNCSQENGCCLQICNNKSGSFIC	180
QY	181	SCHSGFELSSDORTQODIDECDASACGPARCKNPGSYSLCDBGFAYSQEKACRDVD	240
DB	181	SCHSGFELSSDORTQODIDECDASACGPARCKNPGSYSLCDBGFAYSQEKACRDVD	240
QY	241	ECLGRCRQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDDILPCVPFSAKSVKSLYLGRM	300
DB	241	ECLGRCRQVCVNSPGSYTCHCDGRGGLKLSQMDTCEDDILPCVPFSAKSVKSLYLGRM	300
QY	301	FSGTPIRLRFRRLQPTRLVAEFDFRTDPBGILLFAGGHQDSTWIVIALRAGRLEQLR	360
DB	301	FSGTPIRLRFRRLQPTRLVAEFDFRTDPBGILLFAGGHQDSTWIVIALRAGRLEQLR	360
QY	361	YNGVGRVYSSGPIVNHGMQTTISVEELARNVYIKNRDVMKIAVAGDLFOBERGLYHLN	420
DB	361	YNGVGRVYSSGPIVNHGMQTTISVEELARNVYIKNRDVMKIAVAGDLFOBERGLYHLN	420
QY	421	LTVGGIPFHEKDLVOPINPRLDGCMRSWMNLGEBDTTIDETVKVNTRMQCFSTERGSPY	480
DB	421	LTVGGIPFHEKDLVOPINPRLDGCMRSWMNLGEBDTTIDETVKVNTRMQCFSTERGSPY	480
QY	481	PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVTFALMAPLRAVPLSVALY	540
DB	481	PGSGFAFYSLDYMRTPLDVGSTWEEVVAHIRPAADTGVTFALMAPLRAVPLSVALY	540
QY	541	DYHSTRKKLKKOVLVAVENTALAMEIKVCDQOEHVTVSLDGEATLEVDGTRGSEVS	600
DB	541	DYHSTRKKLKKOVLVAVENTALAMEIKVCDQOEHVTVSLDGEATLEVDGTRGSEVS	600
QY	601	AAQOLERLAVLERHLSPLYTFAGGLPDVPTSAPTYAFYRCMTLEVNRLDLDEAAY	660
DB	601	AAQOLERLAVLERHLSPLYTFAGGLPDVPTSAPTYAFYRCMTLEVNRLDLDEAAY	660
QY	661	KHSDITAHSCPVEPAA 678	
DB	661	KHSDITAHSCPVEPAA 678	

RESULT 13

ADQ67207 standard; protein; 624 AA.

ADQ67207;

07-OCT-2004 (first entry)

Novel human protein sequence #2180.

osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

gene therapy; diagnostic marker; morbid state; osteoporosis;

neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

Homo sapiens.

EP1440981-A2.

28-JUL-2004.

PF 21-JAN-2004; 2004EP-00001196.
 XX
 XX 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA Isegaki T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX WPI: 2004-535376/52.
 DR N-PSDB; AD065019.
 XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 4368; 2449bp; English.
 XX
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 XX Sequence 624 AA;

Query Match 85.6%; Score 3146; DB 8; Length 624;
 Best Local Similarity 99.8%; Pred. No. 5.5e-211;
 Matches 584; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 94 DCINXGSPYTKXSGFATCQNLPDCTPNCORRGTQACODLGMNFCCLKKMGWGRIC 153
 DB 40 NCINXGSPYTKXSGFATCQNLPDCTPNCORRGTQACODLGMNFCCLKKMGWGRIC 99
 QY 154 DKDVNCSQENGGCLOICHNKPGSFCHSGFELSDGRTCODIDECADSEACGEARCK 213
 DB 100 DKDVNCSQENGGCLOICHNKPGSFCHSGFELSDGRTCODIDECADSEACGEARCK 159
 QY 214 NLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQCVNPSGYTCHCDGRGLKLSQD 273
 DB 160 NLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQCVNPSGYTCHCDGRGLKLSQD 219
 QY 274 MDTCEBILPCVPSVAKSVKSLVIGMFSCTPIRLRFKQLQPTRLVAEPDFPTPEGI 333
 DB 220 MDTCEBILPCVPSVAKSVKSLVIGMFSCTPIRLRFKQLQPTRLVAEPDFPTPEGI 279
 QY 334 LIFAGGHODSTWVLLRAGRLLOLRVNGVGRVTSGGPYNHGMOTTISVEELARLVY 393
 DB 280 LIFAGGHODSTWVLLRAGRLLOLRVNGVGRVTSGGPYNHGMOTTISVEELARLVY 339
 QY 394 KVNRAVMKIAVAGDLFOBERGLYHNLTVGGLPFHEKDLVQPINRLDGCNRSNMWNG 453
 DB 340 KVNRAVMKIAVAGDLFOBERGLYHNLTVGGLPFHEKDLVQPINRLDGCNRSNMWNG 399
 QY 454 EDTTIOETKVNTRMOCFSYTERGSPYPSGGAFLSLDYKRYLVDGTESTWEVVAHI 513
 DB 400 EDTTIOETKVNTRMOCFSYTERGSPYPSGGAFLSLDYKRYLVDGTESTWEVVAHI 459
 QY 514 RPAADTGVLFALWAPDLRAVPLSVLVDSYHSTKCLKKOLVLAVERHTALALMEIKYCDGQ 573
 DB 460 RPAADTGVLFALWAPDLRAVPLSVLVDSYHSTKCLKKOLVLAVERHTALALMEIKYCDGQ 519
 QY 574 EHVVTVSLDGEATLEVDGTGSGSEVSAQLOERLAVLERHLSPVLTFAAGLPDVPVTS 633
 DB 520 EHVVTVSLDGEATLEVDGTGSGSEVSAQLOERLAVLERHLSPVLTFAAGLPDVPVTS 579
 QY 634 APVTAAYRCMTLENNRRLLDLEAAYKISDITAHSCCPVEPAAA 678
 DB 580 APVTAAYRCMTLENNRRLLDLEAAYKISDITAHSCCPVEPAAA 624

RESULT 14

AAW46462
 ID AAW46462 standard; protein; 673 AA.

AAW46462;

15-MAY-1998 (first entry)

Murine growth arrest specific-gene 6 (gas6) protein.

Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
 KW growth regulation; serum-free culture medium; human; Schwann cell;
 KW receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
 KW treatment; nervous system injury.

Mus sp.

US5714385-A.

03-FEB-1998.

10-MAY-1995; 95US-00435434.

10-MAY-1995; 95US-00435434.

(GENTH) GENENTECH INC.

Chen J, Mather JP, Li R;

WPI; 1998-129864/12.

Medium for culturing human Schwann cells - is serum-free and contains Rse
 PT receptor activator and other mitogens.

Disclosure; Fig 2; 51pp; English.

The present sequence represents a murine growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Rsa and Axl receptor. Rsa is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rsa/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries

Sequence 673 AA;

Query Match 80.4%; Score 2955.5; DB 2; Length 673;
 Best Local Similarity 81.6%; Pred. No. 1.2e-197;
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY 7 PGPAURARAPOLLILLALAECAALLPAREATQFLRPPORAFQVFEAKQCHLRECV 66
 DB 5 PGPAURARAPOLLILLALAECAALLPAREATQFLRPPORAFQVFEAKQCHLRECV 63
 QY 67 EELCSREAREVENDPETYPRYLDCINKYSGPYTKNSGFATCQNLPDCTBNPCD 126
 DB 64 EELCSREAREVENDPETYPRYLDCINKYSGPYTKNSGFATCQNLPDCTBNPCD 123
 QY 127 RKGTOACODLGMNFCCLKKMGWGRICDKDVNCSQENGGCLOICHNKPGSFCHSGHSP 186
 DB 124 RKGTOACODLGMNFCCLKKMGWGRICDKDVNCSQENGGCLOICHNKPGSFCHSGHSP 183
 QY 187 ELSSDGRTCODIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGR 246

Db	184	SIASGQCCODIDECTSDPTCDARKNLPGSISCLCDGYYTSSKEKTCODVDECOQDR	243
Qy	247	CEQVCVNSPGSXYTCHCDRGGLKLSQMDMTCEDILPCVEFVSAKSYKSLYLGFMFSGTPV	306
Db	244	CEQTCVNSBGSYTCCHCDRGGLKLSBDMTCEDILPCVEFPMKSKSLYLGFMFSGTPV	303
Qy	307	IRLRFKRLOPTRLVAEFPDRTTDPBGILLPAGKHODSTWVIALRGRLELQLRNGYGR	366
Db	304	IRLRFKRLOPTRLVAEFPDRTDPEBVLPEFAGGRSDSTWVIGLRGRLELQLRNGYGR	363
Qy	367	VTSSEPVINHGMWMTI SVBELARNLYTKYNRBDVMKIIAAGDLPQBERGLYHNLFTVGGI	426
Db	364	ITSSGPTINHGMWMTI SVBELERNLYTKYKKAQVMKIIAAGELFQLEBGLYHNLFTVGGI	423
Qy	427	PFEHEDLVOPINPRLDGCMRSNMNLNGBDTTIOETVKVNTRMOCFSYTERGSEFYPQSFA	486
Db	424	PFEKSELVQPINPRLDGCMRSNMNLNGEDSALGETKANTKMQCFSYTERGSEFFPGNGFA	483
Qy	487	FYSLDYMRTPDLVCGTSESTVEVVAHIRPADTGVLPALMAPLRAVPLSVALVDYHSTK	546
Db	484	TYRLMYTRTSLDVGTETTEVVKVARIRAPADTGVALLAVGDD--DVLSVALVDYHSTK	541
Qy	547	KLKQOLVVLVAEHTALALMEIKVCQDOEHVYTSRLDEGATLEVDGTRGQSEVSAQLOE	606
Db	542	KLKQOLVVLVAEDVALALMEIKVCQDOEHVYTSRLBGEATLEVDGTRGQSEVSTQLOE	601
Qy	607	RLAVIERHLRSPVLTFAAGLPDVVPVTSAPVTAAYRGCMTELVNRRLIDDEAAVYKSDIT	666
Db	602	RLDTLKTHLQGSVHTVYVGGIPEVSVTSAPVTAAYRGCMTELVNGKILIDLTASYAKSHDIT	661
Qy	667	AHSCPPVEPA 676	
Db	662	SHSCPEVEPA 671	


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Db 361 YNGVGRVTSSSGPGVINHGMMQTTISVEELARNLVIKNRDAVMKIAVAGDLFOGERGLYHLN 420
Qy 421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWNLGEBDTTIOETVKVNTRMOCFSVTERGSFY 480
Db 421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWNLGEBDTTIOETVKVNTRMOCFSVTERGSFY 480
Qy 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVVAHIRPAADGVLPALMAPLRAVPLSVALLY 540
Db 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVVAHIRPAADGVLPALMAPLRAVPLSVALLY 540
Qy 541 DYHSTRKCLKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
Db 541 DYHSTRKCLKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
Qy 601 AAQOERLAVLERHRLSPVLTFRAGGLPDVPTVSAPVTATYRGCMTELVNRLLDDEAY 660
Db 601 AAQOERLAVLERHRLSPVLTFRAGGLPDVPTVSAPVTATYRGCMTELVNRLLDDEAY 660
Qy 661 KHSDDITAHSCPVEPAAADYKDDDDK 686
Db 661 KHSDDITAHSCPVEPAAADYKDDDDK 686
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RESULT 2

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US-10-671-054-3
; Sequence 3, Application US/10671054
; Publication No. US20040157774A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-3
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Query Match 98.7%; Score 3628; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.9e-289;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MAPSLSPGPAALRRAPQOLLLLLLAECALAAALLPAREATQFLRPRORAFQVFEAKQGH 60
Db 1 MAPSLSPGPAALRRAPQOLLLLLLAECALAAALLPAREATQFLRPRORAFQVFEAKQGH 60
Qy 61 LRECEVEELCSRBEAREVEFENDPETDYFYPRIYDCINKTGSPTTKNSGFATCYQNLPDQC 120
Db 61 LRECEVEELCSRBEAREVEFENDPETDYFYPRIYDCINKTGSPTTKNSGFATCYQNLPDQC 120
Qy 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Db 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Qy 181 SCHSGFELSSDRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAVSSOEKACRDV 240
Db 181 SCHSGFELSSDRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAVSSOEKACRDV 240
Qy 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEBLLPCVPPSVAKSVKSLYLGNN 300
Db 241 ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEBLLPCVPPSVAKSVKSLYLGNN 300
Qy 301 PGSTPIYIRLRFKRLQOTRLVAEFDEFTPEBEGILLFAGGHODSTWTLVALRAGRLLEQLR 360
Db 301 PGSTPIYIRLRFKRLQOTRLVAEFDEFTPEBEGILLFAGGHODSTWTLVALRAGRLLEQLR 360
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Qy 361 YNGVGRVTSSSGPGVINHGMMQTTISVEELARNLVIKNRDAVMKIAVAGDLFOGERGLYHLN 420
Db 361 YNGVGRVTSSSGPGVINHGMMQTTISVEELARNLVIKNRDAVMKIAVAGDLFOGERGLYHLN 420
Qy 421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWNLGEBDTTIOETVKVNTRMOCFSVTERGSFY 480
Db 421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWNLGEBDTTIOETVKVNTRMOCFSVTERGSFY 480
Qy 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVVAHIRPAADGVLPALMAPLRAVPLSVALLY 540
Db 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVVAHIRPAADGVLPALMAPLRAVPLSVALLY 540
Qy 541 DYHSTRKCLKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
Db 541 DYHSTRKCLKQOLVLAVENTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGSEVS 600
Qy 601 AAQOERLAVLERHRLSPVLTFRAGGLPDVPTVSAPVTATYRGCMTELVNRLLDDEAY 660
Db 601 AAQOERLAVLERHRLSPVLTFRAGGLPDVPTVSAPVTATYRGCMTELVNRLLDDEAY 660
Qy 661 KHSDDITAHSCPVEBPAA 678
Db 661 KHSDDITAHSCPVEBPAA 678
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RESULT 3

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US-10-696-909A-41
; Sequence 41, Application US/10696909A
; Publication No. US20050118604A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Atchison, Robert E.
; APPLICANT: Frieria, Anabella
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-005820US
; CURRENT APPLICATION NUMBER: US/10/696,909A
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/512,251
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/421,989
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: growth arrest-specific 6 (GAS6), AXL stimulatory
US-10-696-909A-41
```

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Query Match 98.7%; Score 3628; DB 5; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.9e-289;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MAPSLSPGPAALRRAPQOLLLLLLAECALAAALLPAREATQFLRPRORAFQVFEAKQGH 60
Db 1 MAPSLSPGPAALRRAPQOLLLLLLAECALAAALLPAREATQFLRPRORAFQVFEAKQGH 60
Qy 61 LRECEVEELCSRBEAREVEFENDPETDYFYPRIYDCINKTGSPTTKNSGFATCYQNLPDQC 120
Db 61 LRECEVEELCSRBEAREVEFENDPETDYFYPRIYDCINKTGSPTTKNSGFATCYQNLPDQC 120
Qy 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Db 121 TNPDCDRKGTQACODLMGNFCLCKRAGWGRLCDKDVNCSQENGGCLQICHKPKGSFHC 180
Qy 181 SCHSGFELSSDRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAVSSOEKACRDV 240
Db 181 SCHSGFELSSDRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAVSSOEKACRDV 240
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QY 241 ECLQRCBOYCVNSPGSYTCHCDRGGI.KLSQDMTCEBLLPCVPFSYAKSVKSL.YLGRM 300
DB 241 ECLQRCBOYCVNSPGSYTCHCDRGGI.KLSQDMTCEBLLPCVPFSYAKSVKSL.YLGRM 300
QY 301 FSGTPTVRLRFKRLQPTRLVAEPDFTFDEBGLL.FAGGHQDSWTWIALRAGRL.EQLR 360
DB 301 FSGTPTVRLRFKRLQPTRLVAEPDFTFDEBGLL.FAGGHQDSWTWIALRAGRL.EQLR 360
QY 361 YNGVGRVTSFGPVINHGMQOTISVEELARNLVIVNRDAMVKIAVADLFQPERGLYHLN 420
DB 361 YNGVGRVTSFGPVINHGMQOTISVEELARNLVIVNRDAMVKIAVADLFQPERGLYHLN 420
QY 421 LTVGGIPEFHKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMOCQSVTERGSFY 480
DB 421 LTVGGIPEFHKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMOCQSVTERGSFY 480
QY 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVLV 540
DB 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVLV 540
QY 541 DYHSTKLLKKQVLYVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600
DB 541 DYHSTKLLKKQVLYVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600
QY 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCMTELVNRRLDLDBAAY 660
DB 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCMTELVNRRLDLDBAAY 660
QY 661 KHSDDTAHSCPYEPAAA 678
DB 661 KHSDDTAHSCPYEPAAA 678

RESULT 4
US-10-756-149-4949
; Sequence 4949, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Azizi, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4949
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4949

Query Match 98.7%; Score 3628; DB 5; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.9e-289;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSISPGPALRRAPQOLLLILIAFCALALIPAREATQTLRQRRAPFQVEBAKQGH 60
DB 1 MAPSISPGPALRRAPQOLLLILIAFCALALIPAREATQTLRQRRAPFQVEBAKQGH 60
QY 61 LERECEVEELCSREAEVEFENDEPTDYFYPRYLDCTINKXGSPYTKSGPATCVQNL.PDCQ 120
DB 61 LERECEVEELCSREAEVEFENDEPTDYFYPRYLDCTINKXGSPYTKSGPATCVQNL.PDCQ 120
QY 121 TENPCDRKQTOACQDLMGNFFCLCKRAGWGRLCDKDVNECSQENGGCLQICNNKPSGPHC 180
DB 121 TENPCDRKQTOACQDLMGNFFCLCKRAGWGRLCDKDVNECSQENGGCLQICNNKPSGPHC 180
QY 181 SCHSGFELSSDGTQDIDECADSEACGEARCNLFGSYSCLCDEGFAVSSQEKACRDVD 240
DB 181 SCHSGFELSSDGTQDIDECADSEACGEARCNLFGSYSCLCDEGFAVSSQEKACRDVD 240

QY 241 ECLQRCBOYCVNSPGSYTCHCDRGGI.KLSQDMTCEBLLPCVPFSYAKSVKSL.YLGRM 300
DB 241 ECLQRCBOYCVNSPGSYTCHCDRGGI.KLSQDMTCEBLLPCVPFSYAKSVKSL.YLGRM 300
QY 301 FSGTPTVRLRFKRLQPTRLVAEPDFTFDEBGLL.FAGGHQDSWTWIALRAGRL.EQLR 360
DB 301 FSGTPTVRLRFKRLQPTRLVAEPDFTFDEBGLL.FAGGHQDSWTWIALRAGRL.EQLR 360
QY 361 YNGVGRVTSFGPVINHGMQOTISVEELARNLVIVNRDAMVKIAVADLFQPERGLYHLN 420
DB 361 YNGVGRVTSFGPVINHGMQOTISVEELARNLVIVNRDAMVKIAVADLFQPERGLYHLN 420
QY 421 LTVGGIPEFHKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMOCQSVTERGSFY 480
DB 421 LTVGGIPEFHKDLVQPINPRLDGCMSNMNLNGEDTTIOETVKVNTMOCQSVTERGSFY 480
QY 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVLV 540
DB 481 PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVLV 540
QY 541 DYHSTKLLKKQVLYVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600
DB 541 DYHSTKLLKKQVLYVAVEHTALALMEIKVCDGQEHVTVSLRDGEATLEVDGTRGQSEVS 600
QY 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCMTELVNRRLDLDBAAY 660
DB 601 AAQLOERLAVLEHRLSPVLTFAAGLPDVPTSAPTYAFYRGCMTELVNRRLDLDBAAY 660
QY 661 KHSDDTAHSCPYEPAAA 678
DB 661 KHSDDTAHSCPYEPAAA 678

RESULT 5
US-10-223-085-48
; Sequence 48, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02

; PRIOR APPLICATION NUMBER: US 09/643,657
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 383
 ; SEQ ID NO 48
 ; LENGTH: 673
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; US-10-223-085-48

Query Match 80.4%; Score 2955.5; DB 4; Length 673;
 Best Local Similarity 81.6%; Pred. No. 1.4e-233;
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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QY 7 PGPALRRAPOLLILLIAECALALLPAREATOFLLPRQRAFOVFEAKGHLERECV 66
DB 5 PGPAA-ALGTALLILLIAESSHTVLLRAREAAQFLRPQRAFOVFEAKGHLERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCLNKYSPTKNSGFATCVQNLPOCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEFYPRQECMRKXGRPEEKNPDPACVQNLPOCTPNPCD 123
QY 127 RKGTOACODLMGNFCLCAKMGGRCLCDVNECQENGGCIQICHNKGSFHCSHSGF 186
DB 124 KKGTHICODLMGNFCLCAKMGGRCLCDVNECQENGGCIQICHNKGSFHCSHSGF 183
QY 187 ELISDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECTLOGR 246
DB 184 SLASDQTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECTLOGR 243
QY 247 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSYKSLYLGRMFSGTPV 306
DB 244 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSYKSLYLGRMFSGTPV 303
QY 307 IRLRFRLOPTRLVAEFDRTDPBGILLFAGHDSSTIIVLALRAGRIELQLRVNGVR 366
DB 304 IRLRFRLOPTRLVAEFDRTDPBGILLFAGHDSSTIIVLALRAGRIELQLRVNGVR 363
QY 367 VTSAGPVLNMGWOTISVEELARNLVIKVRDVAVMKIAVAGDLFQPERGLYHLNLTVGSI 426
DB 364 ITSSGPTINMGWOTISVEELARNLVIKVRDVAVMKIAVAGDLFQPERGLYHLNLTVGSI 423
QY 427 PPEHEDVOPINPRLDGCMRSNMNLGEBDTTIOETVYKVRNQCFSVTERGSPYSGGPA 486
DB 424 PPEHEDVOPINPRLDGCMRSNMNLGEBDTTIOETVYKVRNQCFSVTERGSPYSGGPA 483
QY 487 FVSLDYMRTPLDVGESTVEVEVAHIRPAADGVLFALMAPDLRAVPLSVALLVDYHSTK 546
DB 484 FVSLDYMRTPLDVGESTVEVEVAHIRPAADGVLFALMAPDLRAVPLSVALLVDYHSTK 541
QY 547 KLLKQOLVLAVENTALALMEIKVCGQEHVVTVSLRDEGATLEVDTRGQSEVSAQLOE 606
DB 542 KLLKQOLVLAVENTALALMEIKVCGQEHVVTVSLRDEGATLEVDTRGQSEVSAQLOE 601
QY 607 RLAVTERHRLSRPVLTFAGGLPDVPTVSAPVTAFTYRCQMTLEVNRLLDIDEAAYKASDIT 666
DB 602 RLAVTERHRLSRPVLTFAGGLPDVPTVSAPVTAFTYRCQMTLEVNRLLDIDEAAYKASDIT 661
QY 667 AHSCEPVEBA 676
DB 662 SHSCEPVEBA 671
  
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RESULT 6
 US-10-223-084-48
 ; Sequence 48, Application US/10223084
 ; Publication No. US20030105011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-084-48
  
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Query Match 80.4%; Score 2955.5; DB 4; Length 673;
 Best Local Similarity 81.6%; Pred. No. 1.4e-233;
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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QY 7 PGPALRRAPOLLILLIAECALALLPAREATOFLLPRQRAFOVFEAKGHLERECV 66
DB 5 PGPAA-ALGTALLILLIAESSHTVLLRAREAAQFLRPQRAFOVFEAKGHLERECV 63
QY 67 BELCSREAREVENDPETDYFYPRLDCLNKYSPTKNSGFATCVQNLPOCTPNPCD 126
DB 64 BEVCSKEAREVENDPETEFYPRQECMRKXGRPEEKNPDPACVQNLPOCTPNPCD 123
QY 127 RKGTOACODLMGNFCLCAKMGGRCLCDVNECQENGGCIQICHNKGSFHCSHSGF 186
DB 124 KKGTHICODLMGNFCLCAKMGGRCLCDVNECQENGGCIQICHNKGSFHCSHSGF 183
QY 187 ELISDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECTLOGR 246
DB 184 SLASDQTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECTLOGR 243
QY 247 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSYKSLYLGRMFSGTPV 306
DB 244 CEQVCNPSGSYTCHCDGRGGLKLSQDMOTCEDILPCVPSVAKSYKSLYLGRMFSGTPV 303
QY 307 IRLRFRLOPTRLVAEFDRTDPBGILLFAGHDSSTIIVLALRAGRIELQLRVNGVR 366
  
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Db 304 IRLAFKRLQPTRLLAEPDFRTPEDEGVLFPAAGRSDSITWIVLGLRAGRLLEQLRYNGVR 363
Qy 367 VTSSGPVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHMLTYVGI 426
Db 364 ITSSGPTINHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHMLTYVGI 423
Qy 427 PFHEKDIWOPINRLDGCMSNMWLNGETTTIOETKVNTRMQCFSTYTERGSPYPSGFA 486
Db 424 PFKESEIVQPINRPLDGCMSNMWLNGETDSAIQETVKANTMOCFSTYTERGSPFGNGFA 483
Qy 487 FYSLDYWRTPLDVGTSTWEEVVAHIRPADTGVLFALMAPDLRANPLSALVDYHSTK 546
Db 484 TYRLNTRYISLDVGTSTWEEVVAHIRPADTGVLFALVGD--DVVISVALVDYHSTK 541
Qy 547 KLKKQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 606
Db 542 KLKKQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSTAOLOE 601
Qy 607 RLAVLEHRLSPVLTFAGGLPDVPTSAVTAFAFYRGCMTELVNRLLDLDEAAVXSHDIT 666
Db 602 RLDTLKTHLQSGVHTVYGGLEPEVSISAPVTAFAFYRGCMTELVNKKIIDLDTASYKSHDIT 661
Qy 667 AHSCPVEPA 676
Db 662 SHSCPVEHA 671

RESULT 7

US-10-223-088-48
Sequence 48, Application US/10223088
Publication No. US20030105012A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Petarra, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scott A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: P3235PIC6
CURRENT APPLICATION NUMBER: US/10/223,088
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-223-088-48

Query Match 80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

Qy 7 PGPAALRRAPDQLLLLLAECALALLPAREATQFLPRQRARQVEEAKQHLERECV 66
Db 5 PGPAALRRAPDQLLLLLAECALALLPAREATQFLPRQRARQVEEAKQHLERECV 63
Qy 67 BELCSREABEVFNDEDTDFYFRYLDCKNKYSGPYTKSGFRATCYQNLPDQCTPNPCD 126
Db 64 BEVCSKEAREVEFNDEDTDFYFRYLDCKNKYSGPYTKSGFRATCYQNLPDQCTPNPCD 123
Qy 127 RKGTQACODLMGNFPCCKXGWMGRLCDKVNESQONGGCTQIHNKPKSFGHCSHGF 186
Db 124 RKGTQACODLMGNFPCCKXGWMGRLCDKVNESQONGGCTQIHNKPKSFGHCSHGF 183
Qy 187 ELSSDGRTCODIDECADSEACGEARCKNLPGYSCLCEGFAYSQKACRDVDECTQGR 246
Db 184 SLASDGTQCODIDECTSDCTCGARCKNLPGYSCLCEGFAYSQKACRDVDECTQGR 243
Qy 247 CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDTLPVCPSPVAKSVKSLYGRNFGSTPV 306
Db 244 CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDTLPVCPSPVAKSVKSLYGRNFGSTPV 303
Qy 307 IRLAFKRLQPTRLLAEPDFRTPEDEGVLFPAAGHDSITWIVLGLRAGRLLEQLRYNGVR 366
Db 304 IRLAFKRLQPTRLLAEPDFRTPEDEGVLFPAAGHDSITWIVLGLRAGRLLEQLRYNGVR 363
Qy 367 VTSSGPVNHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHMLTYVGI 426
Db 364 ITSSGPTINHGMQOTISVEELARNLVIKNRDAVMKIAVAGDLFQPERGLYHMLTYVGI 423
Qy 427 PFHEKDIWOPINRLDGCMSNMWLNGETTTIOETKVNTRMQCFSTYTERGSPYPSGFA 486
Db 424 PFKESEIVQPINRPLDGCMSNMWLNGETDSAIQETVKANTMOCFSTYTERGSPFGNGFA 483
Qy 487 FYSLDYWRTPLDVGTSTWEEVVAHIRPADTGVLFALMAPDLRANPLSALVDYHSTK 546
Db 484 TYRLNTRYISLDVGTSTWEEVVAHIRPADTGVLFALVGD--DVVISVALVDYHSTK 541
Qy 547 KLKKQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSAOLOE 606
Db 542 KLKKQLVLAVEHTALAMEIKVCDGQEHVTVSLRDEATLEVDGTRGQSEVSTAOLOE 601
Qy 607 RLAVLEHRLSPVLTFAGGLPDVPTSAVTAFAFYRGCMTELVNRLLDLDEAAVXSHDIT 666
Db 602 RLDTLKTHLQSGVHTVYGGLEPEVSISAPVTAFAFYRGCMTELVNKKIIDLDTASYKSHDIT 661
Qy 667 AHSCPVEPA 676
Db 662 SHSCPVEHA 671

RESULT 8

US-10-223-090-48
Sequence 48, Application US/10223090
Publication No. US20030105013A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Petarra, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.

APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilian
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C2
CURRENT APPLICATION NUMBER: US/10/223,090
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-223-090-48

Query Match 80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;
QY 7 PGPAAARRAPOLLILLAAECALAAALPPREATOPFRRPRRRFOVPEEAKOGLRECV 66
DB 5 PGPAA-ALCTALLLLASSSHHTVLLRAEAQFLRPRORRAYOVPEEKQOGLRECV 63
QY 67 BEICSRREAREVENDPETDYFYPRLADCKINKYSGPYTKSGPATCVONLPDOCTPNPCD 126
DB 64 BEVCSKEAREVEVENDPETDYFYPRLQOECMRKXGRBEKNPDAKCVONLPDOCTPNPCD 123
QY 127 RKGTQACQDLGNFCLCAAGWGRLCDKDVNECSQENGGCLQICHNKPGSFHCSGSGF 186
DB 124 KKGTHICQDLGNFCLCAAGWGRLCDKDVNECSQENGGCLQICHNKPGSFHCSGSGF 183
QY 187 ELSSDRTQDIDECADSEACGARKCNLPGSYSCLCDEGAASQEKARQVDECLQGR 246
DB 184 SLASDQOTQDIDECADSEACGARKCNLPGSYSCLCDEGAASQEKARQVDECLQGR 243
QY 247 CEQVCNPSGYSYCHCDGRGGLKLSQMDTCEDILPCVPSVAKSVKSLYIGMFSSTPV 306
DB 244 CBQTCNPSGYSYCHCDGRGGLKLSQMDTCEDILPCVPSVAKSVKSLYIGMFSSTPV 303
QY 307 IRLRFRLOPTRLVAEFDFTEPDEGILLFAGGHQDSTWIVLALRAGRLQLRYNGVR 366
DB 304 IRLRFRLOPTRLVAEFDFTEPDEGILLFAGGHQDSTWIVLALRAGRLQLRYNGVR 363
QY 367 VUSGGVINHGMOQTSVEELARNLVYKNRDAVMKIAVAGDLFOPERGGLYHNLVYGGI 426
DB 364 ITSSGPTINGMMQTSVEELARNLVYKNRDAVMKIAVAGDLFOPERGGLYHNLVYGGI 423
QY 427 PFHEKDLVQPINRDLQCKRSMWNLNGEDTTIOETVKNTRMQCFVTERGSEFPYSGSFA 486

DB 424 PFKESELVQPINRDLQCKRSMWNLNGEDSAIQETVKANTKQCFSVTERGSEFPNGSFA 483
QY 487 FVSLDYMTPLDVGNESTWVEVVAIRPADTGLFLMAPDLAVPLSVLVDYHSRK 546
DB 484 TYRLNVTFTSLDVGNETWVEVVAIRPADTGLFLMAPDLAVPLSVLVDYHSRK 541
QY 547 KKKQVLVAVENTLALMEIKVCDGQEHVTVSLRDGEATLEVDGTRQOSEVSAQLOE 606
DB 542 KKKQVLVAVENTLALMEIKVCDGQEHVTVSLRDGEATLEVDGTRQOSEVSAQLOE 601
QY 607 RLAVERRHRSPLTPAGGLPVYTSAPVTAIFYGCTMLEVNRLLDDEAAYKSDIT 666
DB 602 RLDTLKLHQSQSVHTYVGLPEVYSIAFVTAIFYGCTMLEVNRLLDDEAAYKSDIT 661
QY 667 AHSCEPVEBA 676
DB 662 SHSCPEVEBA 671

RESULT 9
US-10-223-087-48
Sequence 48, Application US/10223087
Publication No. US20030109438A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilian
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C4
CURRENT APPLICATION NUMBER: US/10/223,087
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/232,887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18

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1  PRIOR APPLICATION NUMBER: US 60/242,922
2  PRIOR FILING DATE: 2000-10-24
3  PRIOR APPLICATION NUMBER: US 09/709,238
4  PRIOR FILING DATE: 2000-11-08
5  PRIOR APPLICATION NUMBER: PCT/US00/30952
6  PRIOR FILING DATE: 2000-11-08
7  PRIOR APPLICATION NUMBER: PCT/US00/30873
8  PRIOR FILING DATE: 2000-11-10
9  PRIOR APPLICATION NUMBER: PCT/US00/32678
10 PRIOR FILING DATE: 2000-12-01
11 PRIOR APPLICATION NUMBER: US 09/747,259
12 PRIOR FILING DATE: 2000-12-20
13 PRIOR APPLICATION NUMBER: PCT/US00/34956
14 PRIOR FILING DATE: 2000-12-20
15 PRIOR APPLICATION NUMBER: US 09/767,609
16 PRIOR FILING DATE: 2001-01-22
17 PRIOR APPLICATION NUMBER: US 09/796,498
18 PRIOR FILING DATE: 2001-02-28
19 PRIOR APPLICATION NUMBER: PCT/US01/06520
20 PRIOR FILING DATE: 2001-02-28
21 PRIOR APPLICATION NUMBER: PCT/US01/06666
22 PRIOR FILING DATE: 2001-03-01
23 PRIOR APPLICATION NUMBER: US 09/802,706
24 PRIOR FILING DATE: 2001-03-09
25 PRIOR APPLICATION NUMBER: US 09/808,689
26 PRIOR FILING DATE: 2001-03-14
27 PRIOR APPLICATION NUMBER: US 09/816,744
28 PRIOR FILING DATE: 2001-03-22
29 PRIOR APPLICATION NUMBER: US 09/854,280
30 PRIOR FILING DATE: 2001-05-10
31 PRIOR APPLICATION NUMBER: US 09/866,028
32 PRIOR FILING DATE: 2001-05-25
33 PRIOR APPLICATION NUMBER: US 09/866,034
34 PRIOR FILING DATE: 2001-05-25
35 PRIOR APPLICATION NUMBER: PCT/US01/17092
36 PRIOR FILING DATE: 2001-05-25
37 PRIOR APPLICATION NUMBER: US 09/870,574
38 PRIOR FILING DATE: 2001-05-30
39 PRIOR APPLICATION NUMBER: PCT/US01/17443
40 PRIOR FILING DATE: 2001-05-30
41 PRIOR APPLICATION NUMBER: PCT/US01/17800
42 PRIOR FILING DATE: 2001-06-01
43 PRIOR APPLICATION NUMBER: PCT/US01/19692
44 PRIOR FILING DATE: 2001-06-20
45 PRIOR APPLICATION NUMBER: PCT/US01/21066
46 PRIOR FILING DATE: 2001-06-29
47 PRIOR APPLICATION NUMBER: PCT/US01/21735
48 PRIOR FILING DATE: 2001-07-09
49 NUMBER OF SEQ ID NOS: 383
50 SEQ ID NO 48
51 LENGTH: 673
52 TYPE: PRT
53 ORGANISM: Murine
54 US-10-223-087-48
55
56 Query Match 80.4%; Score 2955.5; DB 4; Length 673;
57 Best Local Similarity 81.6%; Pred. No. 1,4e-233;
58 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2
59
60 7 GPPALRRAPOLLILLILAAECALALTPAREATOPILRPQRAPOVFEAKGCHLERECV 66
61 ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||
62 5 PGPAA-ALGTMILLILLISSESHYULRLRREAAQFLRPGRRAIYQVFEAKGCHLERECV 63
63 ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||
64 67 EELGSRERARVEFENDPETDIYPRYLDCINKYSGPYTKNSGFATCVONLPDQCTPNPCD 126
65 ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||
66 64 EEVCSKEAREAREFENDPETEYFYPRYOECMRYKGRPEEKNPDPFACVQNLPDQCTPNPCD 123
67 ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||
68 127 RKGRQACODLNGNPFCLCKAGGGRLLCKDVNVECOENGGCLQIHNKRGSFHSCGSGGF 186
69 ||||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||

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Qy	187	ELSSNGRGTQDIDDECADSEACGEARCKNLPGSTCLCDEGFAVSQEKACRDYDECLQGR	246
Db	184	SLASDQGTQDIDECTDSDTCDDARCKNLPGSTCLCDEGYTSSKREKTCQDYPDECQDR	242
Qy	247	CEQVCVNSPGSYTCHCDGGRGKLSDQMDTCEDILPCVPSVAKSVKSLVLGMSFSTPV	308
Db	244	CEQTCVNSPGSYTCHCDGGRGKLSPDMDTCEDILPCVPSVAKSVKSLVLGMSFSTPV	303
Qy	307	IRLRFRRLQPTLVAEFDFRTEPDEGILTFAGGHODSTWIVLIRAGRLELQRLYNGVGR	366
Db	304	IRLRFRRLQPTLVAEFDFRTEPDEGVLEFAGGRSSTWIVLGRAGRLELQRLYNGVGR	363
Qy	367	VTSSGPGVINHGWMQITISVEELARNLIVIKVNRDAVMKIAVAGDLFQEPGRGLYHNLTVGGI	426
Db	364	ITSSGPTINHGMQITISVEELRNIVIKVNRDAVMKIAVAGELFQLEGRGLYHNLTVGGI	423
Qy	427	PHENDVQPINRPLDGCGRSWNWLNGEPTTIOETVKNVTRNOCSEVTERGSGTYPSSGFA	486
Db	424	PKSESLVQPINRPLDGCGRSWNWLNGEDSALOETVKNATKQCFSTVTERGSGFPNGFA	483
Qy	487	FYSLDMRPTLDVGTESTEVEVVAHIRPADTGVLFALMAPDLRAVPISVALVDVHSTK	546
Db	484	TYRLNRYTTSLDVGTEETVEVVARIRPATDTGVLLALVGD--DVIVSVALVDVHSTK	541
Qy	547	KLKQQLVLAVENTALALMEIKVCDQGEHVVTLSLDGEATLEVDGTGQSEVSAALQGE	606
Db	542	KLKQQLVLAVEDVALALMEIKVCDQSEHTVLSLRGEATLEVDGTGQSEVSTALQGE	601
Qy	607	RLAVLERLRBSVLTFAGLPDPVPTSAPTVAFYGCMTLEVNRRLLIDEAAYKRSDDT	666
Db	602	RLDTLKTHLQGSVHTVYVGLPEVSVISAPTVAFYGCMTLEVNKGILLDITSAKYSDDT	661
Qy	667	AHSCPEVEPA 676	
Db	662	SHSCPEVEHA 671	
RESULT 10			
US-10-223-083-48			
; Sequence 48, Application US/10223083			
; Publication No. US20030119112A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Marsters, Scott A.			
; APPLICANT: Pan, James			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Matanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Ye, Meilan			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS			
; FILE REFERENCE: P3235P1C8			
; CURRENT APPLICATION NUMBER: US/10/223,083			
; CURRENT FILING DATE: 2002-08-16			
; PRIOR APPLICATION NUMBER: US 10/081,056			
; PRIOR FILING DATE: 2002-02-20			
; PRIOR APPLICATION NUMBER: US 60/213,637			
; PRIOR FILING DATE: 2000-06-23			
; PRIOR APPLICATION NUMBER: US 60/219,556			
; PRIOR FILING DATE: 2000-07-20			
; PRIOR APPLICATION NUMBER: US 60/220,624			
; PRIOR FILING DATE: 2000-07-25			
; PRIOR APPLICATION NUMBER: US 60/220,664			

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; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-083-48

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Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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7  PGPALRRAPOLLILLLAECALALLPAREATOFLEPRORAFQVFEBAKQGHLERECV 66
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5  PGPAA-ALGTALLLLILLLAESSHTVILRRAREAAQFLRPRQRAAYQVFEBAKQGHLERECV 63
67  BELSGREAREVEFENDPETDYFYPRYLDCINKYGSBYTKNSGPFATCVQNLPOQCTPNPCD 126
64  BEVCSKEAREVEFENDPETEYFYPRYOECMRKYGRPEEKNDPFAKCVQNLPOQCTPNPCD 123
127  RKGTQACQDLMGNFPCLCAGMGGRLCDVNECSQENGCGCQICHNKRGSPHCSCHSGF 186
124  KKGTHICQDLMGNFPCVCTDGMGGRLCDVNECVQKNGCSQVCHNKRGSPQACHSGF 183
187  ELSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDGFAFYSOGEAKCRDVEDECLQGR 246
184  SLASDQRTCODIDECADSDPTCGDARCKNLPGSYSCLCDGFAFYSOGEAKCRDVEDECLQGR 243
247  CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDIILPCVPSVAKSYKSLYLGRMPSGTIV 306
244  CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDIILPCVPSVAKSYKSLYLGRMPSGTIV 303
307  IRLRKRLOPRTLVAEFDRTPDPBGILLFAGSHOSTWIVLALRAGRLELQLRVYGVGR 366
304  IRLRKRLOPRTLVAEFDRTPDPBGILLFAGSHOSTWIVLALRAGRLELQLRVYGVGR 363
367  VTSSEGVINHGMMQOTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLNLTVGGI 426
364  ITSSGPTINHGMMQOTISVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLNLTVGGI 423
427  PHEKDLVOPINPRLDGCKRSNMWNLGEPTTIOETKYKVTNROCFSEVTERGSPSSGPA 486
424  PKESSELVOPINPRLDGCKRSNMWNLGEPTTIOETKYKVTNROCFSEVTERGSPSSGPA 483
487  FVSLQVMPRLVGTSTVEVEVAHIRPAADTGVLFALMAPLRAVPISVALVDHSHRK 546
484  TYRLNTRTSLDVGETTVEVKVARIIRPAITDGVLLALVGD--DIVISVALVDHSHRK 541
547  KLLKQDLVLAVEHTALALMEIKVCQDQBEHVTVSLRDGEATLEVDSTRQSEVSAALOGE 606
542  KLLKQDLVLAVEHTALALMEIKVCQDQBEHVTVSLRDGEATLEVDSTRQSEVSAALOGE 601
607  RLAVLERHRLSRPYLTAGGLPDVPTSAVYTAFFRCGCMLELVNRRLDLDEAAYKKSDDT 666
602  RLDTLKLTHLQGSVHTVVGGLPEVSVISAPVTAFFRCGCMLELVNRRLDLDEAAYKKSDDT 661
667  AHSCEPVEBA 676
662  SHSCPEVEBA 671

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RESULT 11

US-10-223-089-48

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; Sequence 48, Application US/10223089
; Publication No US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C9
; CURRENT APPLICATION NUMBER: US/10/223,089
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-089-48

```

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Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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7  PGPALRRAPOLLILLLAECALALLPAREATOFLEPRORAFQVFEBAKQGHLERECV 66
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
5  PGPAA-ALGTALLLLILLLAESSHTVILRRAREAAQFLRPRQRAAYQVFEBAKQGHLERECV 63
67  BELSGREAREVEFENDPETDYFYPRYLDCINKYGSBYTKNSGPFATCVQNLPOQCTPNPCD 126
64  BEVCSKEAREVEFENDPETEYFYPRYOECMRKYGRPEEKNDPFAKCVQNLPOQCTPNPCD 123
127  RKGTQACQDLMGNFPCLCAGMGGRLCDVNECSQENGCGCQICHNKRGSPHCSCHSGF 186
124  KKGTHICQDLMGNFPCVCTDGMGGRLCDVNECVQKNGCSQVCHNKRGSPQACHSGF 183
187  ELSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDGFAFYSOGEAKCRDVEDECLQGR 246
184  SLASDQRTCODIDECADSDPTCGDARCKNLPGSYSCLCDGFAFYSOGEAKCRDVEDECLQGR 243
247  CEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDIILPCVPSVAKSYKSLYLGRMPSGTIV 306

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Db      244 CEQTCVNSPGSYTCHCGRGGLKLSPMDTCEDILPCVPFSMAKSVSLYGRMFSSTPV 303
Qy      307 IRLRFKRLQPTRLVAEFDPTFPEGILFAGGHODSTWITLALRAGRLQLRYNGVR 366
Db      304 IRLRFKRLQPTRLVAEFDPTFPEGILFAGGHODSTWITLALRAGRLQLRYNGVR 363
Qy      367 VTSSGPVNHGMQOTISVEBELARNLVKVRDAVMKIAVAGDLFQPERGLYHNLTVGGI 426
Db      364 ITSSGPTINHGMOQTISVEBELARNLVKVRDAVMKIAVAGDLFQPERGLYHNLTVGGI 423
Qy      427 PFHEKDLVQPINRPLDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSPYSGGFA 486
Db      424 PFHESELVQPINRPLDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSPYSGGFA 483
Qy      487 FYSIDYMRPTLDVGTSTWEEVVAHTRPADTGVLPALWAPDLRAVPLSVALVDYHSTK 546
Db      484 TYRLNTRISLDVGTSTWEEVVAHTRPADTGVLPALWAPDLRAVPLSVALVDYHSTK 541
Qy      547 KLRKQVLVAVEHTALAMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVSAQLOE 606
Db      542 KLRKQVLVAVEHTALAMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVSAQLOE 601
Qy      607 RLAVLRHLRSPVLTPAGGLPDVPTVSAPVTAIFYRGCMTELVNRLLDLDEAAVKSHDIT 666
Db      602 RLDTLTKHLQGSVHTVYVGLPEVSVISAPVTAIFYRGCMTELVNRLLDLDTASYKSHDIT 661
Qy      667 AHSCLPVEPA 676
Db      662 SHSCPVEHA 671

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RESULT 12

US-10-223-081-48

Sequence 48, Application US/10223081

Publication No. US2003018686A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerilsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Marstere, Scot A.

APPLICANT: Pan, James

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Williams, P. Mickey

APPLICANT: Ye, Weilan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235P1C7

CURRENT APPLICATION NUMBER: US/10/223,081

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 10/081,056

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/213,637

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/219,556

PRIOR FILING DATE: 2000-07-20

PRIOR APPLICATION NUMBER: US 60/220,624

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/220,664

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/222,695

PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: US 09/643,657

PRIOR FILING DATE: 2000-08-17

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; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-081-48

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Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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Qy      7 PGPAALRRADQQLLLIAACALALLPAREATQFLRPRORARQVFEBAKQHLRECV 66
Db      5 PGPAALRRADQQLLLIAACALALLPAREATQFLRPRORARQVFEBAKQHLRECV 63
Qy      67 ELCSREAREVPEDETDYFYPRYLDCINTKYSPTTKSGFATCYQNLPDQCTPNPCD 126
Db      64 ELCSREAREVPEDETDYFYPRYLDCINTKYSPTTKSGFATCYQNLPDQCTPNPCD 123
Qy      127 RKGTACODLMGNFCLCKAGMGRGLCDKDVNECSQENGCLOICHNKPGSFHSCGSHGF 186
Db      124 RKGTACODLMGNFCLCKAGMGRGLCDKDVNECSQENGCLOICHNKPGSFHSCGSHGF 183
Qy      187 ELSSDGRTCODIDECADSEAGEARCNLPGSYCLDCBGFAYSSQEKACRDVDECIQGR 246
Db      184 ELSSDGRTCODIDECADSEAGEARCNLPGSYCLDCBGFAYSSQEKACRDVDECIQGR 243
Qy      247 CEQTCVNSPGSYTCHCGRGGLKLSPMDTCEDILPCVPFSVAKSVSLYGRMFSSTPV 306
Db      244 CEQTCVNSPGSYTCHCGRGGLKLSPMDTCEDILPCVPFSMAKSVSLYGRMFSSTPV 303
Qy      307 IRLRFKRLQPTRLVAEFDPTFPEGILFAGGHODSTWITLALRAGRLQLRYNGVR 366
Db      304 IRLRFKRLQPTRLVAEFDPTFPEGILFAGGHODSTWITLALRAGRLQLRYNGVR 363
Qy      367 VTSSGPVNHGMQOTISVEBELARNLVKVRDAVMKIAVAGDLFQPERGLYHNLTVGGI 426
Db      364 ITSSGPTINHGMOQTISVEBELARNLVKVRDAVMKIAVAGDLFQPERGLYHNLTVGGI 423
Qy      427 PFHEKDLVQPINRPLDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSPYSGGFA 486
Db      424 PFHESELVQPINRPLDCGRSMNWLNGEDTTIOETVKNTRMOCFSYTERGSPYSGGFA 483
Qy      487 FYSIDYMRPTLDVGTSTWEEVVAHTRPADTGVLPALWAPDLRAVPLSVALVDYHSTK 546
Db      484 TYRLNTRISLDVGTSTWEEVVAHTRPADTGVLPALWAPDLRAVPLSVALVDYHSTK 541
Qy      547 KLRKQVLVAVEHTALAMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVSAQLOE 606
Db      542 KLRKQVLVAVEHTALAMEIKVCDQGEHVTVSLRDEGATLEVDGTRGSEVSAQLOE 601
Qy      607 RLAVLRHLRSPVLTPAGGLPDVPTVSAPVTAIFYRGCMTELVNRLLDLDEAAVKSHDIT 666
Db      602 RLDTLTKHLQGSVHTVYVGLPEVSVISAPVTAIFYRGCMTELVNRLLDLDTASYKSHDIT 661
Qy      667 AHSCLPVEPA 676
Db      662 SHSCPVEHA 671

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RESULT 13

US-10-223-082-48

Sequence 48, Application US/10223082

Publication No. US20030191059A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC3
; CURRENT APPLICATION NUMBER: US/10/223,082
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-082-48

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Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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; 7 PGPALRRAPQQLLLLLAECALALPAREATQFLRPRORAFQVFEAKOGHLRECV 66
; 5 PGPAA-ALGTALLILLALLESSTTVLLRREAQFLRPRORAYQVFEAKOGHLRECV 63
; 67 EELCSREARREVENDEPETYPRYLDCINKYSPYTKNSGFATCVQNLDPDCTNPDCD 126
; 64 EEVCSKEARREVENDEPETYPRYQECMRKRGREKKNPDPKACVQNLDPDCTNPDCD 123
; 127 RKGTQACQDLKMGNFCTLCAAGNGRCLCDVNECSENGCCLOICNNKGSFHCCHSGF 186
; 124 KKGTHICQDLKMGNFCTDGMGGRCLCDVNECVCQNGKSCQVCHNKPSSFQACACHSG 183
; 187 ELISDRTQODIDECADSEAGRCNLPGSYSCDCBGFAYSSQEKACRDVDECLQGR 246
; 184 SLASDQOTQODIDECADSEAGRCNLPGSYSCDCBGFAYSSQEKACRDVDECLQGR 243
; 247 CEQVCNPSFGSYTCHCDGRGGLKLSQMDTCEBILPCVPSVAKSVKSLYLGMFSGTVP 306
; 244 CEQVCNPSFGSYTCHCDGRGGLKLSQMDTCEBILPCVPSVAKSVKSLYLGMFSGTVP 303
; 307 IRLRFRLOPTRLVAFDPRTPEGLILPAGGHQSTWLVALLRGRLEQLQRYNGYGR 366
; 304 IRLRFRLOPTRLVAFDPRTPEGLILPAGGHQSTWLVALLRGRLEQLQRYNGYGR 363
; DB

```

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; 367 VTSSGPVINGMQTISVEBELARNLVIKNRDAVAKKIVAGDLFQPERGLYHLNLTVGCI 426
; 364 ITSSGPTINHGMMQITISVEBELARNLVIKNRDAVAKKIVAGDLFQPERGLYHLNLTVGCI 423
; 427 PEHEKDLVOPINPRLDGCKRSNNWLNGBDTTIOETVKNTRQOCSYTERGSFYGSGFA 486
; 424 PEKESELVOPINPRLDGCKRSNNWLNGBDSALQETVKANTKQOCSYTERGSFYGSGFA 483
; 487 FYSLDYMRTPLDVGESTWEEVVAHIRPAADTVGLPALMAPDLAVPLSLVLDYHSTK 546
; 484 TYRLNVTISLDVGESTWEEVVAHIRPAADTVGLPALMAPDLAVPLSLVLDYHSTK 541
; 547 KKKQVLVAVENHTALMEIKVCDGQEHVTVSLRDEATLEVDGTQOSEVSAQLOE 606
; 542 KKKQVLVAVENHTALMEIKVCDGQEHVTVSLRDEATLEVDGTQOSEVSAQLOE 601
; 607 RLAVLERHRSVLTFFAGLPDVPVTSAPVTAFFYGCMTLENNRLLDDEAAYHSDIT 666
; 602 RLDTLKTHLOGSVHTYVGLPEVSVIASPVTAFFYGCMTLENNRLLDDEAAYHSDIT 661
; 667 AHSCPEVEPA 676
; 662 SHSCPEVEPA 671
; DB

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RESULT 14

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; US-10-305-654-48
; Sequence 48, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, J.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P. F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-305-654-48

```

```

Query Match      80.4%; Score 2955.5; DB 4; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.4e-233;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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; 7 PGPALRRAPQQLLLLLAECALALPAREATQFLRPRORAFQVFEAKOGHLRECV 66
; 5 PGPAA-ALGTALLILLALLESSTTVLLRREAQFLRPRORAYQVFEAKOGHLRECV 63
; 67 EELCSREARREVENDEPETYPRYLDCINKYSPYTKNSGFATCVQNLDPDCTNPDCD 126
; 64 EEVCSKEARREVENDEPETYPRYQECMRKRGREKKNPDPKACVQNLDPDCTNPDCD 123
; 127 RKGTQACQDLKMGNFCTLCAAGNGRCLCDVNECSENGCCLOICNNKGSFHCCHSGF 186
; 124 KKGTHICQDLKMGNFCTDGMGGRCLCDVNECVCQNGKSCQVCHNKPSSFQACACHSG 183
; DB

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QY 187 ELASDGRTCODIDECADSEACGEARCKNLPSSYCLCEGFAVSQEKACBVDCECQGR 246
DB 184 SLASDGRTCODIDECTSDTCGDARCKNLPSSYCLCEGFAVSQEKETCQDVDECCQDR 243
QY 247 CEQVCNVSPPSYTCHCGRGGLKLSQDMTCEDILPCVPFSAVSXSVSLYGRMFSSTPV 306
DB 244 CEQVCNVSPPSYTCHCGRGGLKLSQDMTCEDILPCVPFSAVSXSVSLYGRMFSSTPV 303
QY 307 IRLRFKLOPRLVAEPFRTEDEGILLFAGCHODSTWYALRAGRLQLRYNGVR 366
DB 304 IRLRFKLOPRLVAEPFRTEDEGILLFAGCHODSTWYALRAGRLQLRYNGVR 363
QY 367 VTSSGPVNHGMQTTISVEELARNLVKVRNDAMKIAVAGDLFQPERGLYHNLTVGGI 426
DB 364 ITSSGPTNHGMQTTISVEELARNLVKVRNDAMKIAVAGDLFQPERGLYHNLTVGGI 423
QY 427 PFHEKDLVOPINPLDGCMSMNWLNCEDDTTIOETVKNVTRMOCFSYTERGSFPYSGGFA 486
DB 424 PFHEKDLVOPINPLDGCMSMNWLNCEDDTTIOETVKNVTRMOCFSYTERGSFPYSGGFA 483
QY 487 FYSLDVWRTPLDJGTESTWEVAVAHIRPADTGVFLAALAPDLRAVPLSVALVDYHSTK 546
DB 484 FYSLDVWRTPLDJGTESTWEVAVAHIRPADTGVFLAALAPDLRAVPLSVALVDYHSTK 541
QY 547 KKKQOLVLAHEHTALALMEIKVCDGQEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 606
DB 542 KKKQOLVLAHEHTALALMEIKVCDGQEHVTVSLRDEGATLEVDGTRGQSEVSAQLOE 601
QY 607 RLAVLEHRLSPVLTFAGSLPDVPVTSAPYAFYRGCMTELVNRLLDLDEAAKXSDIT 666
DB 602 RLAVLEHRLSPVLTFAGSLPDVPVTSAPYAFYRGCMTELVNRLLDLDEAAKXSDIT 661
QY 667 AHSCPEPEPA 676
DB 662 SHSCPEPEHA 671

RESULT 15
US-10-081-056-48
Publication 48, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanpelece
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P. Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
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PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/00000
PRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-081-056-48

Query Match 80.4%; Score 2955.5; DB 4; Length 673;
 Best Local Similarity 81.6%; Pred. No. 1.4e-233;
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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Db 484 TYRLNTRYTSLDVGERTTWEKVVARIRPAITDGVLLALVGD--DVIISVALVDYHSTK 541
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Db 662 SHSCPVEPA 671

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Search completed: June 29, 2006, 11:31:30
 Job time : 190 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:16:01 : Search time 51 Seconds
(without alignments)
1177.373 Million cell updates/sec

Title: US-10-671-054-1

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents PA:*
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3: /EMC_Celerra_SIDS3/prodata/2/1aa/7_COMB.pep:*
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7: /EMC_Celerra_SIDS3/prodata/2/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3628	98.7	678	1	US-08-282-141-2 Sequence 2, Appl1
2	3628	98.7	678	1	US-08-435-434-2 Sequence 2, Appl1
3	3628	98.7	678	1	US-08-435-436-2 Sequence 2, Appl1
4	3628	98.7	678	1	US-08-438-863-2 Sequence 2, Appl1
5	3628	98.7	678	1	US-08-438-864-2 Sequence 2, Appl1
6	3628	98.7	678	2	US-08-438-862-2 Sequence 2, Appl1
7	3628	98.7	678	2	US-08-402-253-2 Sequence 2, Appl1
8	3628	98.7	678	2	US-08-443-866B-2 Sequence 2, Appl1
9	3620	98.5	678	2	US-08-628-747-2 Sequence 2, Appl1
10	2955.5	80.4	673	1	US-08-282-141-3 Sequence 3, Appl1
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12	2955.5	80.4	673	1	US-08-435-436-1 Sequence 1, Appl1
13	2955.5	80.4	673	1	US-08-438-863-1 Sequence 1, Appl1
14	2955.5	80.4	673	1	US-08-438-864-1 Sequence 1, Appl1
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16	2955.5	80.4	673	2	US-08-402-253-1 Sequence 1, Appl1
17	2955.5	80.4	673	2	US-08-443-866B-1 Sequence 1, Appl1
18	2945.5	80.1	673	2	US-08-628-747-1 Sequence 1, Appl1
19	1547.5	42.1	676	1	US-08-282-141-4 Sequence 4, Appl1
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21	1543	42.0	676	1	US-08-435-436-3 Sequence 3, Appl1
22	1543	42.0	676	1	US-08-438-863-3 Sequence 3, Appl1
23	1543	42.0	676	1	US-08-438-864-3 Sequence 3, Appl1
24	1543	42.0	676	2	US-08-438-862-3 Sequence 3, Appl1
25	1543	42.0	676	2	US-08-402-253-3 Sequence 3, Appl1
26	1543	42.0	676	2	US-08-443-866B-3 Sequence 3, Appl1

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29	1510.5	41.1	635	1	US-07-985-691-2 Sequence 2, Appl1
30	1510.5	41.1	635	1	US-08-436-804-2 Sequence 2, Appl1
31	1510.5	41.1	635	1	US-08-267-387-2 Sequence 2, Appl1
32	1505	41.0	652	2	US-08-267-387-2 Patent No. 5258288
33	1413	38.4	675	7	5258288-1 Patent No. 5258288
34	358.5	9.8	997	2	US-09-747-371-3 Sequence 3, Appl1
35	354.5	9.6	1587	2	US-09-949-002-354 Sequence 354, App
36	353.5	9.6	1581	2	US-09-949-002-414 Sequence 414, App
37	352	9.6	1935	2	US-09-949-016-10403 Sequence 10403, A
38	352	9.6	2871	2	US-09-538-092-1076 Sequence 1076, Ap
39	345.5	9.4	999	2	US-09-747-371-2 Sequence 2, Appl1
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41	344.5	9.4	677	2	US-09-949-016-11370 Sequence 11370, A
42	344.5	9.4	677	2	US-09-949-016-11371 Sequence 11371, A
43	344.5	9.4	677	2	US-09-949-016-11372 Sequence 11372, A
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ALIGNMENTS

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RESULT 1
US-08-282-141-2
; Sequence 2, Application US/08282141
; Patent No. 5538861
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; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Guidalberto
; TITLE OF INVENTION: Stimulating factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-2

Query Match 98.7%; Score 3628; DB 1; Length 678;
Best Local Similarity 100.0%; Pred.No. 1.5e-309; Indels 0; Gaps 0;
Matches 678; Mismatches 0;
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DB 241 ECLQRCBCEVCVNSPGSYTCHDCGRGGLKLSQDMOTCEDILPCVPSVAKSVKSLYLGM 300
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DB 301 FSGTPVIRLRFKRLQPTRLVAEFDFRTFDPBGILLFAGGHODSTWIVLALRAGRLELQJR 360
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DB 361 YNGVRVTSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNL 420
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DB 481 PGSGFAFYSLDYMRTPLDVGTESTWEVEVAHIRPADTGVLFALMAPDLRAVPLSVALV 540
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DB 661 KXSDITAHSCPVEPAAA 678

RESULT 2
US-08-435-434-2
; Sequence 2, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000

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; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-2

Query Match      98.7%; Score 3628; DB 1; Length 678;
Best Local Similarity 100.0%; Pred.No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 361 YNGVRVTSSGPIVNHGMQTTISVEELANLVIKVRDAVMKIAVAGDLFOPERGLYHNL 420
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DB 541 DYHSTYKLLKKOLVLAVEHTALAMEIKVCDQGEHVTVSLRDGEATLEVDGTRGSEVS 600
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RESULT 3
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; Sequence 2, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jjian

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Db      601  AAQOLERLAVLERHLSPLVTFAGGLPDVPTVSAPTAFYRGCMTEVNRRLLDDEAY 660
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RESULT 5
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; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:

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; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929P1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/225-1994
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-864-2

Query Match      98.7%; Score 3628; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  LRECEVBEICSRFEAREVEFENDPETDYPRYLDCINKKGSFYTKNSGFATCVQNLPDQC 120
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Db      121  TPNPCDRKGTQACODLMGNFCLCKAGMGRLCDKDVNCSQENGGCLOICNKGSPFC 180
Qy      181  SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLDCBGFAYSSQEKACRDVD 240
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Db      241  ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSYLYLGM 300
Qy      241  ECLQRCCEQVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSVKSYLYLGM 300
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Db      301  FSGTFVIRLRFKRLQPTRLVAEFDFTPDPEGILLFAGGHQDSTWIVLALRAGRLELQJR 360
Qy      361  YNGVGRVITSSGPVINGHMWQTTISVEELANLVIKVNRDAVMKIAVAGDLFOBERGLYHIN 420
Db      361  YNGVGRVITSSGPVINGHMWQTTISVEELANLVIKVNRDAVMKIAVAGDLFOBERGLYHIN 420
Qy      421  LTVGGIPFHEKDLVOPINRLDGCMSNMWLNGBDITTOETVKVNTRMOCFSVTERGSPY 480
Db      421  LTVGGIPFHEKDLVOPINRLDGCMSNMWLNGBDITTOETVKVNTRMOCFSVTERGSPY 480
Qy      481  PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY 540
Db      481  PGSGFAFYSLDYMRTPLDVGTSTWEVEVAHIRPAADTGVLFALMAPDLRAVPLSVALY 540
Qy      541  DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTRGSEVS 600
Db      541  DYHSTKCLKKQVLVAVEHTALALMEIKVCDQGEHVTVSLRDGEATLEVDGTRGSEVS 600
Qy      601  AAQOLERLAVLERHLSPLVTFAGGLPDVPTVSAPTAFYRGCMTEVNRRLLDDEAY 660
Db      601  AAQOLERLAVLERHLSPLVTFAGGLPDVPTVSAPTAFYRGCMTEVNRRLLDDEAY 660
Qy      661  KHSIDITAHSCPVEPAAA 678
Db      661  KHSIDITAHSCPVEPAAA 678

RESULT 6
US-08-438-862-2
; Sequence 2, Application US/08438862
; Patent No. 6033660
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.

```

```

APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-2

```

```

Query Match      98.7%; Score 3628; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAPSLSPGPAALRRARAPOLLLLLLAACALAAALPAREATOPLRPRORRAFOVFEBAKQGH 60
DB 1 MAPSLSPGPAALRRARAPOLLLLLLAACALAAALPAREATOPLRPRORRAFOVFEBAKQGH 60
QY 61 LERECVEELCSREAREVEFENDEPETYFYPRYLDICINKYGSPTYKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSREAREVEFENDEPETYFYPRYLDICINKYGSPTYKNSGFATCVQNLPDQC 120
QY 121 TNPQCDKRGKTOACODLGNPFCLCKAGWGRLCDKVNNECSQENGCLOICHNKPSFHC 180
DB 121 TNPQCDKRGKTOACODLGNPFCLCKAGWGRLCDKVNNECSQENGCLOICHNKPSFHC 180
QY 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQKACRDYD 240
DB 181 SCHSGFELSSDGRTCODIDECADSEACGEARCKNLPGSYSCLCDEGFAYSSQKACRDYD 240
QY 241 ECLQGRCEOVCVNPSSTYCHCDGRGGLKLSQDMTCEDTLPCVPSVAKSXYLYLGNM 300
DB 241 ECLQGRCEOVCVNPSSTYCHCDGRGGLKLSQDMTCEDTLPCVPSVAKSXYLYLGNM 300
QY 301 FSGTPYIRLRFKRLQOTRLVAEPDFTPDPEGILLFAGGHODSTWLVLAIRAGRLQIR 360
DB 301 FSGTPYIRLRFKRLQOTRLVAEPDFTPDPEGILLFAGGHODSTWLVLAIRAGRLQIR 360
QY 361 YNGVGVTSSTGPIYNGMQTISVEELANLVIKVRDAMVKIAVAGDLFOPERGLYHNL 420
DB 361 YNGVGVTSSTGPIYNGMQTISVEELANLVIKVRDAMVKIAVAGDLFOPERGLYHNL 420
QY 421 LTVGGIPFHEKDLVQINRPLDGCMSNMWLNCEDETTIOETVKNTRMOCFSVTERGSFY 480
DB 421 LTVGGIPFHEKDLVQINRPLDGCMSNMWLNCEDETTIOETVKNTRMOCFSVTERGSFY 480

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```

QY 481 PGSGFARYSLDYMRTPLDVGSTWEVEVVAHTRPADTGVLFAALMAPDLRAVPLSVALLY 540
DB 481 PGSGFARYSLDYMRTPLDVGSTWEVEVVAHTRPADTGVLFAALMAPDLRAVPLSVALLY 540
QY 541 DYSTKKLKKQVLVAEHTALALMEIKVCDGQSHVTVSLRDEATLEVDGTGQSEVS 600
DB 541 DYSTKKLKKQVLVAEHTALALMEIKVCDGQSHVTVSLRDEATLEVDGTGQSEVS 600
QY 601 AAQLOERLAVLERLRSPLVTFAGGLPDVPTSAPVTAFFRGCKTLEVNRLDLDEAY 660
DB 601 AAQLOERLAVLERLRSPLVTFAGGLPDVPTSAPVTAFFRGCKTLEVNRLDLDEAY 660
QY 661 KHSDIATHSCPPVEPAAA 678
DB 661 KHSDIATHSCPPVEPAAA 678

```

```

RESULT 7
US-08-402-253-2

```

```

Sequence 2, Application US/08402253
Patent No. 6211142
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammond, R. Glenn
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,253
FILING DATE: 10-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-402-253-2

```

```

Query Match      98.7%; Score 3628; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 MAPSLSPGPAALRRARAPOLLLLLLAACALAAALPAREATOPLRPRORRAFOVFEBAKQGH 60
DB 1 MAPSLSPGPAALRRARAPOLLLLLLAACALAAALPAREATOPLRPRORRAFOVFEBAKQGH 60
QY 61 LERECVEELCSREAREVEFENDEPETYFYPRYLDICINKYGSPTYKNSGFATCVQNLPDQC 120
DB 61 LERECVEELCSREAREVEFENDEPETYFYPRYLDICINKYGSPTYKNSGFATCVQNLPDQC 120

```

```

Db      61 LERECVEELCSREAREVEFENDPETYFYPRYLDCLINKGSPYTKNSGFATCVQNLPPDC 120
Qy      121 TPNPCDRKGTQACODLMGNFCLCAKMGRLCDXVNECSQENGGCLOI CHNKGSPHC 180
Db      121 TPNPCDRKGTQACODLMGNFCLCAKMGRLCDXVNECSQENGGCLOI CHNKGSPHC 180
Qy      181 SCHSGFELSSDRTCODIDECADSEACGEARKNLPGSYSLCDEGFAVSQEKACRDVD 240
Db      181 SCHSGFELSSDRTCODIDECADSEACGEARKNLPGSYSLCDEGFAVSQEKACRDVD 240
Qy      241 ECLQRCCEOVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSYKSLYLGM 300
Db      241 ECLQRCCEOVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSYKSLYLGM 300
Qy      301 FSGTVIRLRFKRLQPTRLVAEFDRTPDPBEGILLFAGHODSTWVIALRAGRLEQLR 360
Db      301 FSGTVIRLRFKRLQPTRLVAEFDRTPDPBEGILLFAGHODSTWVIALRAGRLEQLR 360
Qy      361 YNGVRVTSSSGPIVNHGMQTI SVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Db      361 YNGVRVTSSSGPIVNHGMQTI SVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Qy      421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWLNGBDITTIQETVKVNTRMOCFSVTERGSFY 480
Db      421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWLNGBDITTIQETVKVNTRMOCFSVTERGSFY 480
Qy      481 PGSGFAFSLDYMRTPLDVGSTEWEEVVAHIRPAADGVLFALMAPDLRAVPLSVALLY 540
Db      481 PGSGFAFSLDYMRTPLDVGSTEWEEVVAHIRPAADGVLFALMAPDLRAVPLSVALLY 540
Qy      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLDGEATLEVDGTRGSEVS 600
Db      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLDGEATLEVDGTRGSEVS 600
Qy      601 AAQOLERLAVLERHLRSPVLTTFAGGLPDVPTSAPTYAFYRGCMTELVNRLLDLDEAAY 660
Db      601 AAQOLERLAVLERHLRSPVLTTFAGGLPDVPTSAPTYAFYRGCMTELVNRLLDLDEAAY 660
Qy      661 KHSIDTAHSCPVEPAAA 678
Db      661 KHSIDTAHSCPVEPAAA 678

```

RESULT 8

US-08-443-866B-2

Sequence 2, Application US/08443866B

Patent No. 6255068

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Hammonds, R. Glenn

APPLICANT: Mark, Melanie R.

TITLE OF INVENTION: RSE RECEPTOR ACTIVATION

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/443,866B

FILING DATE: 31-May-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/402253

FILING DATE: 10-MAR-1995

ATTORNEY/AGENT INFORMATION:

```

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0929D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-443-866B-2

Query Match      98.7%; Score 3628; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.5e-309;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAPSLPGPALRRAPOLLILLLAAECALALPPAREATQFLRPRORAFQVFEAKQGH 60
Db      1 MAPSLPGPALRRAPOLLILLLAAECALALPPAREATQFLRPRORAFQVFEAKQGH 60
Qy      61 LERECVEELCSREAREVEFENDPETYFYPRYLDCLINKGSPYTKNSGFATCVQNLPPDC 120
Db      61 LERECVEELCSREAREVEFENDPETYFYPRYLDCLINKGSPYTKNSGFATCVQNLPPDC 120
Qy      121 TPNPCDRKGTQACODLMGNFCLCAKMGRLCDXVNECSQENGGCLOI CHNKGSPHC 180
Db      121 TPNPCDRKGTQACODLMGNFCLCAKMGRLCDXVNECSQENGGCLOI CHNKGSPHC 180
Qy      181 SCHSGFELSSDRTCODIDECADSEACGEARKNLPGSYSLCDEGFAVSQEKACRDVD 240
Db      181 SCHSGFELSSDRTCODIDECADSEACGEARKNLPGSYSLCDEGFAVSQEKACRDVD 240
Qy      241 ECLQRCCEOVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSYKSLYLGM 300
Db      241 ECLQRCCEOVCVNSPGSYTCHCDGRGGLKLSQDMTCEDILPCVPSVAKSYKSLYLGM 300
Qy      301 FSGTVIRLRFKRLQPTRLVAEFDRTPDPBEGILLFAGHODSTWVIALRAGRLEQLR 360
Db      301 FSGTVIRLRFKRLQPTRLVAEFDRTPDPBEGILLFAGHODSTWVIALRAGRLEQLR 360
Qy      361 YNGVRVTSSSGPIVNHGMQTI SVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Db      361 YNGVRVTSSSGPIVNHGMQTI SVEELARNLVIKVRDAVMKIAVAGDLFOBERGLYHLN 420
Qy      421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWLNGBDITTIQETVKVNTRMOCFSVTERGSFY 480
Db      421 LTVGGIPFHEKDLVOPINRDLGCKRSNMWLNGBDITTIQETVKVNTRMOCFSVTERGSFY 480
Qy      481 PGSGFAFSLDYMRTPLDVGSTEWEEVVAHIRPAADGVLFALMAPDLRAVPLSVALLY 540
Db      481 PGSGFAFSLDYMRTPLDVGSTEWEEVVAHIRPAADGVLFALMAPDLRAVPLSVALLY 540
Qy      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLDGEATLEVDGTRGSEVS 600
Db      541 DYHSTKCLKKQOLVLAVENTALALMEIKVCDGQEHVTVSLDGEATLEVDGTRGSEVS 600
Qy      601 AAQOLERLAVLERHLRSPVLTTFAGGLPDVPTSAPTYAFYRGCMTELVNRLLDLDEAAY 660
Db      601 AAQOLERLAVLERHLRSPVLTTFAGGLPDVPTSAPTYAFYRGCMTELVNRLLDLDEAAY 660
Qy      661 KHSIDTAHSCPVEPAAA 678
Db      661 KHSIDTAHSCPVEPAAA 678

```

RESULT 9

US-08-628-747-2

Sequence 2, Application US/08628747

Patent No. 6169070

GENERAL INFORMATION:

APPLICANT: Chen, Jian

APPLICANT: Godowski, Paul J.
 APPLICANT: Hammond, R. Glenn
 APPLICANT: Mark, Melanie
 APPLICANT: Mather, Jennie P.
 APPLICANT: Li, Ronghao
 TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: One DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/628,747
 FILING DATE: 17-APR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/402,253
 FILING DATE: 10-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/438,861
 FILING DATE: 10-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 00,000
 REFERENCE/DOCKET NUMBER: P929P2PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-225-1994
 TELEFAX: 650-952-9881
 TELEX: 910-371-7168
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 678 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-628-747-2

Query Match 98.5%; Score 3620; DB 2; Length 678;
 Best Local Similarity 99.9%; Pred. No. 7.8e-309;
 Matches 677; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MAPSLSPGPAALRRAPQLLLLLAECALAAALPAREATQFLPRORARFOVEEAKQGH 60
 1 MAPSLSPGPAALRRAPQLLLLLAECALAAALPAREATQFLPRORARFOVEEAKQGH 60
 61 LERECEVEELCSREAREVEFENDEPETYFYPRYLDCINKYSGPYTKNSGFATCVQNLPPDC 120
 61 LERECEVEELCSREAREVEFENDEPETYFYPRYLDCINKYSGPYTKNSGFATCVQNLPPDC 120
 121 TTPPCDCKRGTOAQCDLGNFCLCKAGWGRLCDKDVNCSQENGGLQIHNKPGSFGHC 180
 121 TTPPCDCKRGTOAQCDLGNFCLCKAGWGRLCDKDVNCSQENGGLQIHNKPGSFGHC 180
 121 TTPPCDCKRGTOAQCDLGNFCLCKAGWGRLCDKDVNCSQENGGLQIHNKPGSFGHC 180
 181 SCHSGFELSDGRTCODIDECADSEACGEARCKNLGSGVSCLEDGFAVSSQKACARDV 240
 181 SCHSGFELSDGRTCODIDECADSEACGEARCKNLGSGVSCLEDGFAVSSQKACARDV 240
 241 ECLQGCCEQVCVNSPGSYTCHCDGRGLKLSQMDTCEBILPCVPSPVAHSVSLYIGRM 300
 241 ECLQGCCEQVCVNSPGSYTCHCDGRGLKLSQMDTCEBILPCVPSPVAHSVSLYIGRM 300
 301 FSGTPIVIRLRFKRLQTRIVAEFDFRTDEBEGILLPAGGHQDSTWIVLAIARGLQLQR 360
 301 FSGTPIVIRLRFKRLQTRIVAEFDFRTDEBEGILLPAGGHQDSTWIVLAIARGLQLQR 360

361 YNGVGRVTSVSGPVINHGMMQRTISVEBLARNLVIKVNDAYVKIYVAGDLFQPERGLYHN 420
 361 YNGVGRVTSVSGPVINHGMMQRTISVEBLARNLVIKVNDAYVKIYVAGDLFQPERGLYHN 420
 421 LTVGIPFHEKDLVQPINPRLDGCRSMNMGEDDTTIOETVKVNTMQCSYTERGSFY 480
 421 LTVGIPFHEKDLVQPINPRLDGCRSMNMGEDDTTIOETVKVNTMQCSYTERGSFY 480
 481 PGSGFAFYSUDYMTPTLDVGSTWEEVYVAHIPPADTGVLFALMAPDLRAVPLSVLV 540
 481 PGSGFAFYSUDYMTPTLDVGSTWEEVYVAHIPPADTGVLFALMAPDLRAVPLSVLV 540
 541 DYHSTKLLKQVLAVEHTALAMEIKVCGOEHVTVSLRDEATLLEVNGTRGQSEVS 600
 541 DYHSTKLLKQVLAVEHTALAMEIKVCGOEHVTVSLRDEATLLEVNGTRGQSEVS 600
 601 AAQLQERLAVLERHLSRSPVLTFAAGLPDVPVTSAPVTAFFRGCTLEVNRLDLDEAY 660
 601 AAQLQERLAVLERHLSRSPVLTFAAGLPDVPVTSAPVTAFFRGCTLEVNRLDLDEAY 660
 661 KHSDTIHNSCPVEPPAAA 678
 661 KHSDTIHNSCPVEPPAAA 678

RESULT 10
 US-08-282-141-3
 Sequence 3, Application US/08282141
 Patent No. 5538861
 GENERAL INFORMATION:
 APPLICANT: Schneider, Claudio
 APPLICANT: Varnum, Brian
 APPLICANT: Avanzi, Giancarlo
 APPLICANT: Branchini, Claudio
 APPLICANT: Manfioletti, Guido
 TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amgen Inc.
 STREET: 1840 Dehavenland Drive
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: United States
 ZIP: 91320-1789
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/282,141
 FILING DATE:
 CLASSIFICATION: 435
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-282-141-3

Query Match 80.4%; Score 2955.5; DB 1; Length 673;
 Best Local Similarity 81.6%; Pred. No. 1.7e-250;
 Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

7 PGPAALRRAPQLLLLLAECALAAALPAREATQFLPRORARFOVEEAKQGHLEBEV 66
 5 PGPAALRRAPQLLLLLAECALAAALPAREATQFLPRORARFOVEEAKQGHLEBEV 63
 67 EELCSREAREVEFENDEPETYFYPRYLDCINKYSGPYTKNSGFATCVQNLPPDC 126
 EELCSREAREVEFENDEPETYFYPRYLDCINKYSGPYTKNSGFATCVQNLPPDC 126


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Db      64  BEVCSKEARBEVFNDEPTEYFYPRYOBCMRKYGRPEEKNPDFAVCQNLDPQCTPNPCD 123
QY      127  RKGTQACODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 186
Db      124  KKGTHICODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 183
QY      187  ELSSDGRFCODIDECADSEACGEARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGR 246
Db      184  SLASDGQTCODIDECADSEACGEARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGR 243
QY      247  CEQVCVNSPGSYTCHCDGRGGLKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGTPV 306
Db      244  CEQVCVNSPGSYTCHCDGRGGLKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGTPV 303
QY      307  IRLRFRLOPTRLVAFDFRTPDPBGILLFAGGHODSTWIVLALAGRLLEQLRNGVGR 366
Db      304  IRLRFRLOPTRLVAFDFRTPDPBGILLFAGGHODSTWIVLALAGRLLEQLRNGVGR 363
QY      367  VTSSEPVINHGMQOTISVEELARNLVIKNRDAVKKIAVAGDLFQPERGLYHLNTLVGGI 426
Db      364  ITSSGPTINHGMQOTISVEELARNLVIKNRDAVKKIAVAGDLFQPERGLYHLNTLVGGI 423
QY      427  PFHEKDLVOPINPRLDGCKRSWNLNGEDTTIOETVKVNTRMQCFSVTERGSFPBGSGRA 486
Db      424  PFHEKDLVOPINPRLDGCKRSWNLNGEDTTIOETVKVNTRMQCFSVTERGSFPBGSGRA 483
QY      487  FYSLDYMRTPLDVGESTWEVVAHIRPAADTGVLFALMAPDLRAVPLSVALVDYHSTRK 546
Db      484  TYRLNTRTSLDVGESTWEVVAHIRPAADTGVLFALMAPDLRAVPLSVALVDYHSTRK 541
QY      547  KKKKQVLVAVENTALALMEIKVCDQOEHVTVSLRDGEATLEVDGTRQSEVSAALQOE 606
Db      542  KKKKQVLVAVENTALALMEIKVCDQOEHVTVSLRDGEATLEVDGTRQSEVSAALQOE 601
QY      607  RLAVLERHLSFVLPFAGGLPDVPTSAVTAFFYRCMTELVNRRLLDDEAAYKXSDIT 666
Db      602  RLAVLERHLSFVLPFAGGLPDVPTSAVTAFFYRCMTELVNRRLLDDEAAYKXSDIT 661
QY      667  AHSCEPVEPA 676
Db      662  SHSCPEVEHA 671

RESULT 11
US-08-435-434-1
; Sequence 1, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-1

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY      7  PGPALRRAAPOLLILLILALAECAALALPAREATQFLRPRORARFQVFEAKQHLRECEV 66
Db      5  PGPAL-ALGTALLILLILASSESHVTLARAREAQFLRPRORARFQVFEAKQHLRECEV 63
QY      67  BEVCSKEARBEVFNDEPTEYFYPRYOBCMRKYGRPEEKNPDFAVCQNLDPQCTPNPCD 126
Db      64  BEVCSKEARBEVFNDEPTEYFYPRYOBCMRKYGRPEEKNPDFAVCQNLDPQCTPNPCD 123
QY      127  RKGTQACODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 186
Db      124  KKGTHICODLMGNFCLCKAGNGRLCDKDVNECSQENGGCLQICHNKGSHGCHSGF 183
QY      187  ELSSDGRFCODIDECADSEACGEARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGR 246
Db      184  SLASDGQTCODIDECADSEACGEARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGR 243
QY      247  CEQVCVNSPGSYTCHCDGRGGLKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGTPV 306
Db      244  CEQVCVNSPGSYTCHCDGRGGLKLSQDMDTCEDIIPCVPFSAKSVKSLYLGRMFSGTPV 303
QY      307  IRLRFRLOPTRLVAFDFRTPDPBGILLFAGGHODSTWIVLALAGRLLEQLRNGVGR 366
Db      304  IRLRFRLOPTRLVAFDFRTPDPBGILLFAGGHODSTWIVLALAGRLLEQLRNGVGR 363
QY      367  VTSSEPVINHGMQOTISVEELARNLVIKNRDAVKKIAVAGDLFQPERGLYHLNTLVGGI 426
Db      364  ITSSGPTINHGMQOTISVEELARNLVIKNRDAVKKIAVAGDLFQPERGLYHLNTLVGGI 423
QY      427  PFHEKDLVOPINPRLDGCKRSWNLNGEDTTIOETVKVNTRMQCFSVTERGSFPBGSGRA 486
Db      424  PFHEKDLVOPINPRLDGCKRSWNLNGEDTTIOETVKVNTRMQCFSVTERGSFPBGSGRA 483
QY      487  FYSLDYMRTPLDVGESTWEVVAHIRPAADTGVLFALMAPDLRAVPLSVALVDYHSTRK 546
Db      484  TYRLNTRTSLDVGESTWEVVAHIRPAADTGVLFALMAPDLRAVPLSVALVDYHSTRK 541
QY      547  KKKKQVLVAVENTALALMEIKVCDQOEHVTVSLRDGEATLEVDGTRQSEVSAALQOE 606
Db      542  KKKKQVLVAVENTALALMEIKVCDQOEHVTVSLRDGEATLEVDGTRQSEVSAALQOE 601
QY      607  RLAVLERHLSFVLPFAGGLPDVPTSAVTAFFYRCMTELVNRRLLDDEAAYKXSDIT 666
Db      602  RLAVLERHLSFVLPFAGGLPDVPTSAVTAFFYRCMTELVNRRLLDDEAAYKXSDIT 661
QY      667  AHSCEPVEPA 676
Db      662  SHSCPEVEHA 671

RESULT 12
US-08-435-436-1
; Sequence 1, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.

```



```

APPLICANT: Li, Ronghao
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-436-1

```

```

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

```

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QY 7 PGPAA-ALGTALLLLLSSESHYVLLRRAEAQFLRPRORAYOVFEBAKQGHLEBECV 66
DB 5 PGPAA-ALGTALLLLLSSESHYVLLRRAEAQFLRPRORAYOVFEBAKQGHLEBECV 63
QY 67 EELCSREAREVENDPETDYFYPRLDCLNKYSGPYTNSGFATCVQNLPOQCTPNPCD 126
DB 64 EEVCSKEAREVENDPETEYFYPRYOECMRKYGRPEEKNPDAKCVQNLPOQCTPNPCD 123
QY 127 RKGTAQCOLMGNFCLCKAGNGRLCDVNECSQENGGCLQICNNKSGSPFCSCHSQF 186
DB 124 KKGTHICOLMGNFCLCKAGNGRLCDVNECSQENGGCLQICNNKSGSPFCSCHSQF 183
QY 187 ELSDGRTQODIDECADSEACGEARCKNPGSYSCLEDGFAYSQEKACRDVDECLQGR 246
DB 184 SLASDQGTQODIDECADSEACGEARCKNPGSYSCLEDGFAYSQEKACRDVDECLQGR 243
QY 247 CEQVCNPSGSGYTCCHDGRGGLKLSQMDTCEDLIPCVFSPVAKSYKSLYLGMFSGTPV 306
DB 244 CEQVCNPSGSGYTCCHDGRGGLKLSQMDTCEDLIPCVFSPVAKSYKSLYLGMFSGTPV 303
QY 307 ILRFRPRLQPTLVAFEDFRTDPBGLILFAGHDSSTIVLALRAGRIELQLRNNGVR 366
DB 304 ILRFRPRLQPTLVAFEDFRTDPBGLILFAGHDSSTIVLALRAGRIELQLRNNGVR 363
QY 367 VTSSEPVINHGMMQITISVELARNLVIKYNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 426
DB 364 ITSSGPTINHGMMQITISVELARNLVIKYNRDAVMKIAVAGDLFQPERGLYHLNLTVGSI 423
QY 427 PHEKDLVQPIPRLDGCKRSMWMLNGEPTTIOETVYKVTNMOCSFVTERGSPFPGSGFA 486
DB 424 PKKESLQVQPIPRLDGCKRSMWMLNGEPTTIOETVYKVTNMOCSFVTERGSPFPGSGFA 483

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QY 487 FVSLDWMRTPLDVGSTSEWEVVAHTRPADGVLFAIMAPDLRAVPLSAIVDYHSTK 546
DB 484 TYRLNTRYISLDVGSTSEWEVVAHTRPADGVLFAIMAPDLRAVPLSAIVDYHSTK 541
QY 547 KKKQOLVLAVENTALAMEIKVCDGQEHVVTSLRDEATLEVDGTRGQSEVSAQLOE 606
DB 542 KKKQOLVLAVENTALAMEIKVCDGQEHVVTSLRDEATLEVDGTRGQSEVSAQLOE 601
QY 607 RLAVLERHLSRSPVLTGAGLPDVVPTSAPTYAFYRGCTLEVNRRLLDLDEAAVKSQIT 666
DB 602 RLDTLKTGHQSGVHTVYGLPEVSVISAPVAFYRGCTLEVNRRLLDLDEAAVKSQIT 661
QY 667 AHSCPPVEPA 676
DB 662 SHSCPPVEHA 671

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RESULT 13

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US-08-438-863-1
Sequence 1, Application US/08438863
Patent No. 5849585

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GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,863
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

```

```

REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168

```

```

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-863-1

```

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Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

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```

QY 7 PGPAA-ALGTALLLLLSSESHYVLLRRAEAQFLRPRORAYOVFEBAKQGHLEBECV 66
DB 5 PGPAA-ALGTALLLLLSSESHYVLLRRAEAQFLRPRORAYOVFEBAKQGHLEBECV 63
QY 67 EELCSREAREVENDPETDYFYPRLDCLNKYSGPYTNSGFATCVQNLPOQCTPNPCD 126
DB 64 EEVCSKEAREVENDPETEYFYPRYOECMRKYGRPEEKNPDAKCVQNLPOQCTPNPCD 123

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QY 127 RKGTOACODLMGNFCLCKAGGRLCDKDVNECSQENGGCLQICHNRPSTHSCCHSGF 186
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 KKGTHICODLMGNFCTLDGGRGLCDKDVNECVQXKNGCSQVCHNRPSTQCACHSGF 183
QY 187 ELSSDRTCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVDECLQGR 246
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 184 SLASDQTCODIDECTSDTCGDARCKNLPSSYSLCDEGYTSSKEKTCQDVDECCQDR 243
QY 247 CEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRMFSGPV 306
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 244 CEQTCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSMAKSVKSLYLGRMFSGPV 303
QY 307 IRLRFRLOPTRLVAEFPFRTPDPBGILLFAGHODSTMIVATLRAGRLEQLRYNGVR 366
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 304 IRLRFRLOPTRLVAEFPFRTPDPBGILLFAGHODSTMIVATLRAGRLEQLRYNGVR 363
QY 367 VTSSEPTINHGMMQITISVEELARNLVYKVRDANKIAVAGDLFQPERGLYHNLTVGGI 426
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 364 ITSSGPTINHGMMQITISVEELARNLVYKVRDANKIAVAGDLFQPERGLYHNLTVGGI 423
QY 427 PFHEKDLVOPINRDLGCKRSNMWLNGBEDTTIOETVKVNTMOCFSVTERGSPYSGGFA 486
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 424 PFKESELVOPINRDLGCKRSNMWLNGBEDSAIOETVKANTKMOCFSVTERGSPFGNGFA 483
QY 487 FYSLDYMRTPLDVGESTSTEVEVVAHIRPAADTVGLFALMAADLRAVPLSVALLVDYHSRK 546
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 484 TYRLNTRYTSLDVGESTSTEVEVVAHIRPATDTGILLALVGD--DVIVSVALVDYHSRK 541
QY 547 KKKKOLVLAVENTALALMEIKVCDGQEHVVTSLRDEGATLEVDTRGQSEVSAALOQ 606
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 542 KKKKOLVLAVENTALALMEIKVCDGQEHVVTSLRDEGATLEVDTRGQSEVSAALOQ 601
QY 607 RLAVLERHLRSPVLTFFAGGLPDVPTVSAPVTAFFRCGMLTVNRRLLIDEAAYKSDIT 666
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 602 RLDTLKLTHLGQSVHTVVGGLPEVSVISAPVTAFFRCGMLTVNRRLLIDEAAYKSDIT 661
QY 667 AHSCEPVEPA 676
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 662 SHSCPVEHA 671
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-08-438-864-1
; Sequence 1, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253

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; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929P1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-864-1

Query Match      80.4%; Score 2955.5; DB 1; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

QY 7 PGPALRRAPQLLLLLAABCALAALLPARENTOPFLRPRORRAFOVFEAKQHLRECV 66
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 PGPAA-ALGTALLLLSSSHVLLRAREAPQFLRPRORRAVYFEAKQHLRECV 63
QY 67 EELCSREAREVEFENDPEPTYDYFPRVYLDICINKYGSPTYKNSGFATCVONLPDQCTPNPCD 126
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 EEVCSKEAREVEFENDPEPTYDYFPRVYLDICINKYGSPTYKNSGFATCVONLPDQCTPNPCD 123
QY 127 RKGTOACODLMGNFCLCKAGGRLCDKDVNECSQENGGCLQICHNRPSTHSCCHSGF 186
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Db 124 KKGTHICODLMGNFCTLDGGRGLCDKDVNECVQXKNGCSQVCHNRPSTQCACHSGF 183
QY 187 ELSSDRTCODIDECADSEACGEARCKNLPSSYSLCDEGFAYSSQEKACRDVDECLQGR 246
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 184 SLASDQTCODIDECTSDTCGDARCKNLPSSYSLCDEGYTSSKEKTCQDVDECCQDR 243
QY 247 CEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSVAKSVKSLYLGRMFSGPV 306
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Db 244 CEQTCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFSMAKSVKSLYLGRMFSGPV 303
QY 307 IRLRFRLOPTRLVAEFPFRTPDPBGILLFAGHODSTMIVATLRAGRLEQLRYNGVR 366
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Db 304 IRLRFRLOPTRLVAEFPFRTPDPBGILLFAGHODSTMIVATLRAGRLEQLRYNGVR 363
QY 367 VTSSEPTINHGMMQITISVEELARNLVYKVRDANKIAVAGDLFQPERGLYHNLTVGGI 426
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 364 ITSSGPTINHGMMQITISVEELARNLVYKVRDANKIAVAGDLFQPERGLYHNLTVGGI 423
QY 427 PFHEKDLVOPINRDLGCKRSNMWLNGBEDTTIOETVKVNTMOCFSVTERGSPYSGGFA 486
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Db 424 PFKESELVOPINRDLGCKRSNMWLNGBEDSAIOETVKANTKMOCFSVTERGSPFGNGFA 483
QY 487 FYSLDYMRTPLDVGESTSTEVEVVAHIRPAADTVGLFALMAADLRAVPLSVALLVDYHSRK 546
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 484 TYRLNTRYTSLDVGESTSTEVEVVAHIRPATDTGILLALVGD--DVIVSVALVDYHSRK 541
QY 547 KKKKOLVLAVENTALALMEIKVCDGQEHVVTSLRDEGATLEVDTRGQSEVSAALOQ 606
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 542 KKKKOLVLAVENTALALMEIKVCDGQEHVVTSLRDEGATLEVDTRGQSEVSAALOQ 601
QY 607 RLAVLERHLRSPVLTFFAGGLPDVPTVSAPVTAFFRCGMLTVNRRLLIDEAAYKSDIT 666
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Db 602 RLDTLKLTHLGQSVHTVVGGLPEVSVISAPVTAFFRCGMLTVNRRLLIDEAAYKSDIT 661
QY 667 AHSCEPVEPA 676
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 662 SHSCPVEHA 671
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
US-08-438-862-1
; Sequence 1, Application US/08438862
; Patent No. 6033660

```

```

GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: pacin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-1

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Query Match      80.4%; Score 2955.5; DB 2; Length 673;
Best Local Similarity 81.6%; Pred. No. 1.7e-250;
Matches 547; Conservative 45; Mismatches 75; Indels 3; Gaps 2;

Qy 7 PGPALRRAPQULLLLAALALPAREATOPLRPRORARFOVPEAKOGHLEBECV 66
Db 5 PGPAA-ALGTALLLLASBSHTVLRAREAAQFLPRORARVOVPEAKOGHLEBECV 63
Qy 67 BELCSREAREVENDEPETDYFYPRYLDCINKYGSPTTKNSGFATCVQNLPDCTPNPCD 126
Db 64 EEVCSKEAREVENDEPETDYFYPRYQECMRKXGRPEKRPDPKACVQNLPDCTPNPCD 123
Qy 127 RKGTQACODLMGNFCLCAAGWGRILCDKDVNCSQENGGCLQICHNKPGSPHCSCHSGF 186
Db 124 KKGTHICODLMGNFCLCAAGWGRILCDKDVNCSQENGGCLQICHNKPGSPHCSCHSGF 183
Qy 187 ELSSDRTCODIDECADSEACGEARKNPGSYSCLDSEFAYSOAKACRDVDECLQGR 246
Db 184 SLASDQOTCODIDECADSEACGEARKNPGSYSCLDSEGYTSSKEXTQDVDECOQDR 243
Qy 247 CEQVCNPSGYSYCHCDGRGGLKLSQDMTCEDILPCVPPSVAKSVKSLYLGRMFSSTPV 306
Db 244 CEQTCVNSPGSYCHCDGRGGLKLSQDMTCEDILPCVPPSVAKSVKSLYLGRMFSSTPV 303
Qy 307 IRLRFRLQPTRLVAFFDRTPDEGILLPAGSHQDSTWIVLALRAGRLLEQLRYNGVR 366
Db 304 IRLRFRLQPTRLVAFFDRTPDEGILLPAGSHQDSTWIVLALRAGRLLEQLRYNGVR 363
Qy 367 VTSSEGVINHGMMQTSVELEARNLYIKNRDAVMKIAVAGLFOPERGILYHNLTVGGI 426
Db 364 ITSSGPTINHGMQTSVELEARNLYIKNRDAVMKIAVAGLFOPERGILYHNLTVGGI 423
Qy 427 PFHEKDLVQPINRDLDCMRSMNWLNGEDTTIOETVKVNTRMQCFVTERGSPYPSGFA 486

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Db 424 PFKESELVQPINRDLDCMRSMNWLNGEDSAIQETVKANTMKGCFVTERGSPFGNGFA 483
Qy 487 FYSLDYMRTPLDVGTSTESTWEYVVAHIRPAADTVLFALNAPDLRAVPLSVALVDYHSTK 546
Db 484 TYRLNTRYTSIDVGTETWEVKVARIIRPATDGLVLLALVDD--DVVISVALVDYHSTK 541
Qy 547 KLKKQVLVLAVEHTALAMEIKVCDGQEHVTVSLRDEGATLEVDGTRGSEVSAAOLOE 606
Db 542 KLKKQVLVLAVEDVALAMEIKVCDSEHTVTVSLRDEGATLEVDGTRGSEVSAAOLOE 601
Qy 607 RLAVLERHLRSPVLTFAAGLPDVYVTSAPYTAFFRGCMTELVNRLDLDEAAVYKSHDIT 666
Db 602 RLDTLKTHLGSSVHTYVGLPEVSVISAPYTAFFRGCMTELVNKGKIIDLDTASTYKSHDIT 661
Qy 667 AHSCEPVEPA 676
Db 662 SHSCPPVEHA 671

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Job time : 53 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:28:31 ; Search time 20 Seconds
(without alignments)
810.155 Million cell updates/sec

Title: US-10-671-054-1

Perfect score: 3675
Sequence: 1 MAPSLSPGPAALRRAPQLL.....AHSCPPVEPAADYKDDDK 686

Scoring table:

BLOSUM62

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA New:

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2: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US06_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	323.5	8.8	448	7	US-11-267-942-5
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4	320	8.7	493	7	US-11-267-942-2
5	319	8.7	448	6	US-10-196-749-408
6	319	8.7	493	7	US-11-267-942-4
7	316	8.6	1418	7	US-11-217-997-38
8	316	8.6	5635	6	US-10-766-760-2
9	300	8.2	444	6	US-10-511-937-2962
10	296	8.1	444	6	US-10-511-937-3014
11	296	8.1	444	7	US-11-183-218-8
12	296	8.1	444	7	US-11-183-218-10
13	277.5	7.6	462	7	US-11-217-997-18
14	275.5	7.5	1594	7	US-11-217-997-18
15	275.5	7.5	2003	7	US-11-217-997-28
16	272.5	7.4	289	7	US-11-264-243-8
17	272.5	7.4	472	7	US-11-217-997-26
18	272.5	7.4	1198	7	US-11-217-997-14
19	272.5	7.4	1398	7	US-11-217-997-4
20	272.5	7.4	1403	7	US-11-217-997-12
21	272.5	7.4	1404	7	US-11-217-997-2
22	272.5	7.4	1450	7	US-11-217-997-6
23	272.5	7.4	1547	7	US-11-217-997-22
24	272.5	7.4	1577	7	US-11-217-997-16
25	272.5	7.4	1577	7	US-11-217-997-20

26	272.5	7.4	1620	7	US-11-217-997-42	Sequence 42, Appl
27	272.5	7.4	1653	7	US-11-217-997-40	Sequence 40, Appl
28	267	7.3	1218	7	US-11-178-724-21	Sequence 21, Appl
29	263.5	7.2	2556	7	US-11-264-243-6	Sequence 6, Appl
30	263	7.2	1247	6	US-10-505-928-371	Sequence 371, App
31	262.5	7.1	439	7	US-11-293-697-2765	Sequence 2765, Ap
32	261.5	7.1	1953	7	US-11-264-243-16	Sequence 16, Appl
33	255	6.9	509	6	US-10-196-749-52	Sequence 52, Appl
34	251	6.8	406	6	US-10-512-754-2	Sequence 2, Appl
35	249	6.8	575	6	US-10-511-937-2625	Sequence 2625, Ap
36	247	6.7	1238	7	US-11-178-724-22	Sequence 22, Appl
37	246.5	6.7	713	7	US-11-175-714-5	Sequence 5, Appl
38	246.5	6.7	720	7	US-11-175-714-4	Sequence 4, Appl
39	246.5	6.7	786	6	US-10-504-973-31	Sequence 31, Appl
40	238.5	6.5	801	6	US-10-504-973-38	Sequence 38, Appl
41	234.5	6.4	1523	6	US-10-196-749-290	Sequence 290, App
42	233	6.3	729	7	US-11-175-714-8	Sequence 8, Appl
43	231.5	6.3	229	7	US-11-293-697-4810	Sequence 4810, Ap
44	231.5	6.3	724	7	US-11-293-697-3263	Sequence 3263, Ap
45	231	6.3	723	7	US-11-178-724-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-505-928-451
; Sequence 451, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OR INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIORITY APPLICATION NUMBER: US 60/363,019
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 451
; LENGTH: 1821
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-451

Query Match 8.9%; Score 325.5; DB 6; Length 1821;
Best Local Similarity 26.8%; Pred. No. 7.3e-18;
Matches 84; Conservative 35; Mismatches 77; Indels 117; Gaps 13;

QY 83 PENTDYFPRRLDCLINKYGSPTKNSGPAATVONLPD-----Q 119
DB 832 PSTDVLTSTPGIDRCAGATVNCGPTCV-NLPDGYRCVSPGYQLHPSQAYCTDDNE 890
QY 120 CTNPCCDKKGTQACODIMGNFCLCKRAG-----GRL--- 152
DB 891 CLADPC--KKGKGCINRVGSYSCTCPGTYLATSGATQECODINECQDPVCSGGCTNT 948
QY 153 -----CD-----KDVNECSQ-----ENGCC 167
DB 949 EGSYHCECDGQYIMVRKKGHCODINECHPCTPCDRCVNSPGSYTCLACEGYRGCGSC 1008
QY 168 LQI-----CHKPGSFHSGHGFSLSSGRICODIDEADSEACGEARCKN 214
DB 1009 VDNECTPQVCAHGCCTINSGSFRCSEGGYEVTSDEKCCQVDECAASASCPPTGCLN 1068
QY 215 LPESYSC-LCDEGFAYSSQKACRDVDEC-LQGRCEQ-VCVNSPGSYTC-HCDGRGGLKL 270
DB 1069 TEGSFPACACENGYWNBQSTACEDJDECAFPVCPGSGVCTNAGSFSCDCD--GGYRP 1126
QY 271 SQDMTCEDILPC 283
DB 1127 SPUGDSCEVDDEC 1139

RESULT 2
 US-11-267-942-5
 ; Sequence 5, Application US/11267942
 ; Publication No. US20060094054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiemann, William P.
 ; APPLICANT: Albis, Allan R.
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof
 ; FILE REFERENCE: 2879-109
 ; CURRENT APPLICATION NUMBER: US/11/267,942
 ; CURRENT FILING DATE: 2005-11-04
 ; PRIOR APPLICATION NUMBER: 60/625,598
 ; PRIOR FILING DATE: 2004-11-04
 ; PRIOR APPLICATION NUMBER: 60/687,129
 ; PRIOR FILING DATE: 2005-06-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-267-942-5

Query Match 8.8%; Score 323.5; DB 7; Length 448;
 Best Local Similarity 33.6%; Pred. No. 1.6e-18;
 Matches 87; Conservative 31; Mismatches 94; Indels 47; Gaps 15;

QY 55 EAKQGHLEECYBE---LC---SREARVFEHDEPTDYF-----YP--- 90
 DB 51 EACRG--DMVCVQNGYLCIPRTNPNVYKGPYSNPSTSGPYPAAPVPASNPPTS 108
 QY 91 RYLDICNKKXSGPTKXSGFATCYQNLPDCTPNCORKGQAQODLMDGNPFLCKXAGW-- 148
 DB 109 RLPLVC--RFG--YQDEBG--NQVD--VDECATDSHOCNPTQICINIEGGYTSCCTGTGWL 161
 QY 149 --GGRLCDKDVNECSQENGGLQICHNKKGSPHCSCHSGFELSDDRTCODIDECADSEA 206
 DB 162 LBGQCL---DIEBC--RYGVCQQLCANVPGSYCTCNPGFTLINDDRSCQDVNECETEMP 216
 QY 207 CGBARKNLPGSYSLCDEBFAVSQEKACRDVDEC--LOGRCEQVCVNSPFSYTHCHG 264
 DB 217 CVQTL--CVNTYSGFICRCDEPYELEEDGHCSDMDECSFSEFLCQHCVCVNPQSGYFSCP- 274
 QY 265 RGGLKLSQDMPTCEDILPC 283
 DB 275 -PGYVLLDNRSCQDINEC 292

RESULT 3
 US-10-505-928-676
 ; Sequence 676, Application US/10505928
 ; Publication No. US20060088532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ludwig Institute for Cancer Research et al.
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
 ; FILE REFERENCE: 28967/39178
 ; CURRENT APPLICATION NUMBER: US/10/505,928
 ; CURRENT FILING DATE: 2004-08-27
 ; PRIOR APPLICATION NUMBER: US 60/363,019
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 676
 ; LENGTH: 493
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-505-928-676

Query Match 8.7%; Score 321; DB 6; Length 493;
 Best Local Similarity 38.2%; Pred. No. 3e-18;
 Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;

QY 118 DOCTNPDCRKGTQAQODLMDGNPFLCKXAGW--GGRLCDKDVNECSQENGGLQICHNKP 175
 DB 175 DECTAGTHNCRADQVCINIRGSPACQCPGYQKRGQC--VDIECTIP--PYCHQRCVNTP 232
 QY 176 GSFHCSCHSGFELSDGRTCODIDECADSEACGEARKNLPSSYSLCDEBFAVSQEK 235
 DB 233 GSFYCCSPGFQLAANNVTCVDINECDASNQCAQ--QCVNIILSFLCQCNQGYELSDRLN 291
 QY 236 CRDVDECLQGR--CEQVCVNSPFSYTHCHDGRGLKLSQDMPTCEDILPC 283
 DB 292 CEDIDECRTSSYLQYQVCVNEBPKFSCMCP--QGYQVRSR--TCQDINEC 338

RESULT 4
 US-11-267-942-2
 ; Sequence 2, Application US/11267942
 ; Publication No. US20060094054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiemann, William P.
 ; APPLICANT: Albis, Allan R.
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof
 ; FILE REFERENCE: 2879-109
 ; CURRENT APPLICATION NUMBER: US/11/267,942
 ; CURRENT FILING DATE: 2005-11-04
 ; PRIOR APPLICATION NUMBER: 60/625,598
 ; PRIOR FILING DATE: 2004-11-04
 ; PRIOR APPLICATION NUMBER: 60/687,129
 ; PRIOR FILING DATE: 2005-06-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 493
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-267-942-2

Query Match 8.7%; Score 321; DB 7; Length 493;
 Best Local Similarity 38.2%; Pred. No. 3e-18;
 Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;

QY 118 DOCTNPDCRKGTQAQODLMDGNPFLCKXAGW--GGRLCDKDVNECSQENGGLQICHNKP 175
 DB 175 DECTAGTHNCRADQVCINIRGSPACQCPGYQKRGQC--VDIECTIP--PYCHQRCVNTP 232
 QY 176 GSFHCSCHSGFELSDGRTCODIDECADSEACGEARKNLPSSYSLCDEBFAVSQEK 235
 DB 233 GSFYCCSPGFQLAANNVTCVDINECDASNQCAQ--QCVNIILSFLCQCNQGYELSDRLN 291
 QY 236 CRDVDECLQGR--CEQVCVNSPFSYTHCHDGRGLKLSQDMPTCEDILPC 283
 DB 292 CEDIDECRTSSYLQYQVCVNEBPKFSCMCP--QGYQVRSR--TCQDINEC 338

RESULT 5
 US-11-267-942-3
 ; Sequence 3, Application US/11267942
 ; Publication No. US20060094054A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiemann, William P.
 ; APPLICANT: Albis, Allan R.
 ; TITLE OF INVENTION: Fibulin-3 and Uses Thereof
 ; FILE REFERENCE: 2879-109
 ; CURRENT APPLICATION NUMBER: US/11/267,942
 ; CURRENT FILING DATE: 2005-11-04
 ; PRIOR APPLICATION NUMBER: 60/625,598
 ; PRIOR FILING DATE: 2004-11-04
 ; PRIOR APPLICATION NUMBER: 60/687,129
 ; PRIOR FILING DATE: 2005-06-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3
 ; LENGTH: 493
 ; TYPE: PRT


```

; CURRENT FILING DATE: 2005-08-31
; PRIOR APPLICATION NUMBER: 10/453,372
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curation version 0.1
; SEQ ID NO 38
; LENGTH: 1418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-38
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Query Match      8.6%; Score 316; DB 7; Length 1418;
Best Local Similarity 29.8%; Pred. No. 3.1e-17;
Matches 78; Conservative 29; Mismatches 97; Indels 58; Gaps 11;
```

```

QY 59 GHLRECVBELCSR-----EAREVEFENDPETYPRYLDCINKYSGYTXN 106
   |||:||||:|
Db 215 GGCCHNCVQULTYTHRCQCRPGFOLDEDRHCVRRSP-----CANNRSGSMHC 263
   |||:||||:|
QY 107 S---GPATGVQNL-----PDQCTPN--PCDRKGTQACDMLGNFPLCKAKAM 148
   |||:||||:|
Db 264 QVVRGLARCEHVGYQLAADGKACEDVDCAAGLAQC---AHGCLNTGSGFRCVCHAGI 319
   |||:||||:|
QY 149 ----GGRLCDK----DVNECSQENGGCLOICHNKPGSFHCSHGFEISSDGRTCODIDE 200
   |||:||||:|
Db 320 ELGAGRGQCYRTEMELVNSCEANNNGSCSHGSHTSAGPLCTCPRGVELTDQRTCTDVG 379
   |||:||||:|
QY 201 CADSEACGEARKCNLPGSYSCLCDEGFAVSSOEKACRDVDECL--OGRBEQCVNSPGSY 258
   |||:||||:|
Db 380 CADSPCCQOV--CTNNGGYEGCGYAGYRLSADGCCEDVDECASSRGCGEHHCTNLAGSF 438
   |||:||||:|
QY 259 TCHCDRGGLKLSQMDTCEDI 280
   |||:||||:|
Db 439 QCSCE--AGYRLHEDRRGCSPL 458
   |||:||||:|
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RESULT 9
US-10-766-760-2
; Sequence 2, Application US/10766760
; Publication No. US20060127915A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Michael
; APPLICANT: Schultz, Dennis
; TITLE OF INVENTION: Gene Mutation Associated with
; TITLE OF INVENTION: Age-Related Macular Degeneration
; FILE REFERENCE: 49321-117
; CURRENT APPLICATION NUMBER: US/10/766,760
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 60/443,214
; PRIOR FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5635
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-760-2
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```

Query Match      8.2%; Score 300; DB 6; Length 5635;
Best Local Similarity 29.0%; Pred. No. 3.8e-15;
Matches 78; Conservative 37; Mismatches 100; Indels 54; Gaps 13;
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QY 50 FQVFEAKQGHLERC-----VEELCSREAREVEENDEPETYFYPRYLDCKINKYS 101
   |||:||||:|
Db 5077 FRTHASISKDRSNOCPSGFTLDSVGFPCADD--ECAAAGNCSH-----SCHNAMGT 5127
   |||:||||:|
QY 102 PYTKNSGFATGVQNL-----DQCTPNPCDRKGTQACQDMLGNFPLCKAGMG 150
   |||:||||:|
Db 5128 YX-----CSCPKGTLTAADGRTCODIDECALGRHTCHAGQDCDNTIGSYRCVVRGSGSF 5181
   |||:||||:|
QY 151 R-----LCDKDVNECSQENGGCLOICHNKPGSFHCSHGFEISSDGRTCODIDECADSE 205
   |||:||||:|
Db 5182 RRTSDGLSCQDINEC--QSSSPCHORCFNAGISFHGCEBPGYOLK--GRKCMVNECRQNV 5238
   |||:||||:|
QY 206 ACGEARKCNLPGSYSCLCDEGFAVSSOEKACRDVDECLQ8----RCEQVCVNSPGSYT 259
   |||:||||:|
Db 5239 CRPDQHCANTRGSGYCTIDLCFPGMT--KAENGCTIDIECKDGTGCRVYQICENTRGSYR 5297
   |||:||||:|
QY 260 CHCD-----GRGGLKLSQMDTCEDI-LPC 283
   |||:||||:|
Db 5298 CVCPRGYRSQGVGRPCMDINECEQVPRKC 5326
   |||:||||:|
```

```

RESULT 10
US-10-511-937-2962
; Sequence 2962, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2962
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2962
```

```

Query Match      8.1%; Score 296; DB 6; Length 444;
Best Local Similarity 35.5%; Pred. No. 2.7e-16;
Matches 66; Conservative 27; Mismatches 65; Indels 28; Gaps 4;
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QY 14 RAPQILILILAAECALAILLPAREATQFLRPRORAFQVFEAKQGHLERCVYELCSRE 73
   |||:||||:|
Db 4 QALRLICLLIGQGCIAAVFVQEBAGVILHRRRRRANALFELRPSLSRECKEEQCSFE 63
   |||:||||:|
QY 74 EAREVEENDPETYPRYLDCINKYSGYTKNSGFATGVQNLDPDQCTPNPCDRKGTQAC 133
   |||:||||:|
Db 64 EAREIFKDAERTKLFMTISYD-----GDQCASSPCQNGG--SC 99
   |||:||||:|
```

QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSQENGGLQICHNKPGRFH-CSCHSGFELS 189
 Db 100 KDQLQSYICFCCLPAFEGRNCFETHKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSL 159
 QY 190 SDGRTC 195
 Db 160 ADGVSC 165

RESULT 11

US-10-511-937-3014
 ; Sequence 3014, Application US/10511937
 ; Publication No. US20060088836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
 ; APPLICANT: Mohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; APPLICANT: Prentice, James
 ; APPLICANT: Morris, Macdonald
 ; APPLICANT: Rosenberg, Steven
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
 ; FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
 ; FILE REFERENCE: 5061200104
 ; CURRENT APPLICATION NUMBER: US/10/511,937
 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946
 ; PRIOR FILING DATE: 2003-04-24
 ; PRIOR APPLICATION NUMBER: US 10/131,831
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: US 10/325,899
 ; PRIOR FILING DATE: 2002-12-20
 ; NUMBER OF SEQ ID NOS: 3117
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3014
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-511-937-3014

Query Match 8.1%; Score 296; DB 6; Length 444;
 Best Local Similarity 35.5%; Pred. No. 2,7e-16;
 Matches 66; Conservative 27; Mismatches 65; Indels 28; Gaps 4;

QY 14 RAPQLLLILAAACALALIPAREATOFLRPRORAPQVFEBAKQGHLEBCEVELCSRE 73
 Db 4 QALRLCLLILGLQGCCLAAVFTQBEAHGVLHRRRRANAFLBELRPGSLERBCEKEQCSFE 63
 QY 74 EAREVEFENDEPDTYFYPRIYDCJNKYGSPTKNSGFATCVQNLPDCTPNCDCRKGTOAC 133
 Db 64 EAREIFKDAERTKLFMTSYSD-----GDCASSPCQNG--SC 99
 QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSQENGGLQICHNKPGRFH-CSCHSGFELS 189
 Db 100 KDQLQSYICFCCLPAFEGRNCFETHKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSL 159
 QY 190 SDGRTC 195
 Db 160 ADGVSC 165

RESULT 12

US-11-183-218-8
 ; Sequence 8, Application US/11183218
 ; Publication No. US20060088906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi

APPLICANT: Bove, Caryne
 ; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
 ; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
 ; FILE REFERENCE: 040853-01-5083-US02
 ; CURRENT APPLICATION NUMBER: US/11/183,218
 ; PRIOR FILING DATE: 2005-07-15
 ; PRIOR APPLICATION NUMBER: US 10/410,945
 ; PRIOR FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: PCT/US02/32263
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: US 60/334,301
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 444
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-183-218-8

Query Match 8.1%; Score 296; DB 7; Length 444;
 Best Local Similarity 35.5%; Pred. No. 2,7e-16;
 Matches 66; Conservative 27; Mismatches 65; Indels 28; Gaps 4;

QY 14 RAPQLLLILAAACALALIPAREATOFLRPRORAPQVFEBAKQGHLEBCEVELCSRE 73
 Db 4 QALRLCLLILGLQGCCLAAVFTQBEAHGVLHRRRRANAFLBELRPGSLERBCEKEQCSFE 63
 QY 74 EAREVEFENDEPDTYFYPRIYDCJNKYGSPTKNSGFATCVQNLPDCTPNCDCRKGTOAC 133
 Db 64 EAREIFKDAERTKLFMTSYSD-----GDCASSPCQNG--SC 99
 QY 134 QDLMGNFFCLCKAGWGRLCDKDVNE---CSQENGGLQICHNKPGRFH-CSCHSGFELS 189
 Db 100 KDQLQSYICFCCLPAFEGRNCFETHKDDQLICVNENGGCEQYCSHTGTGRSCRCHEGYSL 159
 QY 190 SDGRTC 195
 Db 160 ADGVSC 165

RESULT 13

US-11-183-218-10
 ; Sequence 10, Application US/11183218
 ; Publication No. US20060088906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bove, Caryne
 ; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
 ; FILE OF INVENTION: GLYCOCONJUGATION OF ERYTHROPOIETIN
 ; FILE REFERENCE: 040853-01-5083-US02
 ; CURRENT APPLICATION NUMBER: US/11/183,218
 ; CURRENT FILING DATE: 2005-07-15

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; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-218-10

Query Match
Best Local Similarity 7.6%; Score 277.5; DB 7; Length 462;
Matches 65; Conservative 30; Mismatches 63; Indels 33; Gaps 6;

QY 12 LRAAPOLLL-----LAAECALALLPAREATQFLRPRORAFQVFEAKQGHLERECV 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 MAESSLITICLLGYLSAECTV--FLDHNANKILNRPKRVNSGLKEEVQGNLRECM 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 EELCSSEAREVENDPETDYFPRLYDCINKXGSPYTKNSGFATCVQMLPDCTNPDC 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 66 EKKCSSEAREVENDPETDYFPRLYDCINKXGSPYTKNSGFATCVQMLPDCTNPDC 103
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 RKGTQACODLMGNFCLCTKAGWGRLCDKDVNECSQENGCLQICHNK- PGSFHCSCHG 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 104 NGG--SCRDINSYECWCFEGFGKNCCLDVT-CNKNKGCEQFCGNSADNKKVVCSTG 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 FELSSDGRTCQ 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 YRLAENQKSC 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-11-217-997-18
; Sequence 18, Application US/11217997
; Publication No. US20060111561A1
; GENERAL INFORMATION:
; APPLICANT: Valerie L. Gerlach
; APPLICANT: Elma R. Fernandes
; APPLICANT: Richard A. Shinkels
; APPLICANT: Weera Patlurajan
; APPLICANT: Vladimir Y. Gusev
; APPLICANT: Stacie (Caeman) Navara
; APPLICANT: Velizar T. Tchernov
; APPLICANT: David W. Anderson
; APPLICANT: Xiaojia (Sasha) Guo
; APPLICANT: Luca Raetelli
; APPLICANT: Mei Zhong
; APPLICANT: Muratichara Padigaru
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODED THEREBY
; FILE REFERENCE: Cura 551 CIP
; CURRENT APPLICATION NUMBER: US/11/217,997
; PRIOR APPLICATION NUMBER: 2005-08-31
; PRIOR FILING DATE: 2003-06-03
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; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Curesqlst version 0.1
; SEQ ID NO 18
; LENGTH: 1594
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-217-997-18

Query Match
Best Local Similarity 7.5%; Score 275.5; DB 7; Length 1594;
Matches 94; Conservative 33; Mismatches 118; Indels 117; Gaps 15;

QY 5 LSPGPAALRRAPQOLLLLLAAECALALLPAREATQFLRPRORAFQVFEAKQGHLERE 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 LBEARAGAAVVALVALLLLLPAVPGASVPRP---LLPLDQGMHVCABQGLTLVGR 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 --CVELL-----CSREAREVENDPETDYFPRLYDCINKXGSPYTKN 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 QPCVQALSHTVPMVRAGCGMAVCVGHERRTVY-----YMG----YROYTYTE 103
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 107 S-GFATVCQN-----LPDQCPNFCDBKG-----TOACODLMGNFCLCTKAGWG 149
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 104 ARTVLRCGGWGTQOPDEBCLASBCSASLCFHGRCVPSADQCH-----CFPGFQ 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 150 GRLCDVDNECSQENGCLQICHNKPSFHCSCSGFELSDDRTCODIDECA----- 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 155 GPRCQYDVDECRTHNGCCQHRVCNTPGSYLCECKPFRLLHTSRTCLAINSCALNGGCQ 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 -----DSEAC-----GEA--RCKNLPGSYSLCDEGF 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 HHCVQLTTRHRCQCRPGFQLOEDGRHCVRRSPCANRNGSCMHRCCVVRGLARCEHVGY 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 AVSSQEKACRDVDECLQG--RCEQVCVNSPGSYTCH-----DGRGGLKLSOD-MPT 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 275 QLAADGKACEDVDECAAGLAQCAHGCLNTQGSFKVCVCHAGYELGADRCOCTRIEMELVNS 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 277 CE 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 335 CE 336
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-11-264-243-8
; Sequence 8, Application US/11264243
; Publication No. US20060134121A1
; GENERAL INFORMATION:
; APPLICANT: Thurston, Gavin
; APPLICANT: Gale, Nicholas
; APPLICANT: Noguera, Irene
; TITLE OF INVENTION: D1d4 Antagonists, Assays and Therapeutic
; FILE REFERENCE: 2070A
; CURRENT APPLICATION NUMBER: US/11/264,243
; PRIOR APPLICATION NUMBER: 2005-10-31
```


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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 11:31:46 ; Search time 195 Seconds
(without alignments)
18.758 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47
Sequence: 1 DYKDDDK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 500 summaries

Database :

A_Geneseq_8: *
1: geneseqp1980s: *
2: geneseqp1980s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	1	AB999240
2	47	100.0	8	1	AA700024
3	47	100.0	8	2	AA809327
4	47	100.0	8	2	AA844496
5	47	100.0	8	2	AA877283
6	47	100.0	8	2	AA877283
7	47	100.0	8	2	AA877283
8	47	100.0	8	2	AA877283
9	47	100.0	8	2	AA877283
10	47	100.0	8	2	AA877283
11	47	100.0	8	2	AA877283
12	47	100.0	8	2	AA877283
13	47	100.0	8	2	AA877283
14	47	100.0	8	2	AA877283
15	47	100.0	8	2	AA877283
16	47	100.0	8	2	AA877283
17	47	100.0	8	2	AA877283
18	47	100.0	8	2	AA877283
19	47	100.0	8	2	AA877283
20	47	100.0	8	2	AA877283
21	47	100.0	8	2	AA877283
22	47	100.0	8	2	AA877283
23	47	100.0	8	2	AA877283

24	47	100.0	8	2	AA899286	AA899286 FLAG pep
25	47	100.0	8	2	AA854280	AA854280 Peptide s
26	47	100.0	8	2	AA844300	AA844300 Human ser
27	47	100.0	8	2	AA859269	AA859269 Type II I
28	47	100.0	8	2	AA854434	AA854434 Human PSI
29	47	100.0	8	2	AA858571	AA858571 FLAG pep
30	47	100.0	8	2	AA876424	AA876424 FLAG affi
31	47	100.0	8	2	AA881752	AA881752 Synthetic
32	47	100.0	8	2	AA879682	AA879682 Human CSI
33	47	100.0	8	2	AA879770	AA879770 FLAG pep
34	47	100.0	8	2	AA856033	AA856033 Chimeric
35	47	100.0	8	2	AA830566	AA830566 FLAG tag
36	47	100.0	8	2	AA875806	AA875806 FLAG pep
37	47	100.0	8	2	AA854266	AA854266 FLAG pep
38	47	100.0	8	2	AA829748	AA829748 Synthetic
39	47	100.0	8	2	AA879562	AA879562 FLAG pep
40	47	100.0	8	2	AA869953	AA869953 FLAG pep
41	47	100.0	8	2	AA848629	AA848629 Chimeric
42	47	100.0	8	2	AA847353	AA847353 FLAG-pep
43	47	100.0	8	2	AA876407	AA876407 Human PAR
44	47	100.0	8	2	AA856251	AA856251 FLAG pep
45	47	100.0	8	2	AA846969	AA846969 Peptide s
46	47	100.0	8	2	AA868289	AA868289 FLAG pep
47	47	100.0	8	2	AA844008	AA844008 FLAG pep
48	47	100.0	8	2	AA880478	AA880478 Peptide s
49	47	100.0	8	2	AA870592	AA870592 FLAG sequ
50	47	100.0	8	2	AA808734	AA808734 FLAG tag
51	47	100.0	8	2	AA894672	AA894672 Human TRA
52	47	100.0	8	2	AA806471	AA806471 Epitope t
53	47	100.0	8	2	AA899020	AA899020 FLAG pep
54	47	100.0	8	2	AA888371	AA888371 FLAG pep
55	47	100.0	8	2	AA897660	AA897660 FLAG pep
56	47	100.0	8	2	AA808479	AA808479 Human BS2
57	47	100.0	8	2	AA881534	AA881534 FLAG pep
58	47	100.0	8	2	AA806792	AA806792 FLAG pep
59	47	100.0	8	2	AA899670	AA899670 FLAG tag
60	47	100.0	8	2	AA895645	AA895645 Human BS1
61	47	100.0	8	2	AA831721	AA831721 FLAG pep
62	47	100.0	8	2	AA831944	AA831944 FLAG pep
63	47	100.0	8	2	AA892256	AA892256 FLAG pep
64	47	100.0	8	2	AA807740	AA807740 Human bre
65	47	100.0	8	2	AA894250	AA894250 FLAG pep
66	47	100.0	8	2	AA882735	AA882735 Adenoviru
67	47	100.0	8	2	AA842254	AA842254 Synthetic
68	47	100.0	8	2	AA849544	AA849544 FLAG pep
69	47	100.0	8	2	AA806609	AA806609 FLAG pep
70	47	100.0	8	2	AA892410	AA892410 Human IL-
71	47	100.0	8	2	AA806911	AA806911 FLAG pep
72	47	100.0	8	2	AA823636	AA823636 Octapepti
73	47	100.0	8	2	AA868029	AA868029 FLAG pep
74	47	100.0	8	2	AA872153	AA872153 Peptide e
75	47	100.0	8	2	AA897648	AA897648 FLAG pep
76	47	100.0	8	2	AA896302	AA896302 C-termina
77	47	100.0	8	2	AA895562	AA895562 FLAG pep
78	47	100.0	8	2	AA809543	AA809543 Human TAB
79	47	100.0	8	2	AA882718	AA882718 Human ZCH
80	47	100.0	8	2	AA806900	AA806900 FLAG affi
81	47	100.0	8	2	AA853528	AA853528 Human pan
82	47	100.0	8	2	AA813471	AA813471 FLAG pep
83	47	100.0	8	2	AA804141	AA804141 Human sli
84	47	100.0	8	2	AA849750	AA849750 Compact s
85	47	100.0	8	2	AA816563	AA816563 Epitope t
86	47	100.0	8	2	AA897673	AA897673 FLAG pep
87	47	100.0	8	3	AA877538	AA877538 FLAG pep
88	47	100.0	8	3	AA803362	AA803362 N-termina
89	47	100.0	8	3	AA899877	AA899877 FLAG pep
90	47	100.0	8	3	AA810961	AA810961 FLAG pep
91	47	100.0	8	3	AA87937	AA87937 Intracell
92	47	100.0	8	3	AA810094	AA810094 Combinato
93	47	100.0	8	3	AA851938	AA851938 FLAG pep
94	47	100.0	8	3	AA822877	AA822877 FLAG pep
95	47	100.0	8	3	AA856126	AA856126 Human TGF
96	47	100.0	8	3	AA828432	AA828432 FLAG pep

97	47	100.0	8	3	AAV5914	AAV95914	FLAG	pept	170	47	100.0	8	4	AAV49284	AAV49284	FLAG	tag
98	47	100.0	8	3	AAV5360	AAV5360	Mouse neu		171	47	100.0	8	4	AAE00931	AAE00931	FLAG	octa
99	47	100.0	8	3	AAV97366	AAV97366	FLAG	pept	172	47	100.0	8	4	AAV73625	AAV73625	FLAG	pept
100	47	100.0	8	3	AAV83142	AAV83142	FLAG	epit	173	47	100.0	8	4	AAV51513	AAV51513	FLAG	epit
101	47	100.0	8	3	AAV67423	AAV67423	FLAG	pept	174	47	100.0	8	4	AAE11989	AAE11989	FLAG	pept
102	47	100.0	8	3	AAV813358	AAV813358	FLAG	epit	175	47	100.0	8	4	ABR00925	ABR00925	FLAG	pept
103	47	100.0	8	3	AAV97132	AAV97132	FLAG	epit	176	47	100.0	8	4	AAV74300	AAV74300	FLAG	pept
104	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	177	47	100.0	8	4	AAE08007	AAE08007	FLAG	pept
105	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	178	47	100.0	8	4	AAV51726	AAV51726	FLAG	pept
106	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	179	47	100.0	8	4	AAV68336	AAV68336	FLAG	pept
107	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	180	47	100.0	8	5	AAV52698	AAV52698	FLAG	pept
108	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	181	47	100.0	8	5	AAE15822	AAE15822	FLAG	tag
109	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	182	47	100.0	8	5	ABE06583	ABE06583	Beta-secr	
110	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	183	47	100.0	8	5	AAV72123	AAV72123	Synthetic	
111	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	184	47	100.0	8	5	AAE24638	AAE24638	Synthetic	
112	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	185	47	100.0	8	5	ABG78473	ABG78473	Bacteriop	
113	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	186	47	100.0	8	5	ABG79204	ABG79204	FLAG	tag
114	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	187	47	100.0	8	5	ABG31625	ABG31625	Human AUC	
115	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	188	47	100.0	8	5	AAE26099	AAE26099	Novel hum	
116	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	189	47	100.0	8	5	ABG96490	ABG96490	Hydrophil	
117	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	190	47	100.0	8	5	AAE14378	AAE14378	FLAG	epit
118	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	191	47	100.0	8	5	AAV81015	AAV81015	FLAG	epit
119	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	192	47	100.0	8	5	AAE21825	AAE21825	peptide #	
120	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	193	47	100.0	8	5	ABE83168	ABE83168	FLAG	epit
121	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	194	47	100.0	8	5	ABG76872	ABG76872	G-protein	
122	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	195	47	100.0	8	5	AAV66037	AAV66037	Amino aci	
123	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	196	47	100.0	8	5	AAV78504	AAV78504	FLAG	epit
124	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	197	47	100.0	8	5	AAV78429	AAV78429	FLAG	pept
125	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	198	47	100.0	8	5	AAV97725	AAV97725	Epitope t	
126	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	199	47	100.0	8	5	ABE52353	ABE52353	peptide r	
127	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	200	47	100.0	8	5	AAO19088	AAO19088	Human P51	
128	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	201	47	100.0	8	5	AAE13526	AAE13526	FLAG	epit
129	47	100.0	8	3	AAV97183	AAV97183	FLAG	epit	202	47	100.0	8	5	AAV47920	AAV47920	MT1-MMP r	
130	47	100.0	8	4	AAE11238	AAE11238	peptide #		203	47	100.0	8	5	AAV48738	AAV48738	FLAG	pept
131	47	100.0	8	4	AAE13081	AAE13081	Epitope t		204	47	100.0	8	5	AAO14438	AAO14438	Synthetic	
132	47	100.0	8	4	AAE13081	AAE13081	Epitope t		205	47	100.0	8	5	AAU78636	AAU78636	Synthetic	
133	47	100.0	8	4	AAE13081	AAE13081	Epitope t		206	47	100.0	8	5	AAE22591	AAE22591	peptide #	
134	47	100.0	8	4	AAE13081	AAE13081	Epitope t		207	47	100.0	8	5	AAO21841	AAO21841	Breast t1	
135	47	100.0	8	4	AAE13081	AAE13081	Epitope t		208	47	100.0	8	5	ABE78099	ABE78099	Amino aci	
136	47	100.0	8	4	AAE13081	AAE13081	Epitope t		209	47	100.0	8	5	ABG94439	ABG94439	Protease	
137	47	100.0	8	4	AAE13081	AAE13081	Epitope t		210	47	100.0	8	5	AAO19170	AAO19170	Human pro	
138	47	100.0	8	4	AAE13081	AAE13081	Epitope t		211	47	100.0	8	5	AAE18133	AAE18133	FLAG-epit	
139	47	100.0	8	4	AAE13081	AAE13081	Epitope t		212	47	100.0	8	5	AAO15234	AAO15234	FLAG	epit
140	47	100.0	8	4	AAE13081	AAE13081	Epitope t		213	47	100.0	8	5	ABG32027	ABG32027	Synthetic	
141	47	100.0	8	4	AAE13081	AAE13081	Epitope t		214	47	100.0	8	5	ABG77003	ABG77003	Bacteriop	
142	47	100.0	8	4	AAE13081	AAE13081	Epitope t		215	47	100.0	8	5	ABG79221	ABG79221	Bacteriop	
143	47	100.0	8	4	AAE13081	AAE13081	Epitope t		216	47	100.0	8	5	ABE53979	ABE53979	FLAG	pept
144	47	100.0	8	4	AAE13081	AAE13081	Epitope t		217	47	100.0	8	5	AAV48731	AAV48731	FLAG	epit
145	47	100.0	8	4	AAE13081	AAE13081	Epitope t		218	47	100.0	8	5	ABE05641	ABE05641	FLAG	pept
146	47	100.0	8	4	AAE13081	AAE13081	Epitope t		219	47	100.0	8	5	AAE21834	AAE21834	peptide #	
147	47	100.0	8	4	AAE13081	AAE13081	Epitope t		220	47	100.0	8	5	AAU79449	AAU79449	FLAG	tag
148	47	100.0	8	4	AAE13081	AAE13081	Epitope t		221	47	100.0	8	5	AAU79449	AAU79449	FLAG	tag
149	47	100.0	8	4	AAE13081	AAE13081	Epitope t		222	47	100.0	8	5	AAU79449	AAU79449	FLAG	tag
150	47	100.0	8	4	AAE13081	AAE13081	Epitope t		223	47	100.0	8	5	ABE81599	ABE81599	Synthetic	
151	47	100.0	8	4	AAE13081	AAE13081	Epitope t		224	47	100.0	8	5	ABE79780	ABE79780	FLAG	tag
152	47	100.0	8	4	AAE13081	AAE13081	Epitope t		225	47	100.0	8	5	ABG32759	ABG32759	FLAG	tag
153	47	100.0	8	4	AAE13081	AAE13081	Epitope t		226	47	100.0	8	5	ABP54337	ABP54337	FLAG	octa
154	47	100.0	8	4	AAE13081	AAE13081	Epitope t		227	47	100.0	8	5	AAU79194	AAU79194	Synthetic	
155	47	100.0	8	4	AAE13081	AAE13081	Epitope t		228	47	100.0	8	5	AAE23793	AAE23793	FLAG	epit
156	47	100.0	8	4	AAE13081	AAE13081	Epitope t		229	47	100.0	8	5	ABE68439	ABE68439	FLAG	pept
157	47	100.0	8	4	AAE13081	AAE13081	Epitope t		230	47	100.0	8	5	ABE83455	ABE83455	FLAG	epit
158	47	100.0	8	4	AAE13081	AAE13081	Epitope t		231	47	100.0	8	5	AAE13365	AAE13365	peptide u	
159	47	100.0	8	4	AAE13081	AAE13081	Epitope t		232	47	100.0	8	5	ABE07133	ABE07133	FLAG	pept
160	47	100.0	8	4	AAE13081	AAE13081	Epitope t		233	47	100.0	8	5	AAV50571	AAV50571	FLAG	tag
161	47	100.0	8	4	AAE13081	AAE13081	Epitope t		234	47	100.0	8	5	AAE18850	AAE18850	FLAG	anti
162	47	100.0	8	4	AAE13081	AAE13081	Epitope t		235	47	100.0	8	5	AAU88019	AAU88019	Tumour ne	
163	47	100.0	8	4	AAE13081	AAE13081	Epitope t		236	47	100.0	8	5	AAU76531	AAU76531	FLAG	tag
164	47	100.0	8	4	AAE13081	AAE13081	Epitope t		237	47	100.0	8	5	AAO15411	AAO15411	FLAG	epit
165	47	100.0	8	4	AAE13081	AAE13081	Epitope t		238	47	100.0	8	5	AAO19059	AAO19059	Mutation	
166	47	100.0	8	4	AAE13081	AAE13081	Epitope t		239	47	100.0	8	5	AAE28605	AAE28605	FLAG	pept
167	47	100.0	8	4	AAE13081	AAE13081	Epitope t		240	47	100.0	8	5	ABJ10902	ABJ10902	K-beta M6	
168	47	100.0	8	4	AAE13081	AAE13081	Epitope t		241	47	100.0	8	5	ABE05002	ABE05002	FLAG	pept
169	47	100.0	8	4	AAE13081	AAE13081	Epitope t		242	47	100.0	8	5	ABE09934	ABE09934	Ptirn pro	

243	47	100.0	8	5	ABB07739	Abb07739 FLAG pept	316	47	100.0	8	6	ABP60044	Abp60044 FLAG epit
244	47	100.0	8	5	AAE14768	Aae14768 FLAG pept	317	47	100.0	8	6	ABP96701	Abp96701 FLAG pept
245	47	100.0	8	5	ABB81468	Abb81468 FLAG pept	318	47	100.0	8	6	ABU11922	Abu11922 FLAG pept
246	47	100.0	8	5	ABG97833	Abg97833 FLAG read	319	47	100.0	8	6	ABU38456	Abu38456 FLAG epit
247	47	100.0	8	5	ABG97824	Abg97824 FLAG tag	320	47	100.0	8	6	ADA03349	Ada03349 FLAG pept
248	47	100.0	8	5	AAE13735	Aae13735 FLAG pept	321	47	100.0	8	6	ABG74451	Abg74451 Flag pept
249	47	100.0	8	5	ABP47227	Abp47227 Anti-DYK	322	47	100.0	8	6	ABU08631	Abu08631 Endophilin
250	47	100.0	8	5	ABP47227	Abp47227 Human Bly	323	47	100.0	8	6	ABR56717	Abu08631 LSI147-gpe
251	47	100.0	8	5	ABG33586	Abg33586 Influenza	324	47	100.0	8	6	ABEO1252	Abu56717 FLAG tag
252	47	100.0	8	5	ABB80696	Abb80696 Amino aci	325	47	100.0	8	6	ABG73775	Abu01252 Zinc flng
253	47	100.0	8	5	ABB76275	Abb76275 FLAG pept	326	47	100.0	8	6	ABU08455	Abg73775 Human CS
254	47	100.0	8	5	AAE24904	Aae24904 Synthetic	327	47	100.0	8	6	ABU62120	Abu08455 FLAG tag
255	47	100.0	8	5	ABU03956	Abu03956 FLAG pept	328	47	100.0	8	6	ABR99043	Abu62120 Immugen
256	47	100.0	8	5	ABP52193	Abp52193 FLAG pept	329	47	100.0	8	6	AAE34694	Abu99043 Peptide t
257	47	100.0	8	5	AAO22928	Aao22928 Human pap	330	47	100.0	8	6	ABU07887	Aae34694 FLAG tag
258	47	100.0	8	5	AAU76908	Aau76908 C-termina	331	47	100.0	8	6	ADA08104	Abu07887 Novel hum
259	47	100.0	8	5	ABE75957	AbE75957 FLAG pept	332	47	100.0	8	6	ABG72134	Ada08104 Epitope t
260	47	100.0	8	5	ABE25322	Abe25322 Bacteriop	333	47	100.0	8	6	AAE31706	Abg72134 Flag pept
261	47	100.0	8	5	ABP77917	Abp77917 Bacteriop	334	47	100.0	8	6	ABU55851	Aae31706 Epitope t
262	47	100.0	8	5	ABP52189	Abp52189 FLAG epit	335	47	100.0	8	6	ABP71104	Abu55851 DYKDDDK
263	47	100.0	8	5	AAU99567	Aau99567 FLAG epit	336	47	100.0	8	6	ABP72095	Abp71104 Amino aci
264	47	100.0	8	5	AAU87053	Aau87053 FLAG epit	337	47	100.0	8	6	ABU08796	Abp72095 FLAG tag/
265	47	100.0	8	5	AAE21098	Aae21098 FLAG epit	338	47	100.0	8	6	ABU08561	Abu08796 C-termina
266	47	100.0	8	5	ABG35334	Abg35334 Thrombopo	339	47	100.0	8	6	ABP56844	Abu08561 FLAG pept
267	47	100.0	8	5	ABG35327	Abg35327 Thrombopo	340	47	100.0	8	6	AAE30830	Abp56844 FLAG pept
268	47	100.0	8	5	AAU98511	Aau98511 Matrix me	341	47	100.0	8	6	ABG72367	Aae30830 FLAG tag
269	47	100.0	8	5	AAE25118	Aae25118 Peptide #	342	47	100.0	8	6	AAO19756	Abg72367 FLAG epit
270	47	100.0	8	5	AAE28630	Aae28630 FLAG pept	343	47	100.0	8	6	ABP58151	Aao19756 Flag pept
271	47	100.0	8	5	AAU11121	Aau11121 Flg epit	344	47	100.0	8	6	ABP56483	Abp58151 FLAG pept
272	47	100.0	8	5	AAU80474	Aau80474 Peptide F	345	47	100.0	8	6	ABU66326	Abp56483 Interfero
273	47	100.0	8	5	AAU807228	Aau807228 Amino aci	346	47	100.0	8	6	ABP60553	Abu66326 FLAG pept
274	47	100.0	8	5	AAE22696	Aae22696 Peptide #	347	47	100.0	8	6	AAE37228	Abp60553 Human tum
275	47	100.0	8	5	AAU79878	Aau79878 Novel fla	348	47	100.0	8	6	AAE32857	Aae37228 FLAG pept
276	47	100.0	8	5	AAE28944	Aae28944 FLAG pept	349	47	100.0	8	6	AAE34830	Aae32857 FLAG pept
277	47	100.0	8	5	AAU11967	Aau11967 Zaiaphal	350	47	100.0	8	6	ABP72586	Aae34830 FLAG pept
278	47	100.0	8	5	AAU1967	Aau1967 Antigenic	351	47	100.0	8	6	AAE33268	Abp72586 FLAG epit
279	47	100.0	8	5	AAU1967	Aau1967 Antigenic	352	47	100.0	8	6	ABG72477	Aae33268 FLAG epit
280	47	100.0	8	5	AAU1967	Aau1967 Antigenic	353	47	100.0	8	6	AAE32770	Abg72477 FLAG mark
281	47	100.0	8	5	AAU76640	Aau76640 FLAG tag	354	47	100.0	8	6	ABG74757	Aae32770 FLAG tag
282	47	100.0	8	5	AAO18219	Aao18219 FLAG pept	355	47	100.0	8	6	ABP97237	Abg74757 HSV-2 HSV
283	47	100.0	8	5	ABG97970	Abg97970 Synthetic	356	47	100.0	8	6	ABU08596	Abp97237 FLAG epit
284	47	100.0	8	5	ABG97970	Abg97970 Human leu	357	47	100.0	8	6	AAE37702	Abu08596 FLAG epit
285	47	100.0	8	5	AAE21868	Aae21868 Peptide #	358	47	100.0	8	6	ABU62645	Aae37702 FLAG sequ
286	47	100.0	8	5	AAO19214	Aao19214 FLAG pept	359	47	100.0	8	6	ADA26311	Abu62645 FLAG epit
287	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	360	47	100.0	8	6	ADA94909	Ada26311 M2 antiibo
288	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	361	47	100.0	8	6	ADA00849	Ada94909 Interfero
289	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	362	47	100.0	8	6	ADA27206	Ada00849 FLAG epit
290	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	363	47	100.0	8	6	ADA28170	Ada27206 FLAG tag
291	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	364	47	100.0	8	6	ADB25837	Ada28170 FLAG epit
292	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	365	47	100.0	8	6	ABU63661	Adb25837 FLAG epit
293	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	366	47	100.0	8	6	ABO42826	Abu63661 Antigenic
294	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	367	47	100.0	8	6	ABO42826	Abu42826 Human G-P
295	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	368	47	100.0	8	6	ADA26385	Abu42826 FLAG pept
296	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	369	47	100.0	8	6	ABU62136	Ada26385 CS198 pur
297	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	370	47	100.0	8	7	ABU08853	Abu62136 Epitope t
298	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	371	47	100.0	8	7	ADA09664	Abu08853 C-termina
299	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	372	47	100.0	8	7	ADA09664	Ada09664 FLAG tag
300	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	373	47	100.0	8	7	ADA09807	Ada09664 FLAG pept
301	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	374	47	100.0	8	7	ADA09807	Ada09807 FLAG pept
302	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	375	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
303	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	376	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
304	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	377	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
305	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	378	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
306	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	379	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
307	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	380	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
308	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	381	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
309	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	382	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
310	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	383	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
311	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	384	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
312	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	385	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
313	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	386	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
314	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	387	47	100.0	8	7	ADB16982	Ada09807 FLAG pept
315	47	100.0	8	5	ABG32887	Abg32887 FLAG tag	388	47	100.0	8	7	ADB16982	Ada09807 FLAG pept

389	47	100.0	8	7	ADC42904	Adc42904 FLAG epit	462	47	100.0	8	8	ADH76245	Adh76245 FLAG pep
390	47	100.0	8	7	ADC33452	Adc33452 FLAG epit	463	47	100.0	8	8	ADJ34693	Adj34693 FLAG pep
391	47	100.0	8	7	ADG39372	Adg39372 Bacteriop	464	47	100.0	8	8	ADJ23660	Adj23660 FLAG tag
392	47	100.0	8	7	ADC72996	Adc72996 FLAG epit	465	47	100.0	8	8	ADJ22519	Adj22519 FLAG-epit
393	47	100.0	8	7	ADC83638	Adc83638 FLAG pep	466	47	100.0	8	8	ADJ62546	Adj62546 FLAG tag
394	47	100.0	8	7	ADC78262	Adc78262 FLAG epit	467	47	100.0	8	8	ADJ36215	Adj36215 Self-coa1
395	47	100.0	8	7	ABW00624	Abw00624 T125 tag	468	47	100.0	8	8	ADJ03828	Adj03828 Amino aci
396	47	100.0	8	7	ABW00757	Abw00757 Metallopr	469	47	100.0	8	8	ADJ36642	Adj36642 Protein P
397	47	100.0	8	7	ADDP67235	Addp67235 FLAG epit	470	47	100.0	8	8	ADJ41404	Adj41404 Human GPC
398	47	100.0	8	7	ADDB8177	Addb8177 C-termina	471	47	100.0	8	8	ADK67988	Adk67988 Synthetic
399	47	100.0	8	7	ABBB80306	Abbb80306 FLAG sequ	472	47	100.0	8	8	ADB88089	Adb88089 Epitope-t
400	47	100.0	8	7	ABW01147	Abw01147 FLAG pep	473	47	100.0	8	8	ADJ57882	Adj57882 FLAG tag
401	47	100.0	8	7	ABW00602	Abw00602 Peptide #	474	47	100.0	8	8	ADJ29443	Adj29443 FLAG epit
402	47	100.0	8	7	ABW01400	Abw01400 Human HEA	475	47	100.0	8	8	ADJ16816	Adj16816 FLAG epit
403	47	100.0	8	7	ABW01459	Abw01459 FLAG pep	476	47	100.0	8	8	ADJ93454	Adj93454 IFN-beta-
404	47	100.0	8	7	ADG03532	Adg03532 FLAG pep	477	47	100.0	8	8	ADJ50914	Adj50914 FLAG pep
405	47	100.0	8	7	ADD93432	Add93432 Octapepti	478	47	100.0	8	8	ADJ88258	Adj88258 FLAG pep
406	47	100.0	8	7	ADDE15841	Adel15841 FLAG pep	479	47	100.0	8	8	ADJ71859	Adj71859 IGF-IR/IR
407	47	100.0	8	7	ADDE1578	Adel1578 FLAG epit	480	47	100.0	8	8	ADJ69052	Adj69052 IGF-IR/IR
408	47	100.0	8	7	ADDF71827	Adff71827 FLAG epit	481	47	100.0	8	8	ADJ68820	Adj68820 IGF-IR/IR
409	47	100.0	8	7	ADDF6666	Adff6666 FLAG tag	482	47	100.0	8	8	ADJ68121	Adj68121 FLAG epit
410	47	100.0	8	7	ABW02218	Abw02218 Bacteriop	483	47	100.0	8	8	ADJ27230	Adj27230 FLAG tag
411	47	100.0	8	7	ADDF69357	Adff69357 Goodpastu	484	47	100.0	8	8	ADK43172	Adk43172 FLAG pep
412	47	100.0	8	7	ADBE3708	Adbe3708 Tag pep	485	47	100.0	8	8	ADM83503	Adm83503 FLAG pep
413	47	100.0	8	7	ADFE2087	Adfe2087 Human CCR	486	47	100.0	8	8	ADJ24296	Adj24296 FLAG pep
414	47	100.0	8	7	ADFE5337	Adfe5337 Adeno-ass	487	47	100.0	8	8	ADK15503	Adk15503 FLAG tag
415	47	100.0	8	7	ADFE6626	Adff6626 FLAG pep	488	47	100.0	8	8	ADM38897	Adm38897 FLAG tag
416	47	100.0	8	7	ABR83683	Abtr83683 C-termina	489	47	100.0	8	8	ADM38665	Adm38665 Insulin a
417	47	100.0	8	7	ADG24531	Adg24531 FLAG Tag	490	47	100.0	8	8	ADN06109	Adn06109 C-termina
418	47	100.0	8	7	ADFE83602	Adff83602 Cytokine	491	47	100.0	8	8	ADN17178	Adn17178 Peptide u
419	47	100.0	8	7	ADG30406	Adg30406 FLAG pep	492	47	100.0	8	8	ADM28629	Adm28629 FLAG epit
420	47	100.0	8	7	ADG25291	Adg25291 Methionin	493	47	100.0	8	8	ADO06950	Ado06950 FLAG tag
421	47	100.0	8	7	ADG16157	Adg16157 FLAG pep	494	47	100.0	8	8	ADJ60829	Adj60829 FLAG pep
422	47	100.0	8	7	ADG43833	Adg43833 FLAG pep	495	47	100.0	8	8	ADM28579	Adm28579 FLAG pep
423	47	100.0	8	7	ABU64397	Abu64397 Murine Se	496	47	100.0	8	8	ADN16201	Adn16201 FLAG pep
424	47	100.0	8	7	ADG98054	Adg98054 Peptide r	497	47	100.0	8	8	ADN75213	Adn75213 FLAG pep
425	47	100.0	8	7	ADG98834	Adg98834 FLAG pep	498	47	100.0	8	8	ADM97181	Adm97181 Anti-ADAM
426	47	100.0	8	7	ADH34359	Adh34359 FLAG pep	499	47	100.0	8	8	ADN48989	Adn48989 FLAG epit
427	47	100.0	8	7	ADG87507	Adg87507 FLAG pep	500	47	100.0	8	9	AEEO2117	Aeeo2117 Flag tag
428	47	100.0	8	7	ADG68023	Adg68023 Human TRP							
429	47	100.0	8	7	ADG46717	Adg46717 FLAG pep							
430	47	100.0	8	7	ADH69531	Adh69531 C-termina							
431	47	100.0	8	7	ADH50761	Adh50761 FLAG tag							
432	47	100.0	8	7	ADH53326	Adh53326 FLAG epit							
433	47	100.0	8	7	ADH44607	Adh44607 FLAG tag							
434	47	100.0	8	7	ADH62212	Adh62212 FLAG pep							
435	47	100.0	8	7	ADJ23513	Adj23513 FLAG pep							
436	47	100.0	8	7	ADH96361	Adh96361 Insulin r							
437	47	100.0	8	7	ADH96129	Adh96129 Insulin r							
438	47	100.0	8	7	ADI00943	Adi00943 Human zal							
439	47	100.0	8	7	ADI26319	Adi26319 Chimeric							
440	47	100.0	8	7	ADJ59016	Adj59016 Amino aci							
441	47	100.0	8	7	ADJ74026	Adj74026 FLAG-like							
442	47	100.0	8	7	ADK41232	Adk41232 G-CSF rel							
443	47	100.0	8	7	ADJ64018	Adj64018 Epitope t							
444	47	100.0	8	7	ADJ58647	Adj58647 FLAG pep							
445	47	100.0	8	7	ADM31004	Adm31004 FLAG tag							
446	47	100.0	8	7	ADJ26600	Adj26600 Multimeri							
447	47	100.0	8	7	ADJ66798	Adj66798 Shg prote							
448	47	100.0	8	7	ADM35466	Adm35466 Human LY1							
449	47	100.0	8	7	ADN62798	Adn62798 FLAG tag							
450	47	100.0	8	8	ADPF51135	Adff51135 Human PS2							
451	47	100.0	8	8	ADG45053	Adg45053 Synthetic							
452	47	100.0	8	8	ADJ78074	Adj78074 Peptide u							
453	47	100.0	8	8	ADG47239	Adg47239 FLAG pep							
454	47	100.0	8	8	ADG82594	Adg82594 FLAG pep							
455	47	100.0	8	8	ADG20761	Adg20761 FLAG epit							
456	47	100.0	8	8	ADG93200	Adg93200 Novel exp							
457	47	100.0	8	8	ADG71731	Adg71731 FLAG pep							
458	47	100.0	8	8	ADG75430	Adg75430 Human HbL							
459	47	100.0	8	8	ADH70791	Adh70791 Peptide t							
460	47	100.0	8	8	ADH53864	Adh53864 FLAG epit							
461	47	100.0	8	8	ADJ32464	Adj32464 Prostate							

ALIGNMENTS

RESULT 1

ID ABB99240 standard; peptide; 8 AA.

AC ABB99240;

DT 17-DEC-2002 (first entry)

DE Identification peptide.

KW Recombinant; protein production; identification peptide.

OS Unidentified.

PN EP150126-A.

PD 31-JUL-1985.

PF 23-JAN-1985; 85EP-00300432.

PR 24-JAN-1984; 84US-00573825.

XX 23-JUL-1987; 87US-00076811.

PA (IMMV) IMMUNEX CORP.

PI Hopp TP, Bektesh SL, Conlon PJ, March CJ;

DR WPI; 1985-185385/31.

PT Synthesis of proteins with identification peptide - using recombinant DNA
 PT techniques for economic prodn. and efficient purification. by affinity
 chromatography.

XX Example 1; Page 25; 44pp; English.

CC The invention relates to a novel process for producing protein molecules
 CC by recombinant DNA techniques. The invention also relates to a novel DNA
 CC expression vector capable of expressing a heterologous polypeptide in a
 CC transformed host cell, the polypeptide consisting of a constituent
 CC polypeptide and an attached identification peptide. The identification
 CC peptide has an antigenic terminal portion of amino acids. Recombinant DNA
 CC techniques are used for the economic production of a desired protein. It
 CC is then efficiently purified in a single affinity chromatography step
 CC with high yields. The sequence represents an identification peptide of
 CC the invention, used in the preparation of a recombinant plasmid
 CC containing the human Interleukin 2 gene

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
 DB 1 DYKDDDK 8

RESULT 2

AAP70024 standard; peptide; 8 AA.

XX AAP70024;

DT 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 12-FEB-1991 (first entry)

XX N-terminal fusion construct comprising mutant human G-CSF and yeast alpha
 DE -factor leader sequence.

XX Granulocyte-colony stimulating factor; fusion protein;
 KM yeast alpha-factor leader sequence.

XX Saccharomyces cerevisiae.

XX EP243153-A.

XX 28-OCT-1987.

XX 22-APR-1987; 87EP-00303509.

XX 22-APR-1986; 86US-00856643.

XX 14-NOV-1986; 86US-00931458.

XX (IMMV) IMMUNEX CORP.

PI Cerratti DP, Cosman DJ, Gillis S, Mochizuki DY, March CJ;
 PI Price VL, Tushinski RJ, Urdal DL;

XX WPI; 1987-300791/43.

PT New pure human granulocyte colony stimulating factor and mutants - obtd.
 PT by recombinant DNA methods in high yields, used for potentiating immune
 PT responses, treating leukemia(s) etc.

XX Disclosure; Page 13; 37pp; English.

CC The sequence encodes a fusion construct which links a mutant sequence of
 CC human granulocyte-colony stimulating factor to a yeast alpha-factor
 CC leader sequence. Fusion proteins capped with this peptide are resistant
 CC to intracellular degradation. See also AAN70029, AAN70031-35 and

CC AAP70025. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
 DB 1 DYKDDDK 8

RESULT 3

AAR09327 standard; peptide; 8 AA.

XX AAR09327;

DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 29-MAR-1992 (first entry)

XX Sequence of N-terminal octapeptide for compsn. contg. human interleukin-3
 DE (IL-3) analogue.

XX Lymphokine; bone marrow proliferation; cytopenia therapy.

XX Homo sapiens.

XX WO9001039-A.

XX 08-FEB-1990.

XX 14-JUN-1989; 89WO-US002599.

XX 20-JUL-1988; 88US-00221699.

XX (IMMV) IMMUNEX CORP.

PI Anderson DM, Cosman DJ, Price VL;

XX WPI; 1990-067162/09.

PT Compns. contg. recombinant non-glycosylated human interleukin-3 - has
 PT increased biological activity and binding affinity, for treating
 PT cytopenias.

XX Claim 5; Page 18; 23pp; English.

CC The inventors claim a pharmaceutical compsn. which contains an effective
 CC amt. of a recombinant human interleukin-3 protein analogue, rhIL-3,
 CC (Asp15,Asp70). The rhIL-3 analogue has AA SO in AAR09326. The compsn.
 CC may also comprise the N-terminal octapeptide in AAR09327, and a diluent
 CC and 1 or more than 1 biological response modifier. The compsn. has a
 CC biological specific activity of equal to or more than 4.0 x 10 to the 7
 CC mcg/mg in a human bone marrow proliferation assay, and a binding affinity
 CC for human monocyte IL-3 receptors of equal to or more than 4.0 x 10 to
 CC the 10 (M to the minus 1). (Updated on 31-OCT-2002 to add missing OS
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
 DB 1 DYKDDDK 8

RESULT 4
 AAR44496 standard; protein; 8 AA.
 ID AAR44496
 AC AAR44496;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 26-MAY-1994 (first entry)
 DE Sequence of the M2-FLAG epitope.
 KW Epitope; scFv; single chain antibody fragment; composite antibody.
 XX
 XX
 OS Synthetic.
 XX
 XX WO9324630-A1.
 PN
 XX
 PD 09-DEC-1993.
 XX
 XX
 PF 19-MAY-1993; 93WO-AU000228.
 XX
 PR 22-MAY-1992; 92AU-0002551.
 XX
 XX (AGEN-) AGEN LTD.
 PA
 XX
 PI Lilley GG, Hudson PJ, Hillyard CJ;
 XX
 DR WPI; 1993-405821/50.
 XX
 PT Bifunctional recombinant protein - contains particle and analyte binding
 PT moieties, used in agglutination assays pref. on whole blood.
 XX
 PS Example; Fig 7; 42pp; English.
 XX
 XX
 CC Epitopes of the surface protein gp41 from HIV1 and HIV2 virus types may
 CC be combined with epitopes from gp120 surface protein or p24 core protein
 CC or substituted for the M2-FLAG epitope in scFv constructs or added to the
 CC scFv-M2 FLAG construct, thereby producing various bifunctional reagents
 CC capable of binding erythrocytes and serum antibodies which may be present
 CC in patient's serum. The sequences of M2-FLAG, HIV1 and HIV2 epitopes are
 CC given in AAR44496, AAR44497 and AAR44498 respectively. (Updated on 25-MAR
 CC -2003 to correct PN field.)
 CC
 SQ Sequence 8 AA;
 QY
 DB 1 DYKDDDDK 8
 1 DYKDDDDK 8
 1 DYKDDDDK 8
 DB
 RESULT 5
 AAR77283
 ID AAR77283 standard; peptide; 8 AA.
 XX
 AC AAR77283;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 05-DEC-1995 (first entry)
 DE FLAG peptide.
 XX
 XX
 KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
 KW self-tolerance; FLAG; purification.
 XX
 XX
 OS Synthetic.
 XX
 XX WO9518819-A1.
 PN
 XX

PD 13-JUL-1995.
 XX
 XX
 PF 06-JAN-1995; 95WO-US000362.
 XX
 XX
 PR 07-JAN-1994; 94US-00179138.
 PR 01-FEB-1994; 94US-00190559.
 XX
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 XX
 PI Goodwin RG;
 XX
 DR WPI; 1995-255032/33.
 XX
 XX
 PT Human and murine DNA encoding ligand(s) binding to cell surface protein
 PT Fas - useful for studying auto-immune disorder(s) and development of self
 PT -tolerance.
 XX
 PS Disclosure; Page 6; 38pp; English.
 XX
 XX
 CC The highly antigenic FLAG peptide is used to facilitate isolation of
 CC fusion proteins contg. Fas-L proteins. The epitope is reversibly bound by
 CC a specific Mab produced by hybridoma 4E1 (ATCC HB 9259), enabling rapid
 CC assay and purification. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 8 AA;
 QY
 DB 1 DYKDDDDK 8
 1 DYKDDDDK 8
 1 DYKDDDDK 8
 DB
 RESULT 6
 AAR87022
 ID AAR87022 standard; peptide; 8 AA.
 XX
 AC AAR87022;
 XX
 DT 11-JUN-1996 (first entry)
 XX
 DE Flag octapeptide.
 XX
 KW B2LRF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;
 KW major histocompatibility complex; immunoglobulin; cytotoxic T cell;
 KW autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;
 KW systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;
 KW tissue transplant rejection; therapy; cancer; viral disease; mouse;
 KW interleukin-7.
 XX
 XX
 OS Synthetic.
 XX
 XX WO9530015-A2.
 PN
 XX
 PD 09-NOV-1995.
 XX
 XX
 PF 28-APR-1995; 95WO-US005348.
 XX
 PR 28-APR-1994; 94US-00235397.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA (UMOR) UNIV MISSOURI
 PA (USSH) US NAT INST OF HEALTH.
 XX
 XX
 PI Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM,
 PI Hutt-Fletcher LM, Spriggs MK;
 XX
 DR WPI; 1995-393086/50.
 XX
 XX
 PT Epstein-Barr virus B2LRF2 fusion proteins - used for treating e.g. auto-
 PT immune disease, transplant rejection, allergy, asthma, cancer or viral

PT infection.
 XX
 PS Example 1; Page 38; 51pp; English.
 XX
 CC This sequence represents the FLAG octapeptide, and was used in creating a
 CC BZLF2-immunoglobulin Fc fusion protein (BZLF2/Fc). BZLF2 is a Epstein-
 CC Barr virus (EBV) protein. To create BZLF2/Fc, this sequence, a mouse
 CC interleukin-7 (IL-7) leader sequence (see AAR87021), an immunoglobulin Fc
 CC region (see AAR87023) and a flexible linker (see AAR87024) are joined to
 CC the extracellular domain (residues 34 to 223) of the BZLF2 sequence (see
 CC AAR87020). BZLF2 proteins are members of the C-type lectin family. The C-
 CC type lectin domain is found in type II membrane proteins. The BZLF2
 CC protein is capable of binding the beta chain of a major
 CC histocompatibility complex (MHC) class II antigen. Fusion proteins with
 CC an oligomerizing zipper domain (OZD), instead of an immunoglobulin Fc
 CC region, can also be created. BZLF2 proteins inhibit antigen-specific
 CC antibody formation, proliferation of blood mononuclear cells and
 CC cytotoxic T cell responses. They also exhibit superantigen-like activity.
 CC The proteins can be used for treating or preventing autoimmune diseases
 CC such as myasthenia gravis, multiple sclerosis and systemic lupus
 CC erythematosus. Also, for treating organ or tissue transplant rejection
 CC and for treating or preventing allergy or asthma. They can be used for
 CC treating cancer and viral disease, especially EBV infection
 CC
 SQ Sequence 8 AA;
 QY
 Db 1 DYKDDDDK 8
 1 DYKDDDDK 8
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 7
 AAR76469
 ID AAR76469 standard; protein; 8 AA.
 XX
 AC AAR76469;
 XX
 DT 06-MAR-1996 (first entry)
 XX
 DE IBI FLAG epitope.
 XX
 DE Human: tyrosine kinase; receptor; non-differentiated; blood cell;
 KM IBI FLAG epitope.
 XX
 OS Synthetic.
 OS
 PN WO9515386-A1.
 XX
 PD 08-JUN-1995.
 XX
 PF 02-DEC-1994; 94WO-JP002035.
 XX
 PR 02-DEC-1993; 93JP-00302704.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PI Sakano S, Oono M;
 PI WPI; 1995-215266/28.
 DR N-PSDB; AAQ92644.
 XX
 PT Polypeptide and modified versions having a receptor tyrosine kinase
 PT activity - are expressed in a non-differentiated blood cell but undergo a
 PT reduction in the expression level as the non-differentiated cell
 PT differentiates.
 XX
 PS Example 8; Page 39; 73pp; Japanese.
 XX
 CC AAQ92644 encodes AAR76469 the IBI FLAG epitope, used in the prepn. of the

CC human non-differentiated blood cell tyrosine kinase receptor
 XX
 SQ Sequence 8 AA;
 QY
 Db 1 DYKDDDDK 8
 1 DYKDDDDK 8
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 8
 AAM03656
 ID AAM03656 standard; peptide; 8 AA.
 XX
 AC AAM03656;
 XX
 DT 22-FEB-1997 (first entry)
 XX
 DE FLAG-epitope tag.
 XX
 KM FLAG-epitope tag; affinity tag; Fas receptor; FADD; binding;
 KM Fas-associated protein with novel death domain; apoptosis; gene therapy;
 KM antibody; immunosay; drug screening; diagnostic; AIDS.
 KM antitumour; antitumour; cerebroprotective; neuroprotective.
 XX
 OS Synthetic.
 OS
 PN WO9631603-A2.
 XX
 PD 10-OCT-1996.
 XX
 PF 28-FEB-1996; 96WO-US002857.
 XX
 PR 03-APR-1995; 95US-00416379.
 PR 18-MAY-1995; 95US-00443982.
 XX
 PA (UNMT) UNIV MICHIGAN.
 PI
 PI Dixit VM, O'Rourke K;
 PI WPI; 1996-465026/46.
 DR
 XX
 PT FADD protein that binds to cytoplasmic region of Fas receptor - for
 PT identifying inhibitors of Fas-associated apoptosis useful for treating
 PT e.g. AIDS, leukaemia, stroke, etc.
 XX
 PS Example 1; Page 51; 96pp; English.
 XX
 CC This FLAG-epitope tag peptide has been fused to a Fas receptor, which
 CC contains a cytoplasmic region binding a novel FADD protein (Fas-
 CC associating protein with novel death domain, AAT93937), which modulates
 CC apoptosis induced by activation of the receptor by ligand binding. DNA
 CC encoding the tag is fused to the Fas gene and mutants by PCR, downstream
 CC of a putative Fas signal peptide sequence. In a plasmid pcDNA3 vector,
 CC using a 5'-FLAG PCR primer (AAT93938). The resulting fusion protein is
 CC expressed in Escherichia coli and used in an assay to demonstrate in vivo
 CC association of FADD protein and Fas receptor via death domains. FADD DNA
 CC may be used in gene therapy, and FADD protein or a corresponding antibody
 CC functions and Fas-associated apoptosis, for use in therapy of e.g. AIDS,
 CC inflammation, leukaemia, myocardial infarction, degenerative disease, etc
 XX
 SQ Sequence 8 AA;
 QY
 Db 1 DYKDDDDK 8
 1 DYKDDDDK 8
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DYKDDDDK 8

RESULT 9
AAR91066
ID AAR91066 standard; peptide; 8 AA.
XX
AC AAR91066;
XX
DT 23-MAY-1996 (first entry)
XX
DE Affinity tag peptide.
XX
KM Interleukin-1 type-3 receptor; IL-1-3R; immune-associated disease;
KM vector; antibody; therapy; affinity tag.
XX
OS Synthetic.
XX
PN WO9607739-A2.
XX
PD 14-MAR-1996.
XX
PF 11-SEP-1995; 95WO-US012037.
XX
PR 09-SEP-1994; 94US-00303957.
XX
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Lovenberg TW, Oltersdorf T, Liaw CW, Clevenger W, Desouza EB;
XX
DR WPI; 1996-171614/17.
XX
PT Interleukin-1 type 3 receptor proteins - useful for the treatment of
PT immune-associated diseases.
XX
PS Disclosure; Page 7; 64pp; English.
XX
CC An affinity tag (AAR91066) may be linked to interleukin-1 type-3
CC receptors (see e.g. AAR91064 and AAR91054) produced by recombinant DNA
CC technology. The peptide facilitates purification of the expressed
CC recombinant protein
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 10
AAR91045
ID AAR91045 standard; peptide; 8 AA.
XX
AC AAR91045;
XX
DT 25-MAR-2003 (revised)
DT 01-AUG-1996 (first entry)
XX
DE Antigenic N-terminal peptide for fusion to shuIL-1R.
XX
KM Interleukin-1 receptor; human; soluble; N-terminal peptide; antigen;
KM epitope; shuIL-1R; monoclonal antibody; bovine mucosal enterokinase;
KM interleukin-1; IL-1; immune response; mammal; diagnosis; therapy;
KM regulation; immune disease; inflammatory disease.
XX
OS Synthetic.
XX
PN US5492888-A.
XX

PD 20-FEB-1996.
XX
XX 17-JUN-1992; 92US-00904071.
XX
PR 25-NOV-1987; 87US-00125627.
XX
PR 25-FEB-1988; 88US-00160550.
XX
PR 13-OCT-1988; 88US-00258756.
XX
PR 21-DEC-1989; 89US-00455488.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JF, Dower SK, March CJ, Urdal DL;
XX
XX WPI; 1996-150236/15.
XX
DR Use of sol. IL-1 receptors to suppress IL-1-mediated immune responses -
PT e.g. for treatment of inflammation in mammals, esp. humans.
XX
XX Disclosure; Col 8; 22pp; English.
XX
CC This sequence represents an antigenic N-terminal peptide epitope. This
CC sequence can be fused to soluble human interleukin-1 receptor (shuIL-1R).
CC By using this sequence, recombinant shuIL-1R can be assayed and purified
CC easily, by using a monoclonal antibody that reversibly binds this
CC epitope. By using bovine mucosal enterokinase, this sequence can be
CC cleaved from the recombinant shuIL-1R. Proteins capped with this peptide
CC may also be resistant to intracellular digestion in E. coli. The shuIL-1R
CC can be used in a method for suppressing interleukin-1 (IL-1) mediated
CC immune responses in a mammal. The method comprises administering an
CC effective amount of shuIL-1R to the mammal, preferably in a dose of 500ng
CC -5mg/kg/day. The shuIL-1R is effective for use in assay, diagnosis or
CC therapy for regulation of immune or inflammatory activities, in contrast
CC to membrane-bound full-length mature IL-1 receptors. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 11
AAR89288
ID AAR89288 standard; peptide; 8 AA.
XX
AC AAR89288;
XX
DT 13-APR-1996 (first entry)
XX
DE FLAG affinity tag peptide.
XX
KM FLAG; affinity tag; immunoaffinity chromatography; purification;
KM affinity chromatography; immunoassay; monoclonal antibody;
KM fusion protein; cleavage; cattle mucosal enterokinase; LfEK-5; cytokine;
KM elk; hek; protein-tyrosine-kinase; receptor; human fetal brain; cloning;
KM drug delivery; cell targeting; cytostatic; leukaemia; therapy.
XX
OS Synthetic.
XX
PN WO9601839-A1.
XX
XX 25-JAN-1996.
XX
PD 06-JUL-1995; 95WO-US008534.
XX
PF 08-JUL-1994; 94US-00271948.
XX
PR (IMMV) IMMUNEX CORP.
XX

XX	Cerretti DP, Reddy P;
PI	
XX	WPI, 1996-097585/10.
DR	
XX	DNA encoding LERK-5 cytokine capable of binding elk and hek - used as
PT	carrier to deliver attached (anti-leukemic) agents to cells bearing elk
PT	or hek, i.e. human leukaemia cell lines JM and LK63.
PS	
XX	Disclosure; Page 8; 40pp; English.
CC	
XX	The sequence represents a FLAG affinity tail, which may be attached to
CC	e.g. a full-length or soluble LERK-5 cytokine (AAR89287) to facilitate
CC	purification. LERK-5 binds elk and hek receptor protein-tyrosine-kinases
CC	(members of the eph/elk family), and may be isolated e.g. by expression
CC	from a human fetal brain cell cDNA. The FLAG peptide is highly antigenic
CC	and provides an epitope reversibly bound by a specific monoclonal
CC	antibody, enabling rapid immunosassay and purification by immunoaffinity
CC	chromatography. The sequence is specifically cleaved by cattle mucosal
CC	enterokinase at the residue immediately following the Asp-Tyr pairing.
CC	Purified LERK-5 may be used in binding assays to detect elk- or hek-
CC	expressing cells, to measure elk or hek activity, as a drug delivery for
CC	elk or hek receptor-specific cell targeting, e.g. for delivery of
CC	cytostatic agents in leukaemia therapy
SQ	
Sequence 8 AA;	
Query Match	100.0%; Score 47; DB 2; Length 8;
Best Local Similarity	100.0%; Pred. No. 2,le+06;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 DYKDDDK 8 1 DYKDDDK 8
Db	
RESULT 12	
AAR94931	
ID	AAR94931 standard; peptide; 8 AA.
AC	
XX	AAR94931;
XX	23-OCT-1996 (first entry)
DT	
DE	FLAG peptide.
KW	Interleukin-4 receptor; IL-4; interleukin-2 gamma-C receptor; IL-2; allergic rhinitis; asthma; atopic dermatitis; eczema; HIV; FLAG. Synthetic.
OS	
PN	MO9611213-A1.
PD	18-APR-1996.
PF	05-OCT-1995; 95WO-US013101.
PR	07-OCT-1994; 94US-00319496.
PA	(AMGE-) AMGEN BOULDER INC.
Vanderlize RW, Cox GM;	
WPI, 1996-209810/21.	
Dimeric complex having affinity for interleukin-4 - comprises IL-4- receptor homodimer or IL-4-IL2 gamma-C receptor heterodimer, used in treatment of e.g. eczema, asthma and HIV.	
Example 4; Page 21; 53pp; English.	
FLAG is an octapeptide (AAR94931) that is used to facilitate purification of a protein using anti-FLAG monoclonal antibody. A DNA construct was	

CC	produced that coded for IL-2Rgamma-C FLAG comprising the 254-amino acid extracellular domain of human interleukin-2 receptor gamma chain plus an additional C-terminal cysteine and the FLAG peptide. The fusion was expressed in Sf9 cells using a baculovirus expression system and purified by affinity chromatography. IL-2Rgamma-C FLAG can be linked to CC interleukin-4 via a polymeric (PEG) spacer. The resulting dimeric complex CC has affinity for IL-4 and can be used to treat IL-4 mediated disease CC involving elevated IGE levels
SQ	Sequence 8 AA;
Query Match	100.0%; Score 47; DB 2; Length 8;
Best Local Similarity	100.0%; Pred. No. 2.1e+06;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 DYKDDDK 8
Db	1 DYKDDDK 8
RESULT 13	
AAM18236	
ID	AAM18236 standard; peptide; 8 AA.
AC	AAM18236;
DT	01-OCT-1997 (first entry)
DE	FLAG epitope.
KW	Lysosomal enzyme; lysosome; transgenic plant; glucocerebrosidase; alpha-L-iduronidase; IDUA; enzyme replacement therapy; Gaucher disease; Hunter syndrome; FLAG.
OS	Synthetic.
XX	WO9710353-A1.
XX	20-MAR-1997.
PD	
XX	
PX	13-SEP-1996; 96WO-US044730.
PR	14-SEP-1995; 95US-0003737P.
PA	(VIRG) VIRGINIA TECH INTELLECTUAL PTY INC. (CROP-) CROPTech DEV CORP.
PI	Radin DN, Cramer CL, Oishi KK, Weissenborn DL; WPI: 1997-202248/18.
DR	
XX	
PT	Production of enzymatically active (modified) lysosomal enzyme in transgenic plants - useful in treatment of lysosomal storage disorders.
PS	Claim 6; Page 37; 11pp; English.
CC	The FLAG epitope (AAM18236) is utilised in novel constructs for expression of lysosomal enzymes, e.g. human glucocerebrosidase and alpha-L-iduronidase in transgenic plants. The epitope coding sequence is fused in-frame to the C-terminus of the lysosomal enzyme coding sequence (see also AAT71755) in order to facilitate the detection and purification of the gene product. (see also AAM18237). It is designed to be a hydrophilic marker peptide situated on a protein surface to facilitate antibody interactions
CC	
XX	
SQ	Sequence 8 AA;
Query Match	100.0%; Score 47; DB 2; Length 8;
Best Local Similarity	100.0%; Pred. No. 2.1e+06;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 DYKDDDK 8


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Db      1 DYKDDDDK 8

RESULT 14
AAM32484
XX      AAM32484 standard; peptide; 8 AA.
XX
AC      AAM32484;
XX
DT      27-MAR-1998 (first entry)
XX
DE      FLAG epitope.
XX
KW      Catalytic antibody; growth factor; B-cell mitogenesis; LHL; L protein;
KM      hen egg lysozyme; FLAG epitope.
XX
OS      Synthetic.
XX
PN      WO9735887-A1.
XX
PD      02-OCT-1997.
XX
PF      26-MAR-1997; 97WO-AU000194.
XX
PR      26-MAR-1996; 96AU-00008951.
XX
PR      27-FEB-1997; 97AU-00005375.
XX
PA      (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI      Koentgen F, Suesse GW, Tarlinton DM, Treutlein HR;
XX
DR      WPI; 1997-489572/45.
XX
PT      New catalytic antibody precursors - comprising a B-cell surface molecule
PT      binding portion which can induce B-cell mitogenesis.
XX
PS      Example 3; Page 40; 109pp; English.
XX

CC      This peptide comprises the FLAG epitope that is recognised by anti-FLAG
CC      monoclonal antibodies. A form of novel growth factor LHL (see AAM32479)
CC      was generated by PCR that contains the FLAG epitope at its N-terminus and
CC      a strep-tag (see AAM32485) at its C-terminus. The construct is designated
CC      LHL.seq (see AAM32481), where L is the immunoglobulin binding entity from
CC      Peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme.
CC      The FLAG-epitope was added to facilitate the secretion of LHL.seq into
CC      the periplasmic space of host cells. However, this was unsuccessful and
CC      LHL.seq needed to be purified from total bacterial lysate. As a result of
CC      this, the ompA signal peptide was not removed, leading to the formation
CC      of LHL.seq multimers. LHL.seq has identical activity to that of LHL, and
CC      can be used in novel methods for the generation of catalytic antibodies
XX
SQ      Sequence 8 AA:

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
       |||||||
Db      1 DYKDDDDK 8

RESULT 15
AAM00971
ID      AAM00971 standard; peptide; 8 AA.
XX
AC      AAM00971;
XX
DT      12-NOV-1997 (first entry)
XX
DE      FLAG epitope.
XX
KW      DNA binding protein; RNA binding protein; amphipathic peptide;

```

```

KM      acidic extension peptide; gene control; gene regulation; transcription;
KM      dominant negative protein; cancer; drug therapy; drug design;
KM      leucine zipper; FLAG.
XX
OS      Synthetic.
XX
PN      WO9705249-A2.
XX
PD      13-FEB-1997.
XX
PF      31-JUL-1996; 96WO-US012590.
XX
PR      31-JUL-1995; 95US-0001654P.
XX
PR      29-MAY-1996; 96US-0018496P.
XX
PR      31-JUL-1996; 96US-00690011.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Vinson CR, Ktylov D;
XX
DR      WPI; 1997-145687/13.
XX
PT      New nucleic acid binding proteins - having an acidic amino acid sequence
PT      extension at the amino-terminus, to increase ability to regulate gene
PT      transcription, useful e.g. in cancer therapeutics.
XX
PS      Claim 16; Page 58; 144pp; English.
XX

CC      This peptide sequence comprises a FLAG epitope that can be attached to
CC      the N-terminus of a nucleic acid binding protein (NABP) such as a leucine
CC      zipper bZIP protein or bHLH protein. Claimed NABPs having an appended
CC      acidic extension peptide (see AAM00958-65) can regulate the function of a
CC      target nucleic acid or gene to which they are bound, and act as potent
CC      dominant-negative regulators of gene transcription, cell growth and cell
CC      proliferation. They can be used in cancer therapeutics, to treat diseases
CC      caused by eukaryotic microorganisms or by viruses, and as tools for drug
CC      development, rational drug design, and drug and gene therapies
XX
SQ      Sequence 8 AA:

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
       |||||||
Db      1 DYKDDDDK 8

RESULT 16
AAM09824
ID      AAM09824 standard; peptide; 8 AA.
XX
AC      AAM09824;
XX
DT      15-JUL-1997 (first entry)
XX
DE      FLAG epitope tag.
XX
KW      NR4; haemoprotein receptor; interleukin-13 receptor; cytokine; allergy;
KM      asthma; therapy; FLAG.
XX
OS      Synthetic.
XX
PN      WO9715663-A1.
XX
PD      01-MAY-1997.
XX
PF      23-OCT-1996; 96WO-AU000668.
XX
PR      23-OCT-1995; 95AU-00006135.
XX
PR      22-DEC-1995; 95AU-00007276.
XX
PR      09-SEP-1996; 96AU-00002208.

```

XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX
 XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
 XX
 DR WPI, 1997-259018/23.
 XX
 PT DNA encoding animal haemopoietin receptor which interacts with
 PT interleukin-13 - useful to treat asthma, allergy or condition exacerbated
 PT by Ige production.
 XX
 PS Example 2, Page 56; 93pp; English.
 XX
 CC Using PCR, a derivative of novel haemoprotein receptor NR4 cDNA was
 CC generated which encoded the interleukin-3 signal peptide (AAW09823) and
 CC an N-terminal FLAG epitope tag (AAW09824) preceding the mature coding
 CC region (Thr27-Pro424) of murine NR4 (see also AAW09821). The PCR product
 CC was cloned into the mammalian expression vector pBF-BOS
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 17
 AAW46330
 ID AAW46330 standard; peptide; 8 AA.
 XX
 AC AAW46330;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Binding domain of chimeric adenovirus penton base protein.
 XX
 KM Integrin; cell surface receptor; penton base protein; adenovirus;
 KM binding site; binding domain; cell surface binding site; gene therapy;
 KM bispecific molecule; antibody; adenoviral transfer vector; PAT.
 XX
 OS Synthetic.
 XX
 PN US5712136-A.
 XX
 PD 27-JAN-1998.
 XX
 PF 17-APR-1996; 96US-00634060.
 XX
 PR 08-SEP-1994; 94US-00303162.
 XX
 PA (GENV-) GENVEC INC.
 XX
 PI Bruder JT, Mcvey DL, Wickham TJ, Roelivink PW, Kovessi I;
 PI Brough DE;
 XX
 DR WPI, 1998-119984/11.
 XX
 PT Methods for introducing adenovirus into cells - used for genetic
 PT engineering and gene therapy.
 XX
 PS Claim 14; Col 16; 56pp; English.
 XX
 CC The present sequence represents a binding domain of a chimeric adenovirus
 CC penton base protein. The present sequence contains an epitope for an
 CC antibody that is preferably not present in wild type adenovirus protein.
 CC The penton base protein binds to cell surface receptors called integrins.
 CC The integrins not only provide a binding site for the adenoviral penton
 CC base protein, but also mediate cellular adhesion to the extracellular
 CC matrix molecules. The specification describes a method of introducing an

CC adenovirus into a cell in vitro having a particular cell surface binding
 CC site. The adenovirus is contacted with a bispecific molecule (e.g.
 CC bispecific antibody) comprising a component that selectively binds a
 CC binding domain of the penton base protein of the adenovirus and a second
 CC component that selectively binds the cell surface binding site. A complex
 CC of the adenovirus and the bispecific molecule is formed, and the cell is
 CC contacted with it to allow entry of the adenovirus into the cell. The
 CC methods can be used for research and the vectors can be used for gene
 CC therapy
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 18
 AAW80476
 ID AAW80476 standard; peptide; 8 AA.
 XX
 AC AAW80476;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Peptide sequence encoded by an antilease primer.
 XX
 KM EST sequence; CS141; gastrointestinal tract; cancer; Barrett's esophagus;
 KM gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease;
 KM ulcerative colitis; pancreatitis.
 XX
 OS Synthetic.
 XX
 PN WO9844133-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 31-MAR-1998; 98WO-US006337.
 XX
 PR 31-MAR-1997; 97US-00828489.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI, 1998-568280/48.
 XX
 PT New gastrointestinal tract specific polynucleotides, CS141 - used to
 PT develop products for the diagnosis and treatment of e.g. cancers, gastric
 PT ulcer, gastritis, Crohn's disease, ulcerative colitis or pancreatitis.
 XX
 PS Example 10; Page 67; 116pp; English.
 XX
 CC The present sequence represents a peptide sequence encoded by an
 CC antilease primer of the invention. The sequence incorporates a
 CC recognition site to aid in analysis and purification of the CS141
 CC protein. A set of contiguous and partially overlapping EST sequences
 CC (AAV63504-15) are designated CS141. The sequences are isolated from a
 CC cDNA library made from gastrointestinal tract tumour and normal tissues.
 CC The CS141 gene is useful as a marker for gastrointestinal tract
 CC disorders. The methods and products can be used in detecting, diagnosing,
 CC staging, monitoring, prognosticating, preventing, or determining the
 CC predisposition to diseases and conditions of the gastrointestinal tract,
 CC such as gastrointestinal tract cancers, Barrett's esophagus, gastric
 CC ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis,
 CC pancreatitis
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 19
 AAW54166
 ID AAW54166 standard; peptide; 8 AA.
 XX
 AC AAW54166;
 XX
 DT 17-AUG-1998 (first entry)
 XX
 DE FLAG-epitope.
 XX
 KW Protein targeting to glycogen; PTG; PPIC; mouse; diabetes; animal model;
 KM knockout mouse; FLAG epitope.
 XX
 OS Synthetic.
 XX
 PN WO9808948-A1.
 XX
 PD 05-MAR-1998.
 XX
 PF 22-AUG-1997; 97WO-US014142.
 XX
 PR 30-AUG-1996; 96US-0025107P.
 XX
 PR 12-AUG-1997; 97US-0055243P.
 XX
 PA (WARREN) WARNER LAMBERT CO.
 XX
 PI Brady MJ, Printen JA, Saltiel AR;
 XX
 DR WPI; 1998-230264/20.
 XX
 PT Isolated protein targeting to glycogen genes - used to develop products
 for increasing glycogen levels in cells and to develop animal models for
 the study of e.g. diabetes.
 XX
 PS Disclosure; Page 24; 71pp; English.
 XX
 CC This FLAG epitope was introduced into pCI-neo by ligating complementary
 CC oligonucleotides into NheI/EcoRI digested vector. An EcoRI fragment from
 CC murine clone B1-1, which codes for novel protein targeting to glycogen
 CC (PTG) protein (see AAW54164), was cloned at the EcoRI site of the
 CC resulting plasmid. The FLAG epitope-tagged PTG construct was transiently
 CC transfected into CHO cells over-expressing the insulin receptor. Results
 CC showed that PTG can direct PPIC localisation to glycogen both in vivo and
 CC in vitro. PTG can be used to develop products for increasing glycogen
 CC levels in cells and to develop animal models for the study of e.g.
 CC diabetes
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 20
 AAW64456
 ID AAW64456 standard; protein; 8 AA.
 XX

AC AAW64456;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 XX Human CHK protein flag epitope.
 DE
 XX Breast; cancer; matk; CSK homologous kinase; CHK; detection; diagnosis;
 KW cytoplasmic protein; tyrosine kinase; ErbB-2; negative regulator;
 KM mitogenic signalling.
 XX
 OS Homo sapiens.
 XX
 PN WO9830704-A1.
 XX
 PD 16-JUL-1998.
 XX
 PF 07-JAN-1998; 98WO-US000420.
 XX
 PR 08-JAN-1997; 97US-0035228P.
 XX
 PR 16-JUN-1997; 97US-00876882.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Abraham H, Groopman JE;
 XX
 DR WPI; 1998-399149/34.
 XX
 PT Detecting breast cancer by detecting Csk homologous kinase expression -
 especially in humans and use of Csk homologous kinase in treatment or
 PT prophylaxis of breast cancer and for producing medicaments.
 XX
 PS Example 3; Page 26; 54pp; English.
 XX
 CC This sequence represents a CSK homologous kinase (CHK) derived flag
 CC epitope which is used in a method of detecting cancer in breast tissue.
 CC The method allows diagnosis of breast cancer in mammals, especially
 CC humans. It is based on the discovery that a cytoplasmic protein tyrosine
 CC kinase, CHK, is expressed in human breast tissue, but not in adjacent
 CC tissue. This protein can be used to raise antibodies which can be
 CC included in compositions and diagnostic kits for diagnosis of breast
 CC cancer. The presence of CHK in breast tissue can also be determined using
 CC other standard methods (e.g. Northern blotting) or by detecting nucleic
 CC acid sequences encoding all/a portion of the protein (e.g. using
 CC hybridisation probes). Over-expression of the receptor tyrosine kinase
 CC ErbB-2 has previously been associated with the development of breast
 CC cancer, and CHK specifically interacts with activated ErbB-2, and may
 CC function as a negative regulator of ErbB-2 mediated mitogenic signalling.
 CC The compositions may also be used to design drugs (e.g. which incorporate
 CC CHK analogues with greater biological activity than CHK) and to identify
 CC CHK antagonists and agonists for therapeutic use
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 21
 AAW56763
 ID AAW56763 standard; peptide; 8 AA.
 XX
 AC AAW56763;
 XX
 DT 05-AUG-1998 (first entry)
 XX
 DE FLAG peptide epitope used for producing soluble TRAIL polypeptide.
 XX
 KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human;
 XX

KM cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection; FLAG;
 XX epitope.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN US5763223-A.
 XX
 PD 09-JUN-1998.
 XX
 PF 25-JUN-1996; 96US-00670354.
 XX
 PR 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Goodwin RG, Wiley SR;
 XX
 DR WPI; 1998-347322/30.
 XX
 PT DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful
 PT for producing recombinant polypeptides for research and therapy of
 PT leukaemia, lymphoma, melanoma and viral infections.
 XX
 PS Example 7; Col 45; 28pp; English.
 XX
 CC This is a FLAG peptide epitope used in an expression vector for producing
 CC a soluble human tumour necrosis factor related apoptosis ligand (TRAIL)
 CC polypeptide. The human and murine TRAIL polypeptides can induce apoptosis
 CC of Jurkat cells. The encoding nucleic acid sequences are useful for
 CC producing the recombinant TRAIL polypeptides, which may be useful in
 CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells
 CC (e.g. to isolate antigens for vaccine development). The polypeptides can
 CC be used to treat leukaemia, lymphoma or melanoma (e.g. by intracorporeal
 CC treatment of blood or bone-marrow), or to treat viral infections
 CC
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8
 |||||
 RESULT 22
 AAW82555
 ID AAW82555 standard; protein; 8 AA.
 XX
 AC AAW82555;
 XX
 DT 09-FEB-1999 (first entry)
 XX
 DE Human LIR FLAG peptide.
 XX
 DE Immunoregulator; leukocyte immunoglobulin-like receptor; suppressor;
 KM therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhibitor;
 KM cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator;
 KM negative signalling; autoimmune disease; LIR.
 XX
 OS Synthetic.
 XX
 FN WO9848017-A1.
 XX
 PD 29-OCT-1998.
 XX
 PF 23-APR-1998; 98WO-US008244.
 PF 24-APR-1997; 97US-00842248.
 PR
 XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI Cosman DJ;
 XX
 DR WPI; 1998-609990/51.
 XX
 PT Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g.
 PT for treating autoimmune diseases or disease states associated with
 PT suppressed immune function.
 XX
 PS Disclosure; Page 18; 112pp; English.
 XX
 CC This FLAG peptide is used in a method to isolate novel leukocyte
 CC immunoglobulin-like receptor (LIR) polypeptides. These proteins can be
 CC administered therapeutically to treat disorders associated with
 CC insufficient/defective amounts of LIR polypeptide. LIR-P3G2 and certain
 CC other LIR family members contain cytoplasmic immunoreceptor tyrosine-
 CC based inhibitory motifs (ITIMs), whilst other LIR family members lack
 CC ITIMs. By analogy with the structure and function of known MHC Class I
 CC receptor molecules, LIRs having ITIMs are inhibitory receptors mediating
 CC negative signalling, whilst those lacking ITIMs are activatory receptors.
 CC Failure of a receptor that mediates negative signalling could result in
 CC autoimmune diseases, whilst failure of a receptor mediating activatory
 CC signalling could result in suppressed immune function. They are also
 CC useful to produce probes for detecting LIR nucleic acids or isolating LIR
 CC DNA from other species
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8
 |||||
 RESULT 23
 AAW75874
 ID AAW75874 standard; peptide; 8 AA.
 XX
 AC AAW75874;
 XX
 DT 25-MAR-2003 (revised)
 DT 30-OCT-1998 (first entry)
 XX
 DE Peptide used in LU105 expression plasmid construction.
 XX
 DE LU105; lung disease marker; immunoassay; lung disease; cancer; blood;
 KM plasma; serum.
 KM
 XX
 OS Synthetic.
 OS
 PN WO9833926-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JAN-1998; 98WO-US001766.
 PF 31-JAN-1997; 97US-00791710.
 PR
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrapp L;
 PI Russell JC, Stroupe SD;
 XX
 DR WPI; 1998-437479/37.
 XX
 PT New nucleic acid for the lung disease marker LU105 - polypeptides,
 PT antibodies and genes, used for diagnosis, prevention, treatment of lung
 PT disease, specifically cancer.

XX Example 11; Page 98; 123pp; English.

PS This peptide is used in the construction of a plasmid expressing LU105

XX polypeptides. Sequences shown in AAV54616 to AAV54621 represent LU105

CC specific polynucleotide sequences which are used in the method of the

CC invention for detecting target LU105 nucleic acid. The method comprises

CC treating a sample with at least one LU105 specific nucleic acid, or its

CC complement which is at least 50 percent identical with the LU105 specific

CC nucleic acid sequences. LU105 is a lung disease marker. Cells transformed

CC with a recombinant expression system that contains LU105 specific nucleic

CC acid fragments, are used to express recombinant LU105 polypeptides which

CC are used to raise antibodies. The antibodies are used to detect the LU105

CC antigen, and correspondingly this antigen is used to detect specific

CC antibodies, in usual immunoassays. The LU105 polypeptides and nucleic

CC acid sequences are used for diagnosis, staging, monitoring, prognosis,

CC prevention, treatment and determination of susceptibility to, lung

CC disease, specifically cancer. The LU105 polypeptides are also used to

CC screen for specific binding agents, useful therapeutically. LU105 is a

CC marker for lung disease (present at high concentration. In altered form

CC or in an unusual body compartment). LU105 can be detected in blood

CC plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-

CC 2003 to correct PI field.)

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

1 |||||

Db 1 DYKDDDDK 8

RESULT 24

AAB99286

ID AAB99286 standard; peptide; 8 AA.

XX

AC AAB99286;

DT 12-SEP-2001 (first entry)

XX

DE FLAG peptide.

XX

KW TRAIL receptor; TRAIL-R; thrombotic thrombocytopenic purpura;

KW tumour necrosis factor-related apoptosis-inducing ligand; HIV infection;

KW haemolytic-uraemic syndrome; systemic lupus erythematosus; apoptosis;

KW FLAG peptide.

XX

OS Synthetic.

XX

PN WO9835986-A1.

XX

PD 20-AUG-1998.

XX

PF 11-FEB-1998; 98WO-US002239.

XX

PR 13-FEB-1997; 97US-00799861.

XX

PR 12-MAR-1997; 97US-00815255.

XX

PR 28-MAR-1997; 97US-00829536.

XX

PR 04-JUN-1997; 97US-00869852.

XX

PR 26-JUN-1997; 97US-00883036.

XX

PA (IMMUNEX) IMMUNEX CORP.

XX

PI Rauch C, Walczak H;

XX

DR WPI; 1998-480767/41.

XX

PT New TRAIL receptor protein and related oligomers, nucleic acid, vectors -

PT used to inhibit TRAIL activity, e.g. in cases of thrombotic purpura,

PT clotting in small blood vessels etc., also for diagnosis.

XX Example 1; Page 31; 53pp; English.

XX

CC The present invention relates to human TRAIL-receptor polypeptide and

CC coding sequence (TRAIL-R; where TRAIL is tumour necrosis factor-related

CC apoptosis-inducing ligand, see AA46372 and AAB99284). TRAIL-R protein

CC and coding sequence can be used to treat conditions involving defective

CC or inadequate TRAIL-R, e.g. thrombotic thrombocytopenic purpura,

CC haemolytic-uraemic syndrome, clotting of small blood vessels, systemic

CC lupus erythematosus and TRAIL-mediated apoptosis of T cells in human

CC immune deficiency virus infections. The present sequence is the FLAG

CC peptide, which was used in an example from the present invention

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

1 |||||

Db 1 DYKDDDDK 8

RESULT 25

AAW54280

ID AAW54280 standard; peptide; 8 AA.

XX

AC AAW54280;

DT 25-MAR-2003 (revised)

XX

DT 29-JUL-1998 (first entry)

XX

DE Peptide sequence used in constructing a BU101 expression plasmid.

XX

KW BU101; breast cancer; diagnosis; prevention; treatment; gene therapy;

KW immunisation; drug screening.

XX

OS Homo sapiens.

XX

PN WO9807857-A1.

XX

PD 26-FEB-1998.

XX

PF 19-AUG-1997; 97WO-US014665.

XX

PR 19-AUG-1996; 96US-00697105.

XX

PR 15-AUG-1997; 97US-00912276.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Billings-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

PI Russell JC, Stroupe SD;

XX

DR WPI; 1998-169161/15.

XX

PT New BU101 protein over-expressed in breast cancer - useful for, e.g.

PT diagnosis, treatment and prevention of breast cancer.

XX

XX Example 11; Page 66; 105pp; English.

XX

CC The sequence encoding this peptide is incorporated into a primer for

CC constructing a BU101 protein expression plasmid. BU101 is a member of the

CC uteroglobin family of proteins and is over-expressed in breast cancer.

CC Cells transformed with a recombinant expression system comprising a

CC sequence derived from the BU101 open reading frame and with at least 50

CC percent identity to the sequences shown in AAV26458 to AAV26461 are used

CC to produce BU101 polypeptides containing at least 1 epitope. These are

CC used to detect BU101-specific antibodies which are used correspondingly

CC to detect BU101 antigens. The BU101 polynucleotide sequences can be used

CC in a method for detecting the presence of a target BU101 polynucleotide.

CC The various assays are used for diagnosis, prognosis, staging,

CC monitoring, treating and preventing diseases of the breast (especially
CC cancer and its metastases), and also for determining susceptibility. The
CC B101 polypeptides are also useful in drug screening, e.g. to identify
CC antagonists of B101, potentially useful therapeutically and as targets
CC for therapy. The antibodies are also useful for targeted drug delivery
CC and therapeutically to neutralise B101 polypeptides. Fragments of the
CC B101 nucleic acid are useful as probes and primers, e.g. for detection
CC of altered gene expression or in fluorescent in situ hybridisation, also
CC in gene therapy to generate antisense or ribozyme molecules or for
CC genetic immunisation. (Updated on 25-MAR-2003 to correct PI field.)

XX
SQ .Sequence 8 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 2; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
| | | | | | | |
DB 1 DYKDDDDK 8

RESULT 26

ID AAM44300 standard; peptide; 8 AA.
XX
AC AAM44300;

XX
XX 19-JUN-1998 (first entry)

XX
DE Human serrate 2 FLAG peptide.

XX
XX Human; serrate 2; regulation; stem cell; differentiation; neoplasm;

KM Leukemia; endothelial cell; tumour; FLAG.

OS Synthetic.

OS Homo sapiens.

PN WO9802458-A1.

XX
XX 22-JUN-1998.

XX
PF 11-JUL-1997; 97WO-JP002414.

XX
PR 16-JUL-1996; 96JP-00186220.

XX
PR 14-MAY-1997; 97JP-00124063.

PA (ASAH) ASAH1 KASEI KOGYO KK.

PI Sakano S, Itoh A;

PI
DR WPI; 1998-110528/10.

DR N-PSDB; AAV15195.

XX
PT Human serrate-2 gene expression products - used to regulate stem cell
PT differentiation, useful in treating neoplasms, e.g. leukaemia.

XX
PS Example 4; Page 92; 103pp; Japanese.

XX
CC The present sequence represents a FLAG peptide for human serrate 2, used
CC in an example of the present invention which describes human serrate 2.
CC The present invention also describes a method for the preparation of the
CC polypeptides, and antibodies binding to the polypeptide and its
CC fragments. The polypeptide and its fragments expressed by the serrate-2
CC gene can be used to inhibit stem (especially blood stem) cell
CC differentiation and to inhibit endothelial cell growth. They may be
CC incorporated in a cell culture media for culturing undifferentiated stem
CC cells. They can also be used for treatment of neoplasms such as
CC leukaemia. The antibodies can be used for the diagnosis of malignant
CC tumours

XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
| | | | | | | |
DB 1 DYKDDDDK 8

RESULT 27

ID AAM59269 standard; protein; 8 AA.
XX
AC AAM59269;

XX
XX 27-AUG-1998 (first entry)

XX
DE Type II IL-1R protein antigenic motif.

XX
XX Type II interleukin-1 receptor; IL-1R; immune response; inflammation;

KM regulation; soluble; cell surface receptor; treatment; alloantigen;

KM tissue; organ; rejection; transplant; graft-versus-host disease;

KM autoimmune dysfunction; T-cell activation; self antigen;

XX
XX rheumatoid arthritis; diabetes mellitus; multiple sclerosis.

OS Homo sapiens.

OS Mus sp.

PN US5767064-A.

XX
XX 16-JUN-1998.

XX
PF 16-MAY-1995; 95US-00442043.

XX
XX 05-JUN-1990; 90US-00534193.

XX
PR 24-AUG-1990; 90US-00573576.

XX
PR 13-DEC-1990; 90US-00627071.

XX
PR 16-MAY-1991; 91US-00701415.

XX
PR 12-JUL-1993; 93US-00091519.

XX
PR 13-MAY-1994; 94US-00242211.

XX
PA (IMMV) IMMUNEX CORP.

PI Cosman DJ, Lupton SD, Mosley BA, Dower SK, Sims JE;

XX
XX WPI; 1998-361746/31.

XX
PT Regulation of interleukin-1 mediated immune or inflammatory response in

XX
PT mammal - comprises administering soluble IL-1 receptor protein, used in

XX
XX treatment of e.g. graft versus host disease and multiple sclerosis.

XX
PS Disclosure; Col 8; 33pp; English.

XX
XX This sequence represents an antigenic motif found in human and mouse type

XX
XX II interleukin-1 receptor (IL-1R). This receptor is used in a method to

XX
XX investigate the regulation of the immune or inflammatory response in a

XX
XX mammal. This method involves administering a soluble type-II IL-1

XX
XX receptor protein in an amount effective to bind to IL-1 and prevent its

XX
XX binding to cell-surface IL-1 receptors. The process can be used for

XX
XX treating alloantigen-induced rejection of transplanted tissues or organs,

XX
XX graft-versus-host disease and autoimmune dysfunction dependent upon the

XX
XX activation of T cells against self antigens, selected from rheumatoid

XX
XX arthritis, diabetes mellitus or multiple sclerosis

XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
| | | | | | | |
DB 1 DYKDDDDK 8

PT 3, IL-5 or GM-CSF.
 XX
 PS Example 8; Page 48; 112pp; English.
 XX
 CC This represents a FLAG affinity label contained in a recombinant JAK2
 CC protein used in the course of the invention. The invention provides a
 CC method of screening for compounds useful for treating or preventing
 CC asthma. The method comprises contacting a molecule comprising at least
 CC the N-terminal 294 amino acid residues of the JAK2 protein, with another
 CC molecule comprising at least 13 membrane-proximal cytoplasmic amino acids
 CC of interleukin (IL)-3, IL-5 or granulocyte macrophage-colony stimulating
 CC factor (GM-CSF) proteins in the presence of the candidate compound, and
 CC determining whether the first and the second molecules form a complex. If
 CC the compound inhibits complex formation, it can be used to treat asthma
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DYKDDDK 8
 Db 1 DYKDDDK 8
 RESULT 31
 AAW81752
 ID AAW81752 standard; protein; 8 AA.
 XX
 AC AAW81752;
 XX
 DT 27-JAN-1999 (first entry)
 XX
 DE Synthetic FLAG peptide.
 XX
 KW US6; immunomodulator; therapeutic; prophylactic; inhibitor; cell surface;
 KW antigen presentation; major histocompatibility complex; MHC Class I;
 KW immunogenicity; gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO9847914-A2.
 XX
 PD 29-OCT-1998.
 XX
 PF 16-APR-1998; 98WO-EP002225.
 XX
 PR 18-APR-1997; 97EP-00106470.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Hengel H, Koszinowski U;
 XX
 DR WPI; 1998-583601/49.
 XX
 PT New US6 gene of cytomegalovirus - useful for diagnosis and therapeutic or
 PT prophylactic immunomodulation, e.g. to reduce immunogenicity of gene
 PT therapy vectors.
 XX
 PS Example 1; Page 15; 34pp; German.
 XX
 CC This sequence is a FLAG peptide used in a method resulting in the
 CC isolation of a US6 protein from human cytomegalovirus which can be used
 CC as therapeutic or prophylactic immunomodulators, in particular inhibitors
 CC of antigen presentation by MHC Class I on the surface of cells. A
 CC particularly application of this protein is to reduce immunogenicity of
 CC cells being transfected for gene therapy. Fragments of US6 nucleic acid
 CC and its analogues are useful diagnostically as probes and primers, and
 CC also as antisense sequences and ribozymes. US6 proteins are used to raise
 CC antibodies. The US6 protein inhibits a later stage of antigen
 CC presentation than known inhibitors
 XX

SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DYKDDDK 8
 Db 1 DYKDDDK 8
 RESULT 32
 AAW79682
 ID AAW79682 standard; protein; 8 AA.
 XX
 AC AAW79682;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Human CS198 C-terminal peptide fragment.
 XX
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;
 KW pancreatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO9844159-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98WO-US006251.
 XX
 PR 31-MAR-1997; 97US-00828855.
 XX
 PA (ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 1998-542714/46.
 XX
 PT New gastrointestinal polynucleotides, CS198, and their detection - used
 PT for developing products for the diagnosis and treatment of
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis.
 XX
 PS Example 11a; Page 104; 127pp; English.
 XX
 CC This sequence represents a C-terminal fragment of the human CS198 protein
 CC which is used in a method to detect the presence of a target CS198
 CC polynucleotide in a test sample. The CS198 gene is useful as a marker for
 CC gastrointestinal (GI) tract disorders. The methods and products can be
 CC used in detecting, diagnosing, staging, monitoring, prognosticating,
 CC preventing or treating, or determining the predisposition to diseases and
 CC conditions of the GI tract, such as GI tract cancer, Barrett's oesophagus,
 CC gastric ulcer, gastritis, leiomyoma, polyps, Crohn's disease, ulcerative
 CC colitis, and pancreatitis
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DYKDDDK 8
 Db 1 DYKDDDK 8
 RESULT 33
 AAW79770

ID AAW79770 standard; peptide; 8 AA.
 XX
 AC AAW79770;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1999 (first entry)
 XX
 DE FLAG epitope tag for human presenilin 2 protein.
 XX
 KW Proteolytic processing; human; presenilin 2; inhibitor; apoptosis;
 KW cell death; early onset familial Alzheimer's disease; FAD; diagnosis.
 XX
 OS Synthetic.
 XX
 PN WO9847917-A2.
 XX
 PD 29-OCT-1998.
 XX
 PP 24-APR-1998; 98WO-US0008260.
 XX
 PR 24-APR-1997; 97US-0044262P.
 XX
 PA (TANZ/) TANZI R E.
 PA (KIMT/) KIM T.
 PI Tanzi RE, Kim T;
 DR WPI; 1998-583602/49.
 XX
 PT 20 kDa presenilin 2 C-terminal fragment, PS2-CTF - useful to screen for
 PT compounds inhibiting proteolysis of presenilin 2 and to produce
 PT antibodies used in diagnosis of familial Alzheimer's.
 XX
 PS Disclosure; Page 38; 84pp; English.
 XX
 CC The invention relates to a C-terminal fragment from the human 20 kD
 CC presenilin 2 protein (PS2-CTF) which is useful in screening for compounds
 CC that inhibit proteolytic processing of PS2 in cells. Tracking of
 CC presenilin 2 or PS2-CTF, when expressed in cells and in screening assays,
 CC is done by linking a FLAG epitope peptide (this sequence) to the N- or C-
 CC termini of the PS2 protein. The inhibitory compounds can be administered
 CC to prevent proteolytic cleavage of presenilin 2 at a cleavage site which
 CC generates PS2-CTF, and therefore to inhibit apoptotic cell death.
 CC Mutations in the presenilin genes presenilin 1 and presenilin 2 (PS1 and
 CC PS2) cause a major portion (at least 50%) of early onset familial
 CC Alzheimer's disease (FAD), and detection of abnormal PS2-CTF levels can
 CC be indicative of a specific disease, e.g. FAD. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 CC
 SQ Sequence 8 AA;

 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

 RESULT 34
 AAW56033
 ID AAW56033 standard; peptide; 8 AA.
 XX
 AC AAW56033;
 XX
 DT 29-JUL-1998 (first entry)
 XX
 DE Chimeric adenovirus fiber protein non-native amino acid sequence 2.
 XX
 KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
 KW constrained peptide motif; gene therapy; cancer; heart disease;
 KW autoimmune disorder.
 XX
 PA

XX
 OS Synthetic.
 OS Mastadenovirus.
 XX
 PN WO9807865-A1.
 XX
 PD 26-FEB-1998.
 XX
 PP 21-AUG-1997; 97WO-US014719.
 XX
 PR 21-AUG-1996; 96US-00701124.
 XX
 PA (GENV-) GENVEC INC.
 XX
 PI Wicham TJ, Roelvink PW, Kovacs I;
 DR WPI; 1998-169169/15.
 XX
 PD Chimeric adenovirus fibre proteins - containing non-native amino acid
 PT sequence to provide for binding and entry into cells, especially for gene
 PT therapy.
 XX
 PS Claim 7; Page 68; 124pp; English.
 XX
 CC The present sequence represents a specifically claimed non-native amino
 CC acid sequence from a chimeric adenovirus fibre protein (AFP) of the
 CC present invention. The non-native amino acid sequence allows the chimeric
 CC fibre (or a vector comprising the chimeric fibre) to more efficiently
 CC bind to and enter cells. The products can be used for gene therapy, for
 CC treating cancer, e.g. melanoma, glioma and lung cancers as well as
 CC genetic disorders, e.g. cystic fibrosis, haemophilia and muscular
 CC dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and
 CC hepatitis and also for heart disease, to e.g. prevent restenosis
 CC following angioplasty or to promote angiogenesis to reperfuse necrotic
 CC tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis,
 CC rheumatoid arthritis, and Alzheimer's disease
 CC
 SQ Sequence 8 AA;

 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

 RESULT 35
 AAW30566
 ID AAW30566 standard; peptide; 8 AA.
 XX
 AC AAW30566;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE FLAG tag.
 XX
 KW ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;
 KW inflammation; ischaemia; reperfusion injury; FLAG.
 XX
 OS Synthetic.
 OS
 PN WO9844117-A1.
 XX
 PD 08-OCT-1998.
 XX
 PP 27-MAR-1998; 98WO-US006115.
 XX
 PR 28-MAR-1997; 97US-0042862P.
 PR 09-MAY-1997; 97US-0046083P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.

XX Shepard PO;
 PI
 XX
 DR WPI; 1998-557114/47.
 XX
 PT New human chemokine ZS1G-35 - used for, e.g. treating inflammatory
 PT disease, lymphocyte migration and ischaemia/reperfusion injury.
 XX
 PS Example 4; Page 88; 105pp; English.
 XX
 CC This FLAG peptide can be used as a N- or C-terminal tag of novel human
 CC chemokine ZS1G-35 polypeptides (see AAW30565) of the invention. Vectors
 CC have been designed for expression of FLAG-tagged ZS1G-35 in mammalian
 CC host cells. The FLAG peptide acts as a purification aid. ZS1G-35
 CC polypeptides are useful in the regulation of acute and chronic
 CC inflammatory disease conditions, lymphocyte migration and
 CC ischaemia/reperfusion injury
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 1 DYKDDDDK 8
 RESULT 36
 AAW75806
 ID AAW75806 standard; peptide; 8 AA.
 XX
 AC AAW75806;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE FLAG peptide epitope sequence.
 XX
 KM Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
 KM tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KM antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KM hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KM inflammatory skin condition; FLAG.
 XX
 OS Synthetic.
 XX
 PN WO9833812-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 30-JUN-1998; 98WO-US001865.
 XX
 PR 05-FEB-1997; 97US-0037090P.
 XX
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Stevens RL, Huang C;
 XX
 DR WPI; 1998-437390/37.
 XX
 PT Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
 PT inflammatory disorders e.g. asthma.
 XX
 PS Example; Page 18; 69pp; English.
 XX
 CC This represents a FLAG peptide epitope sequence. The invention provides
 CC sequences shown in AAW63160 to AAW63169 that are inhibitors of mouse mast
 CC cell protease (mMCP-6). These peptides which are tryptase-6 complex
 CC inhibitors, can be used for treating a mast cell-mediated inflammatory
 CC disorder. The inhibitors can be used to treat inflammatory disorders
 CC including asthma, allergic rhinitis, urticaria and antioedema, eczematous
 CC dermatitis (atopic dermatitis), anaphylaxis, hyperproliferative skin

CC disease, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness
 CC and inflammatory skin conditions
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 1 DYKDDDDK 8
 RESULT 37
 AAW54266
 ID AAW54266 standard; peptide; 8 AA.
 XX
 AC AAW54266;
 XX
 DT 30-JUL-1998 (first entry)
 XX
 DE FLAG peptide.
 XX
 KM Peptide tag; purification; identification; mutation; breast cancer;
 KM BRCA1; BRCA2; PCR; amplification; primer.
 XX
 OS Synthetic.
 XX
 PN WO9811249-A1.
 XX
 PD 19-MAR-1998.
 XX
 PF 13-SEP-1996; 96WO-US014708.
 XX
 PR 13-SEP-1996; 96WO-US014708.
 XX
 PA (GARV/) GARVIN A M.
 XX
 PI Garvin AM;
 XX
 DR WPI; 1998-207407/18.
 XX
 DR N-PSDB; AAW26454.
 XX
 PT Mutation detection using peptide tagged in vitro synthesised proteins -
 PT useful for identification of mutations in disease causing genes, e.g.
 PT breast cancer susceptibility genes BRCA1 and 2.
 XX
 PS Disclosure; Page 3; 13pp; English.
 XX
 CC The DNA sequences (AAV26452-V26455) are examples of 4 elements which are
 CC present in a unique oligonucleotide sequence. The flag peptide is an
 CC example of a tag which can be encoded by a region of the unique
 CC oligonucleotide sequence. The unique oligonucleotide sequence is used to
 CC amplify desired mutated sequences and to tag the encoded peptide at the N
 CC -terminus. Ligands recognising the peptide can be used to purify the
 CC proteins for further analysis. The method is capable of detecting
 CC mutations that qualitatively alter the protein product or any protein
 CC encoding gene, using genomic DNA or cDNA as the starting material. The
 CC method is useful for identification of mutations in certain disease
 CC causing genes, e.g. the breast cancer susceptibility genes BRCA1 and 2
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 1 DYKDDDDK 8

```

RESULT 38
AAW29748
ID AAW29748 standard; peptide; 8 AA.
XX
XX AAW29748;
AC
XX
XX
XX 27-OCT-1998 (first entry)
XX
XX Synthetic octapeptide recognised by anti-FLAG M2.
DE
XX TNF; endothelium proliferative agent; TREPA; wound healing; cancer;
XX tissue grafting; vascularisation; apoptosis; autoimmunity; birth control.
XX
XX Synthetic.
OS
XX WO9835061-A2.
XX
XX 13-AUG-1998.
XX
XX 12-FEB-1998; 98WO-US002859.
XX
XX 12-FEB-1997; 97US-00798692.
XX
XX 10-FEB-1998; 98US-00021706.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX
XX Wiley SR;
XX
XX WPI; 1998-447255/38.
XX
XX Detecting nucleic acid encoding TREPA - useful for diagnosis and
XX treatment of autoimmune disease, tumours and inflammation.
XX
XX Claim 43; Page 126; 142pp; English.
XX
XX The synthetic octapeptide recognised by anti-FLAG M2 was used in the
XX creation of a plasmid for the expression of secretable TNF-related
XX endothelium proliferative agent (TREPA). TREPA, or its activators or
XX agonists, are used to treat a deficit of TREPA, e.g. to promote wound
XX healing or tissue grafting, by promoting vascularisation, also to induce
XX apoptosis for treating cancer and eliminating autoreactive T cells, as an
XX adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can
XX also be used to target cytotoxic agents or for affinity isolation of the
XX corresponding receptor, the nucleic acid for which can be used to
XX transform tumour cells to render them more responsive to TREPA and to
XX screen for TREPA mimics. Ribozymes, antisense RNA, antibodies or
XX peptides, are used to treat TREPA-associated diseases, e.g. tumours and
XX metastases (by inhibiting vascularisation), inflammation or a wide range
XX of autoimmune conditions, conditions involving abnormal stimulation of
XX epithelial cells (e.g. atherosclerosis), for birth control (inhibiting
XX ovulation and placental formation) or other angiogenic conditions (e.g.
XX ulcers)
XX
XX Sequence 8 AA;
SQ
XX
XX Query Match 100.0%; Score 47; DB 2; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8
XX
XX
XX RESULT 39
XX AAW79562
XX ID AAW79562 standard; peptide; 8 AA.
XX
XX AAW79562;
AC
XX
XX 11-JAN-1999 (first entry)
XX
XX FLAG peptide.
DE

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XX
XX Adenovirus serotype 2; Ad2; hexon; coat protein; gene therapy; vector;
XX FLAG.
XX
XX Synthetic.
XX
XX WO9840509-A1.
XX
XX 17-SEP-1998.
XX
XX 13-MAR-1998; 98WO-US005033.
XX
XX 13-MAR-1997; 97US-00816346.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX (GENV-) GENVEEC INC.
XX
XX Crystal RG, Falck-Pedersen E, Gall J, Kovsed I, Wickham TJ;
XX
XX WPI; 1998-506738/43.
XX
XX N-PSDB; AAV61524.
XX
XX Chimeric adenovirus coat protein - useful in, e.g. vector for gene
XX transfer to treat inherited genetic diseases.
XX
XX Example 4; Page 87; 112pp; English.
XX
XX This is the amino acid sequence of a FLAG peptide. DNA encoding FLAG (see
XX AAV61524) can be introduced into an adenovirus vector. The invention
XX provides a chimeric adenoviral coat protein, particularly a chimeric
XX adenovirus hexon protein (see AAW79538-39), that has a decreased ability
XX or inability to be recognised by a neutralising antibody directed against
XX the corresponding wild-type adenovirus coat protein. The chimeric
XX adenoviral coat protein has a non-native amino acid sequence, especially
XX comprising a deletion of one or more regions of the hexon protein. A
XX vector that comprises the chimeric adenovirus coat protein is claimed,
XX and can be used for gene transfer, for the treatment of inherited
XX diseases
XX
XX Sequence 8 AA;
SQ
XX
XX Query Match 100.0%; Score 47; DB 2; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8
XX
XX
XX RESULT 40
XX AAW69953
XX ID AAW69953 standard; peptide; 8 AA.
XX
XX AAW69953;
AC
XX
XX 08-OCT-1998 (first entry)
XX
XX FLAG peptide epitope for constructing RANK/Fc fusion protein.
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
XX RANK ligand; tumour necrosis factor; FLAG peptide epitope.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9828426-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US023775.
XX
XX

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PR 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Galibert LJ, Maraskovsky E;
 XX
 DR WPI; 1998-377657/32.
 XX
 PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells.
 XX
 PS Example 6; Page 53; 80pp; English.
 XX
 CC This represents a FLAG peptide epitope used in the construction of a
 CC RANK/FC fusion protein. RANK (receptor activator of necrosis factor-
 CC kappab (NF-kB)) is a member of the tumour necrosis factor (TNF) family. A
 CC soluble form of RANK is fused to the FC region of human IgG1. A soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to a
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used
 CC to induce maturation of dendritic cells and enhance their allo-
 CC stimulatory capacity, thereby augmenting an immune response. The soluble
 CC RANK polypeptide composition may also be used for regulating an immune or
 CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
 CC useful in ameliorating negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, or acute inflammatory reactions. They can
 CC also be used in adjunct therapy for disease characterized by neoplastic
 CC cells that express RANK. RANKL polypeptides can also be used to identify
 CC inhibitors of RANK and thus inhibitors of an inflammatory response, and
 CC also for protecting RANK-expressing cells from the negative effects of
 CC chemotherapy or the presence of high levels of TNF-alpha. The products
 CC can also be used for detection and drug screening
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

RESULT 41
 AAM48629
 ID AAM48629 standard; peptide; 8 AA.
 AC AAM48629;
 XX
 DT 11-SEP-1998 (first entry)
 XX
 DE Chimeric adenoviral penton base protein epitope 1.
 XX
 KW Short-shafted adenoviral fibre; ssAF; penton base; cystic fibrosis;
 KW bispecific antibody; HIV; cancer.
 XX
 OS Synthetic.
 XX
 PN MO9807877-A1.
 XX
 PD 26-FEB-1998.
 XX
 PF 21-AUG-1997; 97MO-US014718.
 XX
 PR 21-AUG-1996; 96US-00700846.
 XX
 PA (GENV-) GENVEC INC.
 XX

PI Wickham TJ, Roelink FM, Kovacs I;
 XX
 XX WPI; 1998-169180/15.
 XX
 PT Short-shafted adenoviral fibre constructs - used for producing products
 PT that facilitate entry into target cells, useful for gene therapy of
 PT cellular disorders.
 XX
 PS Disclosure; Page 39; 98pp; English.
 XX
 CC The present sequence is a FLAG octapeptide which is incorporated into an
 CC adenoviral fiber. The fiber protein and its penton base are used by the
 CC adenovirus to interact with distinct cellular receptors to attach to and
 CC efficiently infect a cell. The invention claims for a transfer vector
 CC which contains DNA encoding a short-shafted adenoviral fibre (ssAF). The
 CC adenoviral penton base can be modified by incorporating sequences for a
 CC ligand to a cell surface receptor or sequences that allow binding to a
 CC bispecific antibody. Bispecific antibodies raised against the FLAG
 CC octapeptide allows one end of the antibody molecule to bind to the fiber
 CC and the other end to bind specifically to a cell surface receptor.
 CC Therefore this method enables targeting of the adenovirus to a desired
 CC cell-surface receptor by the introduction of a non-native amino acid
 CC sequence either into the penton base or the fibre knob. The non-native
 CC amino acid sequence can be such that it enables direct or indirect
 CC binding, e.g. by means of a bispecific or multispecific binding agent, of
 CC the adenovirus to the desired cell-surface receptor. Using the a short
 CC shafted adenovirus to attach to a cell and therefore effect entry into
 CC the cell would reduce the level or efficiency of adenoviral fibre binding
 CC to its cell-surface receptor and increase the adenoviral penton base
 CC binding to its cell-surface receptor, thereby increasing the specificity
 CC of binding of the adenovirus to a given cell. The transfer vector is
 CC claimed to be useful for expressing therapeutic genes, for treating
 CC inherited diseases such as cystic fibrosis or for inducing cell death in
 CC pathogenic infections (e.g. HIV infections) and cancers
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

RESULT 42
 AAM47353
 ID AAM47353 standard; peptide; 8 AA.
 AC AAM47353;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE FLAG-peptide.
 XX
 KW EBV; BZLF2; beta-chain; major histocompatibility complex; MHC; class II;
 KW antigen; prevention; treatment; autoimmune disease; transplant rejection;
 KW allergy; asthma; super-antigen; Epstein-barr virus; FLAG-peptide.
 XX
 OS Synthetic.
 XX
 PN US5726286-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 28-APR-1995; 95US-00430633.
 XX
 PR 28-APR-1994; 94US-00235397.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Comeau MR, Alderson M, Farrah TM, Hutt-Fletcher LM, Armitage RJ;

QY 1 DYKDDDDK 8
 XX |||||
 Db 1 DYKDDDDK 8

RESULT 45

AAW46969
 ID AAW46969 standard; protein; 8 AA.
 XX
 AC AAW46969;

DT 06-JUL-1998 (first entry)

DE Peptide sequence of the specification.

XX S11c-like protein; human; diagnosis; treatment; brain-specific disease;
 KM cancer; antibody.

XX Unidentified.

XX JPL0087699-A.

XX 07-APR-1998.

XX 15-JUL-1997; 97JP-00205351.

XX 16-JUL-1996; 96JP-00186219.

XX (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1998-267127/24.

XX Human S11c-like protein - useful for diagnosis and treatment of brain-
 PT specific diseases and cancers.

XX Disclosure; Page 39; 45pp; Japanese.

XX The present sequence appears in the specification. The specification
 CC describes a novel human s11c-like protein (the mature protein is claimed
 CC in Claim 1). The s11c-like polypeptide is useful for diagnosis and
 CC treatment of brain-specific diseases and cancers. Antibodies directed
 CC against the protein, or its fragments can also be used for diagnosing
 CC cancer

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 XX |||||
 Db 1 DYKDDDDK 8

RESULT 46

AAW68289
 ID AAW68289 standard; peptide; 8 AA.

AC AAW68289;

DT 08-OCT-1998 (first entry)

DE FLAG peptide epitope for constructing RANK/Fc fusion protein.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KM immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
 KM RANK ligand; tumour necrosis factor; FLAG peptide epitope.

XX Synthetic.

OS Homo sapiens.

XX

PN W09828424-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US023866.

XX 23-DEC-1996; 96US-005978P.

XX 07-MAR-1997; 97US-0081350P.

XX 14-OCT-1997; 97US-0064671P.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.

XX Example 6; Page 53; 80pp; English.

XX This represents a FLAG peptide epitope used in the construction of a
 CC RANK/Fc fusion protein. RANK (receptor activator of necrosis factor-
 CC kappaB (NF-kB)) is a member of the tumour necrosis factor (TNF) family.
 CC Host cells transformed or transfected with an expression vector
 CC comprising the RANK encoding nucleic acid can be used to produce

CC recombinant RANK protein. A soluble form of RANK is fused to the FC
 CC region of human IgG1. The soluble RANK may be used for inhibiting
 CC activation of NF-kB, by contacting a cell expressing membrane-associated

CC RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble
 CC RANK polypeptide composition may also be used for regulating an immune or

CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
 CC useful in ameliorating negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,

CC graft-versus-host reactions, or acute inflammatory reactions. They can
 CC also be used in adjunct therapy for disease characterized by neoplastic
 CC cells that express RANK. The products can also be used for detection and

CC drug screening

XX Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 XX |||||
 Db 1 DYKDDDDK 8

RESULT 47

AAW44008
 ID AAW44008 standard; peptide; 8 AA.

AC AAW44008;

DT 05-JUN-1998 (first entry)

DE FLAG peptide i used in an epitope tagged prion protein construct.

XX Prion; epitope; FLAG; Strept. poly-histidine; haemagglutinin; recombinant;
 KM transgenic animal; scrapie; Creutzfeldt-Jakob disease; CJD;
 KM bovine spongiform encephalopathy; BSE.

XX Synthetic.

PN W09746572-A1.

XX 11-DEC-1997.

XX 29-MAY-1997; 97WO-US009289.

XX

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PR 06-JUN-1996; 96US-00660626.
XX (REBC ) UNIV CALIFORNIA.
PA Prusiner SB, Telling GC, Cohen FE, Scott MR;
XX MPI; 1998-042112/04.
XX
XX Nucleic acid construct encoding biologically active protein and epitope -
PT especially epitope-tagged prion protein.
XX
XX Claim 4; Page 48; 62pp; English.
XX
XX This sequence represents an artificial FLAG peptide epitope. It is used
CC in a recombinant nucleic acid construct encoding an epitope-tagged prion
CC protein (PrP). The construct comprises a first nucleic acid sequence
CC encoding an amino acid sequence of a biologically active protein fragment
CC and a second nucleic acid sequence encoding a heterologous epitope
CC domain. The heterologous epitope domain is a peptide selected from a
CC peptide group of FLAG, Strep, poly-histidine, human c-myc peptide
CC recognised by monoclonal antibody 9E10 and haemagglutinin peptide
CC synthetic or chimeric PrP molecule. The protein has two different three-
CC dimensional conformations and the epitope domain is spatially positioned
CC relative to the protein such that the epitope domain is more exposed in a
CC first conformation relative to a second conformation. The nucleic acid
CC construct may be used for the production of transgenic animals or cells
CC that are useful in a method for distinguishing between different
CC conformational shapes of a protein. These methods are particularly useful
CC in studying diseases caused by prion proteins, e.g. Creutzfeldt-Jakob
CC disease (CJD), scrapie and bovine spongiform encephalopathy (BSE)
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
   |||||
DB 1 DYKDDDDK 8

RESULT 48
AAW80478 standard; peptide; 8 AA.
XX
XX AAW80478;
AC
XX
XX 28-JAN-1999 (first entry)
DT
XX
XX Peptide sequence encoded by an antisense primer.
DE
XX
XX EST sequence; CS110; gastrointestinal tract; cancer; adenocarcinoma;
KW lymphoma.
XX
XX Synthetic.
OS
XX
XX WO9844160-A1.
PN
XX
XX 08-OCT-1998.
PD
XX
XX 31-MAR-1998; 98WO-US006338.
PF
XX
XX 31-MAR-1997; 97US-00829755.
PR
XX
XX (ABBO ) ABBOTT LAB.
PA
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX
XX MPI; 1998-557139/47.

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XX
XX New CS110 polypeptide(s) - useful for detecting gastrointestinal tract
PT diseases, e.g. gastrointestinal tract cancers and to produce antibodies.
XX
XX Example 11a; Page 67; 116pp; English.
XX
XX The present sequence represents a peptide sequence encoded by an
CC antisense primer of the invention. The sequence incorporates a
CC recognition site to aid in analysis and purification of the CS110
CC protein. A set of contiguous and partially overlapping EST sequences
CC (AA63521-27) are designated CS110. The sequences are isolated from a
CC cDNA library made from gastrointestinal tract tumour and normal tissues.
CC The polypeptides are useful diagnostically to detect CS110 antigen/anti-
CC CS110 antibody in samples, e.g. to detect diseases and conditions of the
CC gastrointestinal tract, especially cancers, e.g. adenocarcinoma and
CC lymphoma
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
   |||||
DB 1 DYKDDDDK 8

RESULT 49
AAW70592
ID AAW70592 standard; peptide; 8 AA.
XX
XX AAW70592;
AC
XX
XX 21-JAN-1999 (first entry)
DT
XX
XX FLAG sequence used in the course of the invention.
DE
XX
XX zsig25; adhesion-modulating protein; prostate cell; prostatic carcinoma;
KW B-cell cancer; infertility; Wolf-Hirschhorn syndrome;
KW chromosome 4 (p16.3).
XX
XX Synthetic.
OS
XX
XX WO9845442-A2.
PN
XX
XX 15-OCT-1998.
PD
XX
XX 10-APR-1998; 98WO-US007117.
PF
XX
XX 10-APR-1997; 97US-0043421P.
PR
XX
XX 11-JUN-1997; 97US-0049288P.
PA
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO;
PI
XX
XX MPI; 1998-557522/47.
XX
XX New zsig25 protein - and antibodies, involved in modulation of adhesion,
PT used for diagnosis and treatment of prostatic and B-cell tumours,
XX stimulation of haematopoietic cells, treatment of immune deficiency etc.
XX
XX Claim 10; Page 120; 161pp; English.
XX
XX The present sequence represents a FLAG sequence used in the course of the
CC invention. The specification describes zsig25 protein, an adhesion-
CC modulating protein expressed at very high level in prostatic cells. The
CC protein is useful as a diagnostic marker for prostatic carcinoma and B-
CC cell cancers, possibly also for infertility, and as a reagent for
CC separating cancerous and non-cancerous cells. The products may also be
CC used to diagnose or treat Wolf-Hirschhorn syndrome, associated with a
CC deletion in the region of chromosome 4 (p16.3) where the zsig25 gene is

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CC located
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 DB 1 DYKDDDK 8
 RESULT 50
 AAE08734
 ID AAE08734 standard; peptide: 8 AA.
 AC AAE08734;
 DT 15-NOV-2001 (first entry)
 XX FLAG tag, used to determine the association of TRAF with RANK.
 DE
 XX Human; receptor activator of nuclear factor kappaB; RANK; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KM immune response; inflammatory response; graft-versus-host reaction;
 KM toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KM anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
 OS Synthetic.
 PN US6271349-B1.
 PD 07-AUG-2001.
 PF 17-DEC-1998; 98US-00215649.
 XX
 PR 23-DEC-1996; 96US-0059978P.
 PR 23-DEC-1996; 96US-00772330.
 PR 07-MAR-1997; 97US-0072181P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 PR 22-DEC-1997; 97US-00996139.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Dougall WC, Galibert L;
 DR WPI; 1998-377655/32.
 XX
 PT New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Example 6; Col 59; 47bp; English.
 CC The parent discloses novel receptor activator of nuclear factor (NF) -
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of
 CC the tumour necrosis factor (TNF) receptor superfamily and associates with
 CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the
 CC regulation of immune and inflammatory response. The receptors are useful
 CC for regulating immune response and in screening for inhibitors of these
 CC receptors. The cytoplasmic domain of RANK is used in developing assays
 CC for inhibitors of signal transduction, e.g. for screening the molecules
 CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and
 CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful
 CC in ameliorating the negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, acute inflammatory reactions and the effects
 CC of bone resorption. RANK acts as an anti-apoptotic signal and rescue the
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are
 CC used in vivo or in vitro based screening tests for agonists or
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B

CC activation, or to inhibit transduction of a signal via RANK. RANK
 CC compositions are used in the development of both agonistic and
 CC antagonistic antibodies, or as an adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. Compounds that
 CC interfere with RANK/TRAF6 interactions are useful for modulating the
 CC formation of osteoclasts from osteoclast precursors and for modulating
 CC osteoclast function and activities. They are used as inhibitors of
 CC diseases associated with excess bone resorption and as immunosuppressants
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression
 CC of recombinant proteins, as probes for analysis of the presence or
 CC distribution of RANK transcripts, while the proteins are useful in
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related
 CC activity. The present sequence is a FLAG tag which is used in the
 CC exemplification of the invention to determine the association of TRAF
 CC with RANK
 CC
 CC SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 DB 1 DYKDDDK 8
 RESULT 51
 AAW94672
 ID AAW94672 standard; peptide: 8 AA.
 AC AAW94672;
 DT 04-MAY-1999 (first entry)
 XX Human TRAIL-BP Flag peptide.
 DE
 XX Human; TNF-related apoptosis-inducing ligand binding protein; clotting;
 KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;
 KM thrombotic microangiopathy; thrombotic thrombocytopenic purpura;
 KM haemolytic-uraemic syndrome; systemic lupus erythematosus.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9900423-A1.
 PD 07-JAN-1999.
 PF 25-JUN-1998; 98WO-US013491.
 PR 26-JUN-1997; 97US-00883529.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Walczak H, Smith CA;
 DR WPI; 1999-095685/08.
 XX
 PT New isolated TRAIL binding protein - which binds to a tumour necrosis
 PT factor-related apoptosis inducing ligand, used in the diagnosis and
 PT treatment of TRAIL-mediated disorders.
 XX
 PS Disclosure, Page 3; 47bp; English.
 CC The present sequence represents a flag peptide from the present
 CC invention. The present invention describes human tumour necrosis factor
 CC (TNF)-related apoptosis-inducing ligand (TRAIL) binding protein (BP).
 CC TRAIL-BP can be used for inhibiting the biological activities of TRAIL or
 CC for purifying TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-
 CC mediated disorder such as T cell death in HIV-infected patients. They can
 CC be used for treating thrombotic microangiopathies such as thrombotic
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small

CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic acids
CC can also be used for gene therapy. They can also be used as carriers for
CC delivering attached agents to cells bearing TRAIL

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 52

AAV06471
ID AAV06471 standard; peptide; 8 AA.

AC AAV06471;

DT 27-SEP-1999 (first entry)

DE Epitope tag.

KW Epitope tag; antibody engineering; yeast; surface display;
KW protein library; peptide library.

OS Synthetic.

PN WO9336569-A1.

PD 22-JUL-1999.

PF 20-JAN-1999; 99WO-US001188.

PR 20-JAN-1998; 98US-0009388.

PR 26-AUG-1998; 98US-00140084.

PA (UNITI) UNITV ILLINOIS FOUND.

PI Witrup KD, Kieke MC, Kranz DM, Shusta E, Boder ET;

DR WPI; 1999-430619/36.

XX Selecting proteins with enhanced phenotypic properties than wild-type
XX proteins, is useful for highly specific cancer diagnosis and therapy.

PS Disclosure; Page 7; 116pp; English.

XX This peptide comprises an epitope tag that can be used in methods of the
XX invention. The invention discloses a powerful new system for engineering
XX antibody affinity and specificity, by constructing a microbial analogue
XX of the mammalian system's B cell repertoire. Antibodies are displayed on
XX the surface of yeast cells by genetic fusion with yeast cell wall
XX proteins, especially agglutinin proteins. After mutation, variants are
XX selected on the basis of improved binding characteristics with
XX fluoresceinly labeled targets. The selection method also identifies
XX proteins with enhanced phenotypic characteristics, proteins that are
XX displayed at higher levels, proteins that are secreted at higher
XX efficiency and proteins of improved stability

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 53
AAW99020
ID AAW99020 standard; peptide; 8 AA.

AC AAW99020;

DT 12-MAY-1999 (first entry)

DE Flag peptide.

KW Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;
KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;
KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;
KW multiple sclerosis.

OS Synthetic.

PN WO9303992-A1.

PD 28-JAN-1999.

PF 10-JUL-1998; 98WO-US014410.

PR 15-JUL-1997; 97US-00892119.

PA (IMMV) IMMUNEX CORP.

PI Degli-Besposti M;

DR WPI; 1999-132236/11.

XX New isolated TRAIL receptor polypeptides - used to develop products for
XX treating e.g. thrombotic microangiopathy, multiple sclerosis, systemic
XX lupus erythematosus or HIV infection.

PS Disclosure; Page 13; 51pp; English.

XX The present invention describes human tumour necrosis factor (TNF) -
XX related apoptosis-inducing ligand (TRAIL) receptors (TRAILR). TRAILR
XX proteins can be used for binding TRAIL, e.g. to measure or inhibit the
XX biological activity of TRAIL. TRAILR proteins can be used for treating
XX thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura
XX (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood
XX vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus
XX or for reducing TRAIL-mediated death of T cells in HIV-infected patients.
XX They can also be used to purify TRAIL or TRAIL-expressing cells or as
XX carriers for delivering agents to cells bearing TRAIL. The present
XX sequence represents a flag peptide form the present invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 54

AAW8371
ID AAW8371 standard; peptide; 8 AA.

AC AAW8371;

DT 26-APR-1999 (first entry)

DE FLAG peptide.

KW Tumour necrosis factor-gamma; TNF-gamma; human; inflammation; cancer;
KW tumour; metastasis; graft versus host disease; drug screening; therapy;
KW diagnosis; FLAG.

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XX OS Synthetic.
XX XX WO900518-A1.
XX PN 07-JUN-1999.
XX PD 12-JUN-1998; 98WO-US012101.
XX PF 26-JUN-1997; 97US-00883086.
XX PR (ABBO ) ABBOTT LAB.
XX PA Wiley SR;
XX PI WPI; 1999-095761/08.
XX DR Tumour necrosis factor gamma detects target polynucleotides - useful for,
XX PT e.g. treating inflammation, cancer and graft versus host disease.
XX PS Claim 43; Page 70; 106pp; English.
XX CC This is a FLAG peptide recognised by monoclonal antibody anti-FLAG M2.
XX CC DNA encoding the FLAG peptide can be ligated to DNA encoding a human
XX CC serum albumin leader sequence (see AAW88370) and the C-terminal portion
XX CC (see AAW88369) of novel human tumour necrosis factor gamma (TNFG, see
XX CC AAW88368) in order to provide a construct for the expression of
XX CC secretable TNFG proteins in mammalian host cells. Such soluble
XX CC polypeptides can be used to treat deficiencies of TNFG and disease
XX CC conditions ameliorated by TNFG. Antibodies, antagonists and inhibitors of
XX CC the polypeptide may be used to treat TNFG-associated diseases, tumours or
XX CC metastases, and to screen for, diagnose and monitor conditions
XX CC attributable to TNFG, especially inflammation, cancer and graft versus
XX CC host disease
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 55
AAW97660
ID AAW97660 standard; peptide; 8 AA.
XX AC AAW97660;
XX DT 10-MAY-1999 (first entry)
XX DE FLAG epitope.
XX KW BL210; urinary tract; cancer; tumour; metastasis; diagnosis; therapy;
XX KM human; epitope; antigen; antibody; FLAG.
XX OS Synthetic.
XX PN WO9902734-A1.
XX PD 21-JAN-1999.
XX PF 08-JUL-1998; 98WO-US014210.
XX PR 08-JUL-1997; 97US-00889866.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;

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PI Stroupe SD, Yu H;
XX WPI; 1999-120934/10.
XX DR Nucleic acid derived from the BL210 gene - used for diagnosis and
XX PT treatment of urinary tract disease, particularly cancer.
XX PF Example 11a; Page 70; 120pp; English.
XX PS
XX CC This peptide comprises a FLAG epitope. An antisense primer incorporating
XX CC a sequence encoding FLAG has been used in the PCR amplification of human
XX CC urinary tract specific BL210 cDNA clones (see also AAX07044-57) for the
XX CC production of a BL210 expression plasmid. The BL210 protein product (see
XX CC also AAW97655) was recovered from transfected mammalian cells using anti-
XX CC FLAG monoclonal antibody M2. The invention provides BL210 cDNA clones and
XX CC polypeptides useful for developing products for detecting, diagnosing,
XX CC staging, in vivo imaging, preventing or treating diseases or conditions
XX CC of the urinary tract, including cancer
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 56
AAV08479
ID AAV08479 standard; protein; 8 AA.
XX AC AAV08479;
XX DT 29-JUL-1999 (first entry)
XX DE Human BS274 protein fragment 1.
XX KW Human; breast tissue; BS274; detection; disease; marker; antitumour;
XX KM breast cancer; metastases; atypical hyperplasia; fibroadenoma; cyst;
XX KM diagnosis; therapy; antagonist; cytotoxin; immunos assay; drug screen;
XX KM chromosomal anomaly; immunisation; antisense; triplex; ribozyme.
XX OS Homo sapiens.
XX PN WO9925850-A1;
XX PD 27-MAY-1999.
XX PF 17-NOV-1998; 98WO-US024562.
XX PR 17-NOV-1997; 97US-00971772.
XX PA (ABBO ) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
XX PI Russell JC, Stroupe SD;
XX DR WPI; 1999-347484/29.
XX PT New BS274 nucleic acid as a marker for breast disease.
XX PS Example 11a; Page 102; 105pp; English.
XX CC This invention describes novel human BS274 protein clones which can be
XX CC used as markers for breast cancer and have antitumour activity. BS274 can
XX CC also be used as a marker of cancer and its metastases, atypical
XX CC hyperplasia, fibroadenoma and cysts, so detection/quantification of BS274
XX CC encoded polypeptides and BS274-specific antibodies are used for
XX CC diagnosis, staging, monitoring, prognosis, in vivo imaging of, and

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determining predisposition to these diseases. Antibodies are useful as therapeutic antagonists (optionally coupled to a cytotoxin), as immunosay reagents and in competitive drug screens. BS274 nucleic acid and its fragments, are used as probes and primers (in diagnostic assays, for quantifying gene expression, for detecting chromosomal anomalies and to isolate related sequences), for genetic immunization, as a source of therapeutic antisense, triplex-forming and ribozyme sequences, and for recombinant production of BS274 polypeptides. BS274 polypeptides are used as immunosay reagents, for generating antibodies, in drug screens for specific binding agents (i.e. antagonists and inhibitors, potentially useful as therapeutic agents) and for rational drug design

Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8
DB

RESULT 57

AAW81534 standard; peptide; 8 AA.

AAW81534;

01-MAR-1999 (first entry)

FLAG peptide epitope.

JIP-1; JNK-interacting protein; c-Jun NH2-terminal kinase;
signal transduction; inhibitor; mouse; neurodegenerative disease;
Parkinson's disease; Alzheimer's disease; blood clot; stroke; malignancy;
cancer; leukaemia; autoimmune disease; inflammation; apoptosis; therapy;
diagnosis; FLAG.

Synthetic.

WO9849188-A1.

05-NOV-1998.

28-APR-1998; 98WO-US008513.

28-APR-1997; 97US-00819177.

(UWMA-) UNTV MASSACHUSETTS.

Davis RJ, Dickens M;

WPI; 1999-024042/02.

c-Jun NH2-terminal kinase (JNK)-interacting protein 1 - used to treat neurodegenerative disease, blood clot, leukaemia, autoimmune disease, and inflammation.

Example 2; Page 48; 95pp; English.

This peptide comprises a FLAG epitope. DNA encoding this epitope has been inserted into mutine JIP-1 cDNA (see AAV69289) between the first 2 codons of the coding region. Recombinant JIP-1 was expressed in bacterial host cells as GST fusion proteins. Experiments demonstrates that JIP-1 (see also AAW81525) specifically binds JNK (c-Jun NH2-terminal kinase) in vivo. JIP-1 polypeptides and nucleic acids are used in the manufacture of medicaments for treating a pathological condition associated with abnormal expression or activity of JNK, such as a neurodegenerative disease (selected from Parkinson's disease and Alzheimer's disease), a blood clot, stroke, malignancy, leukaemia, an autoimmune disease or inflammation

Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8
DB

RESULT 58

AAW6792 standard; peptide; 8 AA.

AAW6792;

22-JUN-1999 (first entry)

FLAG peptide epitope.

Urinary tract; detection; diagnosis in vivo imaging; cancer; keratin;
cytokeratin; cellular apoptosis susceptibility; CAS; mat-8; FLAG.

Synthetic.

WO9914372-A1.

25-MAR-1999.

15-SEP-1998; 98WO-US019362.

15-SEP-1997; 97US-0058925P.

(ABBO) ABBOTT LAB.

Billing-Medel PA, Cohen M, Friedman PN, Gordon J, Hodges SC;

Klaas MR, Kratochvil JD, Russell E, Stroupe SD;

WPI; 1999-229552/19.

Detection and treatment of urinary tract disease, particularly cancer.

Example 12a; Page 69; 109pp; English.

The invention relates to novel methods for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing, treating or determining a predisposition to diseases or conditions of the urinary tract, particularly cancer. The methods use products derived from keratin/cytokeratin, cellular apoptosis susceptibility (CAS) or mat-8-specific polynucleotides (AAW32486 to AAW32498). These polynucleotide sequences are used in the methods for detecting diseases of the urinary tract, especially cancer

Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8
DB

RESULT 59

AAW99670 standard; peptide; 8 AA.

AAW99670;

07-JUN-1999 (first entry)

DE FLAG tag sequence SEQ ID NO:6.
 XX Human; lipocalin; testis; mammary gland; breast tumour; zlipol;
 KM breast cancer; emphysema; skin disease; reproduction; anti-inflammatory;
 KM antimicrobial.
 XX Synthetic.
 OS
 PN MO9907740-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 06-AUG-1998; 98WO-US016425.
 XX
 PR 06-AUG-1997; 97US-0054867P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Conklin DC;
 XX
 DR WPI; 1999-167367/14.
 XX
 PT New lipocalin homologue designated zlipol - whose expression is
 PT restricted to testis and mammary gland tissues, particularly breast
 PT tumour tissue, used to, e.g. predict tumour aggressiveness.
 PS
 XX Example 5; Page 61; 94pp; English.
 CC The present invention describes a lipocalin homologue, designated zlipol.
 CC The lipocalin homologue, zlipol, is specifically expressed in testis and
 CC mammary gland, particularly breast tumour tissue. Based on this tissue
 CC distribution, zlipol may be used as a diagnostic for breast carcinomas
 CC and as a tool for predicting tumour aggressiveness. Agonists can be used
 CC for transportation of small hydrophobic molecules either in vivo or in
 CC vitro, and so are useful in specifically promoting the growth and/or
 CC development of testis-specific cell lineages in culture. Zlipol can be
 CC used to identify inhibitors. Zlipol proteins can also be used to prepare
 CC antibodies (which can be linked to toxins), and can serve as immunogens.
 CC Zlipol proteins can be used as a delivery and encapsulation system to
 CC transport and/or stabilise small lipophilic molecules, e.g. to protect
 CC from gut pH and digestive enzymes. They can also be used to bind small
 CC fatty acids in blood or tissues to modulate their biological function,
 CC e.g. to transport retinoids or steroids to receptors, in particular as
 CC therapy for breast cancer, emphysema and diseases of the skin. They may
 CC also play an important role in reproduction. Other uses include anti-
 CC inflammatory responses, and antimicrobial activities. Zlipol nucleic acid
 CC sequences may be used for gene therapy to increase or inhibit zlipol
 CC activity, to derive probes and primers, to derive antisense sequences,
 CC and to detect genetic abnormalities. The present sequence represents a
 CC FLAG tag sequence which is used in an example from the present invention
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8
 |||||
 RESULT 60
 AAM95645
 ID AAM95645 standard; protein; 8 AA.
 XX
 AC AAM95645;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Human BS124 peptide fragment.
 XX
 KM BS124; breast; cancer; detection; diagnosis; prevention; treatment;

KM peptide; fragment.
 XX
 OS Homo sapiens.
 XX
 PN MO9859049-A1.
 XX
 PD 30-DEC-1998.
 XX
 PF 19-JUN-1998; 98WO-US012862.
 XX
 PR 20-JUN-1997; 97US-00879354.
 XX
 PA (ABBOTT) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell UC;
 PI Scheffel CP, Stroupe SD, Yu H;
 XX
 DR WPI; 1999-105623/09.
 XX
 PT New isolated BS124 polynucleotides and polypeptides - used for detecting,
 PT diagnosing, preventing or treating diseases or conditions of the breast,
 PT such as breast cancer.
 PS
 XX Example 11a; Page 100; 125pp; English.
 CC The sequence is that of a BS124 peptide fragment. It is useful for
 CC detecting, diagnosing, staging, preventing or treating, or determining
 CC predisposition to diseases or conditions of the breast, such as breast
 CC cancer
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8
 |||||
 RESULT 61
 AAY31721
 ID AAY31721 standard; peptide; 8 AA.
 XX
 AC AAY31721;
 XX
 DT 22-NOV-1999 (first entry)
 XX
 DE Flag epitope.
 XX
 KM Fibrinogen domain related protein; FDRG; TANGO 115; angiogenesis;
 KM adipocyte; diabetes; obesity; inflammation; gene therapy; diagnosis;
 KM human; Flag epitope.
 XX
 OS Synthetic.
 XX
 PN WO9945135-A1.
 XX
 PD 10-SEP-1999.
 XX
 PF 02-MAR-1999; 99WO-US004548.
 XX
 PR 02-MAR-1998; 98US-00033539.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Holtzman DA, Spiegelman BM, Yoon CH;
 XX
 DR WPI; 1999-540859/45.

PT New isolated Fibrinogen Domain Related polypeptides, used to develop
 PT products for treating e.g. obesity, diabetes, cancers, angiogenesis or
 PT inflammation.
 XX
 XX
 PS Example 6; Page 93; 152pp; English.
 CC The present sequence represents the FLAG epitope. A human FDRG FLAG
 CC epitope-tagged protein was constructed by PCR amplification of FDRG cDNA
 CC (see AAX87858) using a primer that includes the epitope sequence.
 CC ligation into expression vector pMER stop, and expression in HEK 293T
 CC cells. FDRG is a secreted molecule that is believed to modulate
 CC angiogenesis and to mediate the contribution of adipocytes to various
 CC metabolic processes. The invention provides FDRG proteins, antibodies,
 CC nucleic acid, and transgenic animals. Also provided are methods for
 CC identifying compounds that modulate FDRG activity or which modulate a
 CC metabolic disorder involving FDRG. Claimed methods of treating obesity or
 CC diabetes, and of regulating angiogenesis, involve administering a small
 CC molecule modulator of FDRG, a FDRG nucleic acid molecule or FDRG antibody
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 62
 AAY31944
 ID AAY31944 standard; peptide; 8 AA.
 AC AAY31944;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE FLAG epitope tag.
 XX
 KM Rad17; cell cycle checkpoint; human; modulator; screening; cancer;
 KM cell proliferation; immune disorder; cirrhosis; rheumatoid arthritis;
 KM therapy; diagnosis; FLAG epitope.
 XX
 OS Synthetic.
 XX
 PN WO9949043-A2.
 XX
 PD 30-SEP-1999.
 XX
 PF 29-MAR-1999; 99WO-US006782.
 XX
 PR 27-MAR-1998; 98US-00049760.
 XX
 PA (ICOS-) ICOS CORP.
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Carr AM, Herendeen DR;
 XX
 DR WPI; 1999-591096/50.
 PT Novel human RAD17 gene and protein useful for identifying factors
 PT involved in cell cycle checkpoint control, e.g. for treatment of cell
 PT cycle control disorders such as cancer.
 PS Example 3; Page 28; 75pp; English.
 CC This peptide represents the FLAG epitope tag that was used in fusion
 CC proteins with human Rad17 (see AAY31937) for expression in mammalian host
 CC cells, permitting immuno-detection and immuno-purification. Rad17 is a
 CC novel cell cycle checkpoint control protein. The invention provides rad17
 CC polynucleotides and polypeptides, expression constructs, host cells,
 CC methods for producing Rad17 polypeptides, antibodies, methods for

CC identifying binding partners of the polypeptides, and methods of
 CC screening for modulators of Rad17 activity. Modulators may be
 CC therapeutically useful in treatment of a wide range of diseases, such as
 CC cancer, in which rad17 activity is involved. They may also be useful as
 CC chemotherapy and radiotherapy adjuvants
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 63
 AAW92256
 ID AAW92256 standard; peptide; 8 AA.
 AC AAW92256;
 XX
 DT 21-APR-1999 (first entry)
 XX
 DE FLAG peptide epitope.
 XX
 KM BL172; urinary tract; marker; cancer; recombinant; human; FLAG.
 XX
 OS Synthetic.
 XX
 PN WO9855656-A1.
 XX
 PD 10-DEC-1998.
 XX
 PF 05-JUN-1998; 98WO-US011693.
 XX
 PR 05-JUN-1997; 97US-00869579.
 XX
 PA (ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J,
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L,
 PI Russell JC, Stroupe SD, Yu H;
 XX
 DR WPI; 1999-045802/04.
 XX
 PT New purified polynucleotide BL172 derivatives and encoded polypeptides -
 PT useful in the identification of markers, which are indicative of urinary
 PT tract diseases or conditions.
 XX
 PS Example 11a; Page 68; 114pp; English.
 CC The invention provides polynucleotide sequences from urinary tract tissue
 CC library BL172. The BL172 polynucleotides (AAX01683-87) are used to detect
 CC target BL172 polynucleotides and BL172 mRNA and the BL172 polypeptides
 CC are used to detect BL172 antigens/antibodies in a test sample. The
 CC identification of certain markers in these methods are indicative of the
 CC presence of urinary tract disease, especially cancer. Additionally, the
 CC polypeptides are used to detect antibodies that bind specifically to a
 CC BL172 epitope derived from a BL172 polypeptide. Host cells containing a
 CC recombinant expression vector comprising the BL172 polynucleotide
 CC sequences are used to produce the polypeptides containing BL172 epitopes.
 CC The methods aid in diagnosis, detection, staging, monitoring,
 CC prognostication, in vivo imaging, prevention and treatment of diseases or
 CC conditions associated with BL172, especially urinary tract cancer. The
 CC present sequences represents a FLAG peptide epitope used in a BL172
 CC expression plasmid
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

RESULT 64
 AAY07740
 ID AAY07740 standard; protein; 8 AA.

XX AAY07740;

XX 05-JUL-1999 (first entry)

XX Human breast-specific BS200 derived protein fragment 1.

XX Breast; cancer; BS200; EST; expressed sequence tag; human; detection;

XX diagnosis; prevention; treatment; disease predisposition.

XX Synthetic.

XX Homo sapiens.

XX WO9902714-A1.

XX 21-JAN-1999.

XX 07-JUL-1998; 98WO-US013908.

XX 07-JUL-1997; 97US-00889127.

XX (ABBO) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

XX Granados EN, Hodges SC, Klasse WR, Kratochvil JD, Russell JC;

XX Stroupe SD, Yu H;

XX WPI; 1999-120915/10.

XX New breast specific gene BS200 - used to develop products for detecting,

XX PT diagnosis, staging, preventing or treating diseases or conditions of the

XX breast, e.g. Breast Cancer.

XX Example 11a; Page 119; 124pp; English.

XX This invention describes a novel human breast-specific protein BS200.

XX CC This protein and its encoding nucleic acids are useful for detecting,

XX CC diagnosing, staging, monitoring, prognosticating, preventing or treating,

XX CC or determining predisposition to diseases or conditions of the breast,

XX CC such as breast cancer

XX SQ Sequence 8 AA;

XX Query Match 100.0%; Score 47; DB 2; Length 8;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

XX 15-APR-1999 (first entry)

XX FLAG peptide epitope.

XX p35 protein; cowpox; vaccinia; variola; secreted protein; chemokine;

KW chemotaxis; cytokine; monocyte chemotactic protein; MCP-1; MCP-3; MIP-1;

KW Rantes; Botaxin; macrophage inflammatory protein; inflammation; asthma;

KW lung; allergy; influenza; psoriasis; arthritis; autoimmune disorder.

XX Synthetic.

XX US5871740-A.

XX 16-FEB-1999.

XX 26-SEP-1996; 96US-00720258.

XX 23-SEP-1995; 95US-00537324.

XX 20-DEC-1995; 95US-00575715.

XX (IMMV) IMMUNEX CORP.

XX Smith CA;

XX WPI; 1999-166574/14.

XX The invention provides nucleic acid sequences (AA906698-700) encoding p35

XX proteins of cowpox, vaccinia and variola viruses (AA904242-44)

XX respectively. p35 is a secreted protein that can be produced by usual

XX recombinant techniques. These p35 proteins can bind to a number of

XX chemotaxis-stimulating cytokines (chemokines). The p35 proteins can be

XX used to treat conditions mediated by chemokines such as monocyte

XX chemotactic protein (MCP)-1, MCP-3, Rantes, Botaxin, macrophage

XX inflammatory protein (MIP)-1 alpha, and MIP-1 beta. They can be used to

XX treat inflammation such as inflammation of the lung, e.g. associated with

XX allergy or asthma. They can also be used to treat influenza, skin

XX inflammation, e.g. psoriasis, or arthritis or autoimmune disorders. The

XX p35 polypeptides can also be used as reagents in assays and for purifying

XX chemokines. The present sequence represents a FLAG peptide epitope used

XX during the course of the invention

XX SQ Sequence 8 AA;

XX Query Match 100.0%; Score 47; DB 2; Length 8;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+06;

XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

XX 29-MAR-1999 (first entry)

XX Adenovirus chimeric protein FLAG-peptide.

XX Chimeric protein; adenoviral fibre protein; monomer; infection;

XX trimerisation domain; affinity; substrate; gene therapy vector;

XX attachment; interaction assay.

XX Mastadenovirus.

XX WO9854346-A1.

XX 03-DEC-1998.

PE 28-MAY-1998; 98MO-US011024.
 XX
 PR 28-MAY-1997; 97US-0047849P.
 PR 16-JAN-1998; 98US-0071668P.
 XX
 PA (GENV-) GENVEC INC.
 XX
 F1 Wickham TJ, Kovesdi I, Roelvink PW, Binfeld D, Brough DE;
 P1 Lizonova A, Yonehiro G;
 DR WPI, 1999-059848/05.
 XX
 PR New adenoviral fibre trimer with reduced binding to native substrate -
 PT useful for, e.g. preparing gene therapy vector with minimal ectopic
 PT infection for in vitro applications.
 XX
 PS Example 14; Page 65; 103pp; English.
 XX
 CC This sequence represents a FLAG peptide used in a method to construct
 CC novel monomers having an N-terminus of an adenoviral fibre protein and a
 CC trimerisation domain. Such monomers have lower affinity for native
 CC substrate than the native adenoviral fibre trimer. Cell lines containing
 CC such monomers are used (i) to propagate adenovirus for use as gene
 CC therapy vectors (for in vitro or in vivo applications), (ii) as reagents
 CC for studying adenoviral attachment and infection, and (iii) in receptor-
 CC ligand interaction assays. The new viruses produce minimal ectopic
 CC infection (they can not infect native host cells) so are safer as vectors
 CC and can be engineered for selective targeting to other cells
 XX
 SQ Sequence 8 AA;

Query Match	Similarity	100.0%;	Score 47;	DB 2;	length 8;
Best Local	Similarity	100.0%;	Pred. No. 2.1e+06;		
Matches	8;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0
Qy	1	DYKDDDDK	8		
Db	1	DYKDDDDK	8		
RESULT 67					
AAy42254					
ID	AAy42254	standard;	peptide;	8	AA.
AC	AAy42254;				
XX					
DT	01-DEC-1999	(first entry)			
XX					
DE	Synthetic FLAG octapeptide.				
XX					
KW	Adenovirus; gene therapy; coxsackievirus adenovirus receptor; CAR;				
XX	cancer; cystic fibrosis; muscular dystrophy.				
OS	Synthetic.				
XX					
PN	W09939734-A1.				
XX					
PD	12-AUG-1999.				
XX					
PF	05-FEB-1999;	99WO-US002549.			
XX					
PR	06-FEB-1998;	98US-0073947P.			
XX					
PR	10-SEP-1998;	98US-009801P.			
XX					
PA	(UABR-) UAB RES FOUND.				
XX					
PI	Curjel DT, Krasnykh VN, Dmitriev I;				
XX					
DR	WPI, 1999-539951/45.				
XX					
PT	Recombinant adenovirus vectors with modified fiber knob loops, useful in				
XX	gene therapy.				
XX					

PS Example 14; Page 39; 126pp; English.
 XX
 CC This sequence represents a synthetic FLAG octapeptide. DNA encoding this
 CC sequence was cloned into the sequence encoding the HI loop of the
 CC adenovirus fibre protein knob domain, which was then used in the
 CC construction of plasmids encoding a fibre protein. Recombinant adenovirus
 CC genomes were generated by homologous DNA recombination in *E. coli* before
 CC excision of the newly generated genome for virus rescue. The knob domain
 CC of the adenovirus fibre protein mediates the initial binding and
 CC recognition of the coxsackievirus and adenovirus receptor (CAR) on the
 CC cell surface. The HI loop protrudes from the knob domain and connects
 CC beta-strands involved in the formation of the cell binding site.
 CC Recombinant adenovirus vectors are used in a number of gene therapy
 CC applications; however, the reliance on the CAR means that in certain
 CC situations, recombinant virions are sequestered by high CAR-expressing
 CC non-target cells while the true target cells, if low in CAR, receive
 CC little of the therapeutic gene. Studies of fibre proteins with an HI loop
 CC modified by insertion of the FLAG octapeptide (a widely used detection
 CC and purification tag) suggested that a heterologous peptide sequence at
 CC this location would not affect the structure of the protein and that the
 CC HI loop was still accessible for binding. The infectivity of recombinant
 CC virions carrying this modified fibre protein was unaffected
 CC
 XX
 SQ Sequence 8 AA:
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ	Sequence	8 AA:
Query Match	100.0%;	Score 47;
Best Local Similarity	100.0%;	Pred. No. 2.1e+06;
Matches	8; Conservative	0; Mismatches
		0; Indels
		0; Gaps
OY	1 DYKDDDDK 8 	
Db	1 DYKDDDDK 8	
RESULT 68		
AAY49544		
ID	AAY49544 standard; peptide; 8 AA.	
XX	AAY49544;	
AC		
XX		
DT	12-JAN-2000 (first entry)	
XX		
DE	FLAG epitope for insertion into the N-terminus of Nsp1.	
KM	Human; PRO201, PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; ESR;	
KW	expressed sequence tag; tumour; tumorigenesis; diagnosis; cancer;	
XX	identification; proliferation; neoplastic cell growth.	
OS	Synthetic.	
XX		
PN	WO954467-A1.	
XX		
PD	28-OCT-1999.	
XX		
PF	23-APR-1999; 99WO-US008847.	
XX		
PR	23-APR-1998; 98US-0082767P.	
PR	22-DEC-1998; 98US-0113296P.	
XX	(GETH) GENENTECH INC.	
PA		
PI	Stewart TA, Lu Y;	
XX		
DR	WPI, 1999-620728/53.	
XX		
PT	New human polypeptides useful to screen for antagonists and produce	
XX	antibodies useful to diagnose and treat tumors, e.g. cancers.	
PS	Example 3; Page 54; 152pp; English.	
CC	The present invention describes human proteins designated PRO201, PRO308	
CC	and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are	
CC	encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins were	

Query Match	100.0%	Score 47;	DB 2;	Length 8;
Best Local Similarity	100.0%	Pred. No. 2.1e+05;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	DYKDDDDK	8	
Db	1	DYKDDDDK	8	

DT 26-OCT-1999 (first entry)
XX
DE FLAG peptide.

KW islet cell antigen, IIA2; human; epitope; autoantigen; autoantibody;
 KM insulin-dependent diabetes mellitus, IDDM; immunoassay; diagnosis; FLAG
 XX Synthetic.
 OS
 XX

PF	29-DEC-1998;	98EP-00660149.
XX		
PR	29-JAN-1998;	98US-00015399.
VV		

PI	Hinkkanen A;
XX	
DR	WPI; 1999-481070/41.
XX	

PI mellitus.
XX
PS Disclosure; Page 4; 27pp; English.
XX

This peptide represents a FLAG peptide that is recombinantly expressed by monoclonal antibody M1 (ATCC HB 9259). FLAG has been used in novel fusion proteins of the invention. Such fusion proteins have epitopes of at least 2 of the autogenetic glutamate decarboxylase (GAD65, see AA006607), islet cell antigen (IICA, see AA006605) and pepsinoholinin (PPHNS, see AA006608), the epitopes being connected via linker peptides. The invention also provides the cDNA encoding the fusion protein, a vector and an ischaemic colic cell encompassing the fusion protein. The fusion protein is used in an immunoassay for the simultaneous detection of autoantibodies related to insulin-

[illegible]

```

RESULT 70
AAW92410
ID AAW92410 standard; peptide; 8 AA
vv

```

DT	21-APR-1999	(first entry)
XX		
DE	Human IL-17R	FLAG peptide
XY		

KM 1,2-1/6; human; interleukin-1/ receptor; immunoregulator; inhibitor;
 T cell proliferation; T cell activation; organ; graft; rejection;
 autoimmune disease; allergy; asthma; treatment; inflammatory disease
 B cell proliferation; immunoglobulin secretion; immunogen.

FN 053869286-A.
XX
PD 09-FEB-1999.
XX

PA	(IMMV) IMMUNEX CORP.
XX	
PR	07-AUG-1995; 95US-00538765.
FA	03-MAR-1995; 95US-00410535.

XX WPI; 1999-152766/13.
DR
XX

PT asthma or inflammatory disease.
XX
PS Example 3; Col 29-30; 25pp; English.
V

This sequence represents a human interleukin-1 receptor (IL-1R) FLAG peptide. IL-1R polypeptides have immunoregulatory activity. They can be used for inhibiting T cell proliferation, or for inhibiting T cell activation. In particular they can be used for preventing or treating organ or graft rejection, autoimmune disease, allergy or asthma. They can also be used for the prevention or treatment of inflammatory disease in which activated T cells play a role or for inhibiting B cell proliferation or immunoglobulin secretion. The IL-17 polypeptides can also be used as immunogens, reagents in *in vitro* assays, or as binding agents for affinity purification procedures

Query Match	100.0%;	Score 4.1;	UB 4.1;	Length 8;
Best Local	100.0%;	Pred. No. 2.1e+05;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0.

Qy	1	DYKDDDDK	8
Db	1	DYKDDDDK	8

RESULT 71	
AAV06911	
AAV06911 standard; peptide; 8 AA.	
AAV06911;	
01-JUL-1999 (first entry)	
FLAG peptide epitope.	
Growth factor precursor; B-cell surface; T cell surface; CAb; hepatitis; catalytic antibody; immunoglobulin; tumour necrosis factor; influenza; rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmunity; inflammatory disease; gene therapy; FLAG.	
Synthetic.	
WO9915563-A1.	
01-APR-1999.	
18-SEP-1998; 98WO-AU000783.	
19-SEP-1997; 97AU-00009306.	
(AMRAD OPERATIONS PTY LTD.	
Koentgen F, Sness GM, Tarlinton DM, Treutlein HR;	
WPI; 1999-244394/20.	
Growth factor precursor cleaved by antigen-specific catalytic antibody.	
Example 3; Page 42; 101pp; English.	
The invention relates to a growth factor precursor that comprises B-cell surface binding part, T cell surface binding part, antigen cleavable by a catalytic antibody (CAb), and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part can interact with its target. The growth factor precursors are used to select B cells that produce Ag-specific CAb, and to generate CAb from such cells (by inducing mitogenesis, caused by the growth factor released by specific cleavage). The Ag-specific CAb can be directed against, e.g. tumour necrosis factor (treatment of rheumatoid arthritis or toxic shock syndrome); viral docking receptors (treatment of human immune virus, hepatitis and influenza infections); tumour-specific antigens; amyloid plaque (treatment of Alzheimer's disease or myeloma) or IGE (treatment of allergies such as asthma). CAb may also be used for drug detoxification, to treat autoimmune or inflammatory diseases and to eliminate environmental or industrial pollutants, such as plastics and petroleum. Particularly the growth factor precursors are produced by delivering the corresponding nucleic acid in a viral or other gene therapy vector. The present sequence represents a FLAG peptide epitope	
Sequence 8 AA;	
Query Match 100.0%; Score 47; DB 2; Length 8;	
Best Local Similarity 100.0%; Pred. No. 2.1e+06;	
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 DYKDDDK 8	
1 DYKDDDK 8	
RESULT 72	
AAV23636	
AAV23636 standard; peptide; 8 AA.	
AAV23636;	

DT	06-SEP-1999	(first entry)	
XX			
DE	Ocrapeptide used to make BZLF2 fusion proteins.		
XX			
XX	BZLF2 protein; beta chain; blood mononuclear mononuclear cell;		
KW	Class II major histocompatibility complex antigen; proliferation;		
KM	Cytotoxic T cell response; antigen specific response; asthma;		
KW	autoimmune disease; transplant rejection.		
XX			
OS	Synthetic.		
XX			
FN	US5925734-A.		
XX			
PD	20-JUL-1999.		
XX			
XX			
PF	24-SEP-1997; 97US-00936854.		
XX			
PR	28-APR-1994; 94US-00235397.		
PR	28-APR-1995; 95US-00430633.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
F1	Comeau MR, Hutt-Fletcher LM, Armitage RJ, Farrarh TM, Alderson M;		
P1	Spriggs MK, Cohen JI;		
XX			
DR	WPI; 1999-418295/35.		
XX			
PT	Epstein-Barr virus BZLF2 proteins.		
XX			
PS	Example 1; Col 31-32; 25pp; English.		
XX			
CC	The present sequence represents a peptide used to create fusion proteins		
CC	with the Epstein-Barr virus BZLF2 proteins of the invention. The BZLF2		
CC	protein is capable of binding to a beta chain of a Class II major		
CC	histocompatibility complex antigen to inhibit an antigen-specific		
CC	response. BZLF2 is useful for inhibiting antigen-specific antibody		
CC	formation, the proliferation of blood mononuclear mononuclear cells, and		
CC	cytotoxic T cell responses. BZLF2 is also useful for inhibiting		
CC	undesirable antigen specific responses, e.g. in the treatment or		
CC	prevention of asthma; for preventing or treating autoimmune disease; and		
CC	for preventing tissue or organ transplant rejection		
XX			
SQ	Sequence 8 AA;		
	Query Match 100.0%; Score 47; DB 2; Length 8;		
	Best Local Similarity 100.0%; Pred. No. 2.1e+06;		
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CY	1 DYKDDDDK 8		
DB	1 DYKDDDDK 8		
	RESULT 73		
ID	AAW86029		
XX	AAW86029 standard; peptide; 8 AA.		
AC	AAW86029;		
XX			
DT	23-FEB-1999 (first entry)		
XX			
DE	FLAG peptide epitope.		
XX			
KW	UT116; urinary tract; epitope; antigen; detection; diagnosing;		
KW	monitoring; in vivo imaging; cancer; agonist; antibody; tumour;		
KW	metastasis.		
XX			
OS	Synthetic.		
XX			
FN	W09851824-A1.		
XX			
PD	19-NOV-1998.		
XX			

PF 15-MAY-1998; 98WO-US009972.
 XX
 PR 15-MAY-1997; 97US-00856652.
 XX
 XX (ABBOT) ABBOTT LAB.
 PA Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
 PI Hodges SC, Klaas MR, Kratochvil JD, Roberts-Rapp L, Russell JC;
 PI Stroupe SD;
 XX
 DR WPI; 1999-045237/04.
 XX
 XX New method for detecting diseases of the urinary tract - comprises use of
 PT a U116 polynucleotide, protein or antibodies, used for preventing and
 PT treating urinary tract infections and cancer.
 XX
 PS Example 11; Page 67; 113pp; English.
 XX
 CC The invention relates to a method of detecting the presence of a target
 CC U116 polynucleotide in a test sample using U116 gene-specific sequences
 CC (AAV60386 to AAV80397). Host cells transfected with an expression vector
 CC containing the U116 gene can be used to produce a U116 polypeptide
 CC recombinantly. This polypeptide has at least one U116 epitope which can
 CC be used in a method for detecting U116 antigen in a test sample. The
 CC polynucleotides and polypeptides are useful for detecting, diagnosing,
 CC monitoring, staging, prognosticating, in vivo imaging, preventing,
 CC treating or determining the predisposition of a subject to diseases and
 CC conditions of the urinary tract, such as urinary tract cancer. Antibodies
 CC specifically binding to an epitope of U116 antigen, and agonists are
 CC useful for treating urinary tract diseases, tumours and metastases. The
 CC present sequence represents a FLAG peptide epitope used in the
 CC construction of plasmids for the expression of U116 polypeptide
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 XX
 RESULT 74
 AAY27153
 ID AAY27153 standard; peptide; 8 AA.
 XX
 AC AAY27153;
 XX
 DT 15-SEP-1999 (first entry)
 XX
 DE Peptide encoded by Seq ID No: 24 of JP11164690.
 XX
 KW Vertebrate-derived protein; slit protein; diagnosis; cancer; nerve;
 KW muscle; endocrine system.
 XX
 OS Synthetic.
 XX
 XX JP11164690-A.
 XX
 XX 22-JUN-1999.
 XX
 PD 05-DEC-1997; 97JP-00335435.
 XX
 PR 05-DEC-1997; 97JP-00335435.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 DR WPI; 1999-411830/35.
 DR N-PSDB; AAX89170.
 XX
 PT New vertebrate slit protein - useful for diagnosis and treatment of

PT cancers in nerves, muscle and endocrine system.
 XX
 PS Disclosure; Page 88; 102pp; Japanese.
 XX
 CC The invention relates to a vertebrate-derived protein containing an amino
 CC acid sequence shown in AAY27137 and AAY27139. The vertebrate-derived
 CC protein has at least 55 % homology to one of sequences shown in AAY27141-
 CC Y27143, and has slit protein-like activity. The vertebrate slit proteins
 CC encoding nucleic acid sequences have at least 60% homology to nucleic
 CC acid sequences AAX9161-163. The vertebrate-derived proteins can be
 CC produced recombinantly by transforming host cells with expression vectors
 CC comprising the encoding nucleic acids. The proteins of the invention are
 CC for diagnosing and treating cancer of the nerves, muscle and/or endocrine
 CC system
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 XX
 RESULT 75
 AAW97648
 ID AAW97648 standard; peptide; 8 AA.
 XX
 AC AAW97648;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE FLAG peptide.
 XX
 KW B8202 protein; breast cancer; tumour; metastasis; diagnosis; therapy;
 KW antigen; epitope; human; FLAG.
 XX
 OS Synthetic.
 XX
 XX MO9902559-A1.
 XX
 PD 21-JAN-1999.
 XX
 PF 07-JUL-1998; 98WO-US014046.
 XX
 PR 07-JUL-1997; 97US-00888894.
 XX
 PA (ABBOT) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klaas MR, Kratochvil JD, Russell JC;
 PI Stroupe SD;
 XX
 DR WPI; 1999-120783/10.
 XX
 PT New breast specific gene, B8202 - used to develop products for detecting,
 PT diagnosing, staging, preventing or treating diseases or conditions of the
 PT breast such as breast cancer.
 XX
 PS Example 11a; Page 70; 110pp; English.
 XX
 CC This peptide comprises a FLAG epitope. An antisense primer incorporating
 CC a sequence encoding FLAG has been used in the PCR amplification of human
 CC breast specific B8202 cDNA clones (see also AAX07004-09) for the
 CC production of a B8202 expression plasmid. The B8202 protein product (see
 CC also AAW97643) was recovered from transfected mammalian cells using anti-
 CC FLAG monoclonal antibody M2. The invention provides B8202 cDNA clones and
 CC polypeptides useful for developing products for detecting, diagnosing,
 CC staging, preventing or treating diseases or conditions of the breast,
 CC including breast cancer
 XX

SQ Sequence 8 AA: 100.0%; Score 47; DB 2; Length 8;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DYKDDDDK 8
 1 DYKDDDDK 8
 1 DYKDDDDK 8

RESULT 76
 AAW96302
 ID AAW96302 standard; peptide; 8 AA.
 AC AAW96302;
 DT 28-JUN-1999 (first entry)
 DE C-terminal tagging peptide.
 XX
 KM TANGO-69; herpesvirus entry mediator; HVEM; glycoprotein D; LIGHT;
 KM lymphotoxin; tumour necrosis factor receptor; TNFR; cell proliferation;
 KM programmed cell death; apoptosis; immune response; probe; primer;
 KM antibody; signal transduction; cytokine; leukocyte; cell differentiation;
 KM coagulation.
 XX
 OS Synthetic.
 XX
 PN WO9911662-A1.
 PD 11-MAR-1999.
 XX
 PF 03-SEP-1998; 98WO-US018533.
 XX
 PR 05-SEP-1997; 97US-0057936P.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Busfield SJ;
 DR WPI; 1999-205132/17.
 XX
 PT Newly isolated murine polynucleotide encoding a TANGO-69 polypeptide -
 PT useful for regulating cell proliferation and differentiation, and cell
 PT survival.
 PS
 PS Example 4(b); Page 104; 125pp; English.
 CC The murine TANGO-69 cDNA encodes a type II membrane protein, which is the
 CC murine homolog of the human herpesvirus entry mediator (HVEM) ligand,
 CC LIGHT. LIGHT is a novel cytokine and is termed LIGHT because it shows
 CC homology to lymphotoxins, exhibits inducible expression and competes with
 CC HSV Glycoprotein D for HVEM, a receptor expressed by T-lymphocytes. HVEM
 CC and TANGO-69 are members of the tumour necrosis factor receptor (TNFR)
 CC ligand superfamily. The TANGO-69 protein regulates a variety of cellular
 CC processes including cell proliferation, programmed cell death and immune
 CC responses by binding to a membrane-bound form of HVEM (mHVEM) to inhibit
 CC mHVEM activity. The protein plays an essential role in inhibiting
 CC inflammation. Probes or primers derived from the TANGO-69 coding sequence
 CC are useful for detecting the polynucleotide in samples (especially
 CC mRNA) and antibodies directed against the TANGO-69 polypeptide are useful
 CC for detecting the polypeptide. Compounds which bind to the TANGO-69
 CC polypeptide are useful for modulating the activity of the polypeptide and
 CC TANGO-69 protein variants are useful as (ant)agonists. TANGO-69
 CC polypeptides are useful for interacting with proteins in the TANGO-69
 CC signalling pathway, binding the TANGO-69 receptor, interacting with mHVEM
 CC and mast cells, and for modulating inflammation, cytokine production,
 CC leukocyte activation, MHC I induction, allergic reactions, cellular
 CC differentiation, viral proliferation, cell death adhesion molecule
 CC induction on endothelial cells and coagulation. Two primers (AA08401,
 CC AA08402) were used to amplify the TANGO-69 sequence for its subcloning
 CC into the expression vector pIC2alpha A for expression in Pichia

CC pastoris. The resulting plasmid fused the Pichia pastoris alpha-factor
 CC signal sequence to the mature form of TANGO-69 also comprising this C-
 CC terminal tag
 SQ Sequence 8 AA: 100.0%; Score 47; DB 2; Length 8;
 Query Match Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DYKDDDDK 8
 1 DYKDDDDK 8
 1 DYKDDDDK 8

RESULT 77
 AAW95562
 ID AAW95562 standard; peptide; 8 AA.
 AC AAW95562;
 DT 29-MAR-1999 (first entry)
 DE FLAG peptide epitope used in a Ls170 expression plasmid.
 XX
 KM Ls170 gene; in vivo imaging; lung disease; cancer; drug screening; FLAG.
 XX
 OS Synthetic.
 XX
 PN WO9856951-A1.
 PD 17-DEC-1998.
 XX
 PF 11-JUN-1998; 98WO-US011601.
 XX
 PR 11-JUN-1997; 97US-0049183P.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EM, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
 PI Russell JC, Stroupe SD;
 DR WPI; 1999-060335/05.
 XX
 PT New Ls170 nucleic acid from lung tissue - useful for detecting,
 PT monitoring, preventing and treating lung disease, particularly cancer.
 PS
 PS Example 11; Page 70; 120pp; English.
 CC The present invention relates to the detection of a target Ls170
 CC polynucleotide that comprises treating a test sample with at least one
 CC Ls170-specific nucleic acid that has at least 50 percent identity with
 CC any of the sequences (AA00801-809) which are fragments derived from
 CC Ls170 gene. These Ls170 nucleic acid fragments represent a set of
 CC contiguous, partially overlapping sequences transcribed from lung tissue.
 CC They are used for diagnosis, staging, monitoring, in vivo imaging,
 CC prevention and treatment of lung disease, specifically cancer, and to
 CC indicate predisposition to such disease. Particularly detection of Ls170
 CC polynucleotide, Ls170 antigens, or anti-Ls170 antibodies is indicative of
 CC disease. Cells transformed with an expression system comprising the Ls170
 CC nucleic acid sequences are used to express recombinant polypeptides. The
 CC Ls170 polypeptides containing at least one epitope in their sequences,
 CC are used to raise Ab and for drug screening. Ls170-related nucleic acid
 CC can be used to isolate related sequences; as standards and reagents in
 CC assays; as targets for drug screening, and as components or targets for
 CC therapy, e.g. as antisense, ribozyme or triplex-forming agents. Ab can be
 CC used to deliver therapeutic agents to Ls170-expressing cells; directly as
 CC therapeutic agents (by neutralising Ls170 polypeptides); in competitive
 CC binding drug screens, and to generate anti-idiotypic antibodies for use
 CC in rational drug design. The present sequence represents a FLAG peptide
 CC epitope used in the Ls170 expression plasmids

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8

RESULT 78

AAV09543

ID AAV09543 standard; peptide; 8 AA.

XX AAV09543;

XX 21-JUL-1999 (first entry)

XX Human TAB1 FLAG peptide.

XX Human; TAB1; TAK1; screening; inhibition; TGF-beta;

XX transforming growth factor beta.

XX Homo sapiens.

XX WO921010-A1.

XX 29-APR-1999.

XX 22-OCT-1998; 98WO-JF004796.

XX 22-OCT-1997; 97JP-00290188.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ono K, Ohtomo T, Tsuchiya M;

XX WPI; 1999-312645/26.

PT Screening for TGF- beta inhibitory substances, which are useful as drugs
PT for treatment of diseases relating to its disorder.

XX Example 1; Page 58; 195pp; Japanese.

CC A method has been developed for screening for substances which inhibit
CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
CC comprises: (a) contacting the polypeptide in the presence of a sample;
CC and (b) detecting the amount of bound polypeptide, in which the sample
CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
CC indications e.g. as TGF-beta signal transduction inhibitors or
CC activators, or extracellular matrix protein production enhancement
CC inhibitors, or monocytic migration inhibitors or activators, or
CC physiological activity induction inhibitors or activators, or
CC immunosuppression inhibitors or activators, or amyloid beta protein
CC precipitation inhibitors or activators, and such substances can also be
CC inhibitors of the TAK1 polypeptide function, particularly kinase
CC activity. The present sequence represents a peptide from an example of
CC the present invention

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8

RESULT 79

AAW82718

ID AAW82718 standard; protein; 8 AA.

XX AAW82718;

XX 15-MAR-1999 (first entry)

XX Human ZCHEMO-8 C/N terminal FLAG peptide.

XX Chemokine; ZCHEMO-8; human; pathological condition; infection; cancer;
XX autoimmune disorder; immunodeficiency; myeloproliferic; wound healing;
XX transplant; progenitor cell; HIV infection; AIDS; chemotherapy;
XX radiation therapy; T cell; macrophage activation inhibitor; B lymphocyte;
XX chronic inflammatory disease; infective disease; diagnosis; detection;
XX drug screening; gene therapy; FLAG peptide.

XX Synthetic.

XX WO9854326-A1.

XX 03-DEC-1998.

XX 19-MAY-1998; 98WO-US010329.

XX 29-MAY-1997; 97US-0047860P.

XX (ZYMO) ZYMOGENETICS INC.

XX Shepard PO;

XX WPI; 1999-059841/05.

PT New isolated human beta-chemokine, ZCHEMO-8 - used to develop products
PT for treating e.g. ischemia, reperfusion, wound healing, autoimmune
PT diseases, inflammation, asthma or infections.

PS Claim 10; Page 94; 131pp; English.

CC This sequence represents a FLAG peptide used in the isolation of a
CC novel human beta chemokine, ZCHEMO-8. Altered levels of ZCHEMO-8 may be
CC indicative of pathological conditions, including infections, cancer,
CC myeloproliferic disorders, autoimmune disorders and immunodeficiencies. The
CC ZCHEMO-8 polypeptides can be used, e.g. to reduce the damage in ischemic
CC and reperfusion injuries, in a wound healing regime to stimulate an
CC infiltration of immune cells (e.g. monocytes, neutrophils, T lymphocytes
CC or basophils) to a wound site to facilitate healing. ZCHEMO-8 may be used
CC to mobilize progenitor cells from the marrow into the peripheral blood
CC for transplants. ZCHEMO-8 polypeptides could be used to further define
CC the role of chemokines in mediating suppression of HIV replication in
CC CD4+ T-cells and limiting progression of HIV infection to AIDS. Use may
CC be made of ZCHEMO-8 polypeptides during chemotherapy or radiation
CC therapy, to protect haematopoietic cells. ZCHEMO-8 antagonists may have a
CC beneficial therapeutic effect in diseases where the inhibition of
CC activation of certain macrophages, neutrophils, basophils, B lymphocytes
CC and/or T cells may be effective. Such diseases include autoimmune
CC diseases e.g. multiple sclerosis, insulin-dependent diabetes and systemic
CC lupus erythematosus, rheumatoid arthritis, allergies, asthma or
CC atherosclerosis. Also benefit may be derived from using ZCHEMO-8
CC antagonists for chronic inflammatory and infective diseases. Antagonists
CC may be used to dampen or inactivate ZCHEMO-8 during activated immune
CC response. The products can also be used for detection, diagnosis, drug
CC screening or gene therapy

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
1 DYKDDDDK 8

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RESULT 80
AAV06900
ID AAV06900 standard; peptide; 8 AA.
XX
XX
AC AAV06900;
XX
DT 06-JUL-1999 (first entry)
XX
DE FLAG affinity peptide sequence.
XX
KM Secretory protein; ZSIG-11; ligand polypeptide; testis; endoprotease;
KM prohormone convertase; fertility; therapeutic; human; FLAG.
OS Synthetic.
XX
PN WO916870-A1.
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-US020449.
XX
PR 29-SEP-1997; 97US-0060327P.
PR 29-SEP-1997; 97US-00939897.
PR 19-MAY-1998; 98US-00081310.
PR 19-MAY-1998; 98US-0085966P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO;
XX
DR WPI; 1999-263692/22.
XX
PT Polynucleotide encoding a human secretory protein, ZSIG-11.
XX
PS Example 4; Page 107; 113pp; English.
XX
CC The invention relates to a human secretory protein, ZSIG-11. Host cells
CC containing a vector comprising the ZSIG-11 nucleic acid are used for the
CC recombinant expression of the protein. ZSIG-11 is a novel ligand
CC polypeptide and specific antibodies can be used to detect its presence in
CC a biological sample. Probes derived from ZSIG-11 nucleotide sequences can
CC also be used in detection of ZSIG-11 RNA. ZSIG-11 is expressed at high
CC levels in testis, and could be used to identify/study prohormone
CC convertases or endoproteases that exhibit testis specificity.
CC Antagonists, including antibodies, are useful for inhibiting or
CC eliminating the function of ZSIG-11. It is possible that ZSIG-11 and its
CC antagonists will be useful as fertility inducing therapeutics
XX
SQ Sequence 8 AA:
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

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KW gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO9931274-A2.
XX
XX PD 24-JUN-1999.
XX
XX PF 11-DEC-1998; 98WO-US026441.
XX
XX PR 15-DEC-1997; 97US-00990568.
XX
XX PA (ABBOTT ) ABBOTT LAB.
XX
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EM, Hodges SC, Kلاس MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
XX DR WPI; 1999-405041/34.
XX
XX PT PA153 CDNA transcribed from pancreatic tissue.
XX
XX PS Example 11a; Page 123; 123pp; English.
XX
XX CC This invention describes novel contiguous and partially overlapping cDNA
XX sequences and their encoded polypeptides, designated PA153, transcribed
XX from human pancreatic tissue and which have cytostatic activity. The
XX PA153 polynucleotides, proteins and antibodies are all useful in methods
XX of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
XX antibodies in a sample is indicative of pancreatic disease. PA153
XX antibodies (antagonists) can also be used in vivo for therapeutic use,
XX e.g. treatment of pancreatic disease, tumours or metastases. Antisense
XX PA153 polynucleotides can be used in gene therapy of pancreatic diseases
XX
SQ Sequence 8 AA:
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

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RESULT 81
AAV25328
ID AAV25328 standard; protein; 8 AA.
XX
XX AC AAV25328;
XX
XX DT 03-SEP-1999 (first entry)
XX
XX DE Human pancreatic PA153 derived peptide.
XX
XX KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;
XX anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
KW

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RESULT 82
AAV13471
ID AAV13471 standard; peptide; 8 AA.
XX
XX AC AAV13471;
XX
XX DT 26-JUL-1999 (first entry)
XX
XX DE FLAG peptide sequence.
XX
XX KW BSI06; breast; marker; detection; diagnosis; breast cancer.
XX
XX OS Synthetic.
XX
XX PN WO9923230-A1.
XX
XX PD 14-MAY-1999.
XX
XX PF 19-OCT-1998; 98WO-US022020.
XX
XX PR 31-OCT-1997; 97US-00962094.
XX
XX PA (ABBOTT ) ABBOTT LAB.
XX
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados E, Hodges SC, Kلاس MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Stroupe SD;
XX
XX

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DR WPI; 1999-326991/27.
 XX New isolated BS106 nucleic acids.
 XX
 PS Example 11a; Page 93; 105pp; English.
 CC The invention provides BS106 polynucleotides (AAK55578-82) and
 CC polypeptides (AAV13466-470). The BS106 nucleic acids correspond to a
 CC breast tissue gene and can be used as markers for breast tissue disease.
 CC The products can be used for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing or treating, or determining diseases or
 CC conditions associated with BS106, especially breast cancer
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 1 DYKDDDDK 8

RESULT 83
 ID AAY04141 standard; peptide; 8 AA.
 XX AAY04141;
 AC
 XX 15-JUN-1999 (first entry)
 DT
 XX Human slit 3 peptide.
 DE
 XX Human; slit-like protein; slit 3; slit 1; prevention; treatment; disease;
 KW spinal cord; thyroid gland; ovary; prostate; renal gland;
 KW small intestine; heart; trachea; thymus; lymph node; muscular system;
 KW colon.
 XX
 XX Homo sapiens.
 OS
 XX JP11075846-A.
 PN
 XX 23-MAR-1999.
 PD
 XX 02-SEP-1997; 97JP-00236994.
 PF
 XX 02-SEP-1997; 97JP-00236994.
 PR
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX WPI; 1999-257695/22.
 DR
 XX
 XX PT New slit-like polypeptide - useful for prevention and treatment of
 PT diseases in spinal cord, thyroid gland, ovary, prostate, renal gland,
 PT small intestine, heart, trachea, thymus, lymph node, muscular system and
 PT colon.
 XX
 XX Example 4; Page 47; 48pp; Japanese.
 PS
 CC The present sequence represents a peptide from a human slit-like protein.
 CC slit-like proteins can be used for the prevention and the treatment of
 CC diseases in spinal cord, thyroid gland, ovary, prostate, renal gland,
 CC small intestine, heart, trachea, thymus, lymph node, muscular system and
 CC colon
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 84
 ID AAY49750 standard; peptide; 8 AA.
 XX AAY49750;
 AC
 XX 19-JAN-2000 (first entry)
 DT
 XX Compact structure forming exemplification peptide #43.
 DE
 XX Compact structure forming peptide; dimerisation; stability; scaffold;
 KW library screening; drug screening; gene therapy.
 XX
 XX Synthetic.
 OS
 XX WO9951625-A2.
 PN
 XX 14-OCT-1999.
 PD
 XX 02-APR-1999; 99WO-US007374.
 PF
 XX 02-APR-1998; 98US-0080444P.
 PR
 XX (RIGE-) RIGEL PHARM INC.
 PA
 XX Anderson D;
 PI
 XX WPI; 1999-620191/53.
 DR
 XX Novel dimerization peptides which self-associate are used with other
 PT proteins to effect the formation of compact structures.
 PT
 XX Disclosure; Page 13; 75pp; English.
 PS
 XX The present invention describes peptides which have a moderate or high
 CC affinity for each other, when added as extensions to both the N-terminus
 CC and C-terminus of a protein, can be used to help fold the protein into a
 CC compact structure. This compact structure is more stable to proteases. A
 CC composition (A) comprises at least a first dimerisation peptide (I)
 CC comprising the sequence (SI) that is no more than 8 amino acids long,
 CC where the composition optionally comprises a second dimerisation peptide
 CC (II): NH₂-X1-X2-X3-X4-X5-COOH (SI) where X1 to X4 = Ala, Val, Ile, Leu,
 CC Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu; NH₂-X1-X2-X3-X4-X5-
 CC COOH (II). The compositions of the invention are displayed
 CC intracellularly or extracellularly and are useful to identify binding
 CC proteins and molecules, and to modulate intracellular signalling
 CC pathways. A library of constrained proteins may be evaluated in vivo for
 CC its bioactive potential. The invention can be used to access molecules or
 CC targets within living cells, and then provide for the isolation of the
 CC constrained protein which has a phenotypic effect on the living cells.
 CC The methods are also useful to identify in vitro binding partners of the
 CC constrained protein. The compositions of the invention are useful as a
 CC scaffold for gene therapy and for potential use as a therapeutic in
 CC physiological fluids. The present sequence is used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 1 DYKDDDDK 8

RESULT 85
 AAE16563

```

ID  AA616563 standard; peptide; 8 AA.
XX
AC  AA616563;
XX
DT  09-APR-2002 (first entry)
XX
DE  Epitope tag #7 fused to yeast cell wall protein AGA2.
XX
KW  Yeast cell wall protein; AGA2; T cell receptor; multiple sclerosis;
XX  cancer; sepsis; autoimmune disease; arthritis; diabetes.
XX
OS  Synthetic.
XX
PN  US6331391-B1.
XX
PD  18-DEC-2001.
XX
PF  20-JAN-1998; 98US-00009388.
XX
PR  31-MAY-1996; 96US-0018741P.
XX  30-MAY-1997; 97US-00866398.
XX
PA  (UNII ) UNIV ILLINOIS FOUNO.
XX
PI  Wittrup KD, Kranz DM, Kieke M, Boder ET;
XX  WPI; 1999-430619/36.
XX
PT  Selecting proteins with enhanced phenotypic properties than wild-type
XX  proteins, is useful for highly specific cancer diagnosis and therapy.
XX
PS  Claim 40; Col 60; 59pp; English.
XX
CC  The present invention relates to a method for selecting proteins for
XX  displayability on a yeast cell surface. The method comprises transforming
XX  yeast cells with a vector that expresses a test protein fused to a yeast
XX  cell wall protein (AGA2), contacting the cells with a label that binds to
XX  proteins displayed on the cell wall, and isolating label-bound cells,
XX  where the test protein is from a variegated population generated by
XX  mutagenesis. The invention is also directed to new processes for
XX  engineering T cell receptor for improved binding properties. Improved T
XX  cell receptor molecules are useful in therapies for cancer, sepsis,
XX  autoimmune diseases such as arthritis, diabetes or multiple sclerosis.
XX  The methods are useful to select proteins with altered affinity, altered
XX  specificity or conditional binding. The present sequence is an epitope
XX  tag fused between protein of interest and yeast cell wall protein AGA2
XX
SQ  Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DYKDDDDK 8
    |||||
    1 DYKDDDDK 8
Db

RESULT 86
AAW97673
ID  AAW97673 standard; peptide; 8 AA.
XX
AC  AAW97673;
XX
DT  10-MAY-1999 (first entry)
XX
DE  FLAG epitope.
XX
KW  MKK3, human; mitogen activated protein kinase kinase; MAP kinase kinase;
XX  signal transduction; inflammation; psoriasis; AIDS; cancer; apoptosis;
XX  therapy; FLAG; epitope.
XX
OS  Synthetic.

```

```

XX
PN  WO9902547-A1.
XX
PD  21-JAN-1999.
XX
PF  07-JUL-1998; 98WO-US014101.
XX
PR  07-JUL-1997; 97US-00888429.
XX
PA  (UTMA-) UNIV MASSACHUSETTS.
XX
PI  Davis RJ, Whitmarsh A, Tournier C;
XX  WPI; 1999-120771/10.
XX
DR  WPI; 1999-120771/10.
XX
PT  New isolated mitogen-activated protein kinase kinase isoforms - used to
XX  develop products for treating e.g. inflammatory disorders, oxidative
XX  damage, proliferative disorders or autoimmune disorders.
XX
PS  Example 3; Page 31; 168pp; English.
XX
CC  This peptide comprises a FLAG epitope. DNA coding for the epitope was
XX  inserted between codons 1 and 2 of cDNA clones (see AAX07065 and AAX07067
XX  -69) encoding human mitogen activated protein (MAP) kinase kinase 3 (see
XX  AAW97668) and MKK4 (see AAW97670-72) by insertional overlapping PCR.
XX  Recombinant MKK polypeptides were used in in vitro phosphorylation
XX  experiments. MKK3 phosphorylated p38 MAP kinase but not JNK1 or ERK2.
XX  Human MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72) mediate
XX  the transduction of specific signals from the cell surface to the nucleus
XX  along specific pathways. They are useful for screening reagents which
XX  modulate MKK activity. Such agents can be used to prevent or treat MKK-
XX  mediated disorders, e.g. inflammation, oxidative damage or stress-related
XX  proliferative disorders, e.g. psoriasis, AIDS, malignancies of e.g. the
XX  skin, bone marrow, lung, liver, breast, gastrointestinal system and
XX  genito-urinary tract. Agents which inhibit the activity or expression of
XX  MKK inhibit cell growth or cause apoptosis. MKK7 polynucleotides (see
XX  AAX07059-64) and polypeptides (see AAW97662-67) are claimed
XX
SQ  Sequence 8 AA;

Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DYKDDDDK 8
    |||||
    1 DYKDDDDK 8
Db

RESULT 87
AAW77538
ID  AAW77538 standard; peptide; 8 AA.
XX
AC  AAW77538;
XX
DT  03-MAY-2000 (first entry)
XX
DE  FLAG peptide epitope tag sequence.
XX
KW  Neurotactin; multiple sclerosis; chemokine; inflammation; brain; human;
XX  neuroprotective; antiinflammatory, cytostatic; antibacterial; FLAG.
XX
OS  Synthetic.
XX
PN  US6013257-A.
XX
PD  11-JAN-2000.
XX
PF  16-DEC-1997; 97US-00991426.
XX
PR  07-MAY-1996; 96US-00643798.
XX  05-MAY-1997; 97US-00851160.
XX

```


PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX Pan Y;
 XX WPI; 2000-146535/13.
 DR
 XX Treating multiple sclerosis by administering an antibody that binds the
 PT proinflammatory chemokine neurotactin.
 XX
 XX Example 2; Col 29; 36pp; English.
 CC The invention provides a method of treatment of multiple sclerosis that
 CC comprises administering an antibody that binds to human chemokine
 CC neurotactin. The antibodies inhibit neurotactin, a chemokine that is
 CC associated with inflammation, particularly in the brain. The antibodies
 CC are useful for treatment of multiple sclerosis. The present sequence
 CC represents a FLAG peptide epitope tag
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 89
 AAB03362 standard; peptide; 8 AA.
 ID AAB03362;
 AC AAB03362;
 XX
 XX 05-OCT-2000 (first entry)
 DT
 XX N-terminal sequence of a soluble human IL-1R fusion protein.
 DE
 XX
 XX Surgical irrigation solution; anti-inflammatory; anti-pain; anti-spasm;
 KM anti-restenosis; analgesic; human; IL-1R fusion protein; Interleukin-1.
 XX
 XX Homo sapiens.
 OS
 XX MO200025745-A2.
 PN
 XX 11-MAY-2000.
 PD
 XX 05-NOV-1999; 99WO-US026330.
 PF
 XX 05-NOV-1998; 98US-0107256P.
 PR
 XX (OMER-) OMEROS MEDICAL SYSTEMS INC.
 PA
 XX Demopoulos GA, Palmer PP, Herz JM;
 PI
 XX WPI; 2000-365358/11.
 DR
 XX
 XX Preemptive inhibition of pain and inflammation in surgical procedures
 PT comprising application of soluble receptors, e.g. TNF, optionally with
 PT pain and inflammation inhibitor, directly at the wound site, useful e.g.
 PT in arthroscopy, dentistry.
 XX
 XX Disclosure; Page 70; 122pp; English.
 PS
 XX Various mediators are known to cause pain and inflammation e.g.
 CC prostaglandins, histamine, bradykinin and serotonin. The present
 CC invention relates to inhibition of pain and inflammation at a wound
 CC during surgery by delivering locally and perioperatively to the site a
 CC solution containing at least one soluble receptor antagonist. The
 CC solution would inhibit locally the mediators of pain, inflammation, spasm
 CC and restenosis. The present sequence is the N-terminal sequence of a
 CC soluble human interleukin-1 receptor (IL-1R) fusion protein. IL-1 is

CC proinflammatory and it is thought that IL-1 effects would be prevented by
 CC blocking IL-1 binding to IL-1R, e.g. IL-1 induced inflammation and
 CC cartilage destruction within joints. The IL-1R fusion protein consists of
 CC the IL-1R binding domain and binds to IL-1 with high affinity. Local
 CC delivery of an IL-1R soluble receptor, such as the IL-1R fusion protein
 CC in an irrigation solution during joint surgery may be useful as a
 CC cartilage protective agent
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 DB 1 DYKDDDDK 8
 RESULT 89
 AAY9877 standard; protein; 8 AA.
 ID AAY9877
 XX AAY9877;
 AC AAY9877;
 XX
 XX 16-OCT-2000 (first entry)
 DT
 XX FLAG epitope antibody label.
 DE
 XX Human; hepatitis C virus; HCV; envelope glycoprotein E2; antiviral;
 KM vaccine; immunotherapy; antibody; CBH.
 XX
 XX Synthetic.
 OS
 XX WO200026418-A1.
 PN
 XX 11-MAY-2000.
 PD
 XX 29-OCT-1999; 99WO-US025711.
 PF
 XX 05-NOV-1998; 98US-00187057.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Foung SKI, Hadlock KG;
 PI
 XX WPI; 2000-451625/39.
 DR
 XX
 XX Detection of hepatitis C virus (HCV) infection comprises using monoclonal
 PT antibodies binding to conformational epitope of an envelope protein from
 PT more than one HCV genotype, the monoclonal antibodies are also used as a
 PT vaccine against HCV.
 XX
 XX Disclosure; Page 16; 85pp; English.
 PS
 XX The present sequence is the FLAG epitope which may be fused to antibodies
 CC as a label for their identification and isolation. The label may be added
 CC to monoclonal antibodies which bind to conformational epitopes of the
 CC envelope glycoprotein E2 from multiple HCV genotypes. These antibodies
 CC may be useful in the prevention and treatment of the majority of HCV
 CC infections. For example, a subset of antibodies (CBH-2, CBH-5, CBH-7, CBH
 CC -8C, CBH-8E and CBH-11) have the ability to prevent the binding of HCV E2
 CC proteins of multiple genotypes to human CD81, a possible coreceptor for
 CC HCV infection. Thus the antibodies are useful in passive immunotherapy
 CC strategies for reducing viral load of infected individuals and
 CC interfering with infection of target cells
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 90

AAB10961

ID AAB10961 standard; protein; 8 AA.

AC AAB10961;

DT 07-FEB-2001 (first entry)

DE FLAG epitope tag peptide.

XX APP; amyloid precursor protein; human; alpha-secretase; ADAM 10;
 XX disintegrin-metalloprotease; protease; neurotrophic; neuroprotective;
 KW gene therapy; Alzheimer's disease.
 XX
 OS Synthetic.

DE19910108-A1.

XX 21-SEP-2000.

XX 08-MAR-1999; 99DE-01010108.

XX 08-MAR-1999; 99DE-01010108.

XX 08-MAR-1999; 99DE-01010108.

XX (FAHR/) FAHRENHOLZ F.

XX FAHRENHOLZ F, Postina R;

XX WPI; 2000-588391/56.

XX Recombinant cells, for identifying alpha-secretase active agents and
 PT identifying risk factors associated with Alzheimer's disease, comprise
 PT amyloid precursor protein and alpha-secretase.
 XX

XX Example 4; Page 8; 24pp; German.

XX This invention describes a novel recombinant cell comprising recombinant
 CC nucleic acids encoding a region of human amyloid precursor protein
 CC containing an alpha-secretase cleavage site and a protease or a
 CC heterologous RNA coding for a substrate protein and a protease. The
 CC invention also describes a recombinant cell, characterized in that it
 CC contains recombinant nucleic acids comprising either: (a) a gene for a
 CC substrate protein (SP), which comprises a sequence region of 18 amino
 CC acids of the human amyloid precursor protein (APP) or a homologous
 CC protein, where the sequence region contains the alpha-secretase cleavage
 CC site at a reference of 6 residues at the N-terminal and 12 residues at
 CC the C-terminal; and (b) a gene for a protease protein (PP), that either
 CC comprises a proteolytically active necessary sequence region or a
 CC sequence region of the disintegrin metalloprotease ADAM 10 from a cow
 CC (Bos taurus), from a human or other mammal or a mutant of this, which
 CC shows the same enzymatic properties, where the genes are under the
 CC control of heterologous promoters; or a heterologous RNA coding for a SP
 CC and a PP. The products of the invention have neurotrophic and
 CC neuroprotective activity and can be used for gene therapy. The protease
 CC proteins of the invention are useful for proteolytic cleavage of
 CC substrate proteins, especially human amyloid precursor protein. Dominant
 CC negative forms of bovine, human or other mammalian disintegrin-
 CC metalloprotease ADAM 10 proteins and their coding sequences are useful
 CC for suppressing the alpha-secretase activity of a cell. Nucleic acid
 CC sequences encoding the proteases are useful for constructing vectors for
 CC gene therapy. The proteins and recombinant cells are useful for
 CC identifying secretases and pharmaceutical agents and to identify risk
 CC factors associated with Alzheimer's disease
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 91

AAV87937

ID AAV87937 standard; peptide; 8 AA.

XX AAV87937;

DT 11-SEP-2000 (first entry)

DE Intracellular C-terminal HDL-receptor domain FLAG epitope #1.

XX Intracellular C-terminal HDL receptor domain; cholesterol; bile acid;
 KW high density lipoprotein; lipid metabolism; peroxisome; gene therapy;
 KW treatment; hyperlipidemia.
 XX

OS Synthetic.

XX WO200023475-A1.

XX 27-APR-2000.

XX 22-OCT-1999; 99WO-SE001902.

XX 22-OCT-1998; 98SE-00003609.

XX (CARL/) CARLSSON B.

XX (CARL/) CARLSSON L.

XX (JOHN/) JOHNSON M.

XX Carlsson B, Carlsson L, Johnson M;

XX WPI; 2000-339657/29.

XX New peptide homologous to the intracellular C-terminal domain of a
 PT mammalian HDL-receptor useful in identifying drug targets and the
 PT treatment of hyperlipidemia.
 XX

XX Example 1; Page 8; 23pp; English.

XX This invention describes a novel peptide (P), homologous to the
 CC intracellular C-terminal domain of a mammalian HDL-receptor. The products
 CC of the invention can modulate cholesterol, bile acid and lipid
 CC metabolism. The peptides may alter the activity of the enzymes in the
 CC peroxisome to inhibit cholesterol synthesis and promote cholesterol
 CC elimination. The cDNA encoding the peptide is used in gene therapy and is
 CC also used for the production of the peptide. The peptide can be used in
 CC the treatment of hyperlipidemia and for the modulation of cholesterol,
 CC bile acid and/or lipid metabolism of a patient. The peptide can also be
 CC used for the identification of drug targets for treatment of
 CC hyperlipidemia. The drug targets thus identified are targets for
 CC modulation of the metabolism of cholesterol, bile acid and/or lipids. In
 CC addition the peptide may also be used for the production of a medicinal
 CC product for treatment of hyperlipidemia. This sequence represents a FLAG
 CC epitope used in the method of the invention
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 1 DYKDDDDK 8

RESULT 92

AA10094
ID AAB10094 standard; peptide; 8 AA.
XX
AC AAB10094;
XX
DT 10-NOV-2000 (first entry)
XX
DE Combinatorial chemical library peptide 1.
XX
KM Combinatorial library; diagnosis; disease detection; cancer; infection;
KM autoimmune disease; drug development; diagnostic marker.
XX
OS Synthetic.
XX
PN W0200035940-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-DE003982.
XX
PR 14-DEC-1998; 98DE-01057529.
PR 30-JUL-1999; 99DE-01035553.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (EUWO-) EURO LAB MOLEKULARBIOLOGIE.
PI Pouska A, Breitling F, Gross K, Duebel S, Saffrich R;
PI WPI; 2000-442358/38.
XX
PT Applying materials to a support, useful for combinatorial synthesis of
PT peptides, e.g. for diagnosis, by incorporating materials in meltable
PT particles and delivery through a printer.
XX
PS Disclosure; Page 38; 77pp; German.
XX
CC This invention describes a novel method for applying substances (I),
CC especially monomers for combinatorial synthesis of molecule libraries, to
CC a carrier by embedding (I) in a matrix, an applying the matrix to the
CC carrier either as a solid or a gel. (I) is first embedded in a matrix
CC comprising at least 1 first solvent (S1) that is solid at below 90
CC (preferably 50) plusoc so as to form transport units (TU) that can be
CC moved individually. TU are applied to the carrier as solid, at below 90
CC plusoc or are applied dissolved in second solvent (S2), which at the same
CC temperature is a liquid, so that, after evaporating at least some S2, a
CC solid or gel is formed on the carrier. (I) is then rendered mobile by
CC altering the physical conditions, brought into contact with the carrier
CC surface by a physical process and coupled covalently to molecules (II) on
CC the surface (or it undergoes, or catalyzes, a reaction with (II)). Coupled
CC (I) may be (or may generate) many different substances and application of
CC (I) can be repeated sequentially, with intermediate rinsing off of any
CC uncoupled (I). The method is used to produce combinatorial chemical
CC libraries (e.g. of peptides or oligonucleotides) for use in scientific or
CC medical investigations, e.g. diagnostically for detecting markers of a
CC wide range of diseases (cancer, autoimmune disease or infections, also
CC diseases of unknown or uncertain etiology) in blood samples or for
CC identifying lead compounds (specific binding agents) for drug
CC development. Encapsulation of (I) significantly reduces its diffusion
CC away from its target site on the carrier, resulting in simpler and more
CC compact assembly of a library relatively free of artefacts. The library
CC may have a very high density, increasing the chances of detecting
CC diagnostic markers or potential therapeutic agents and allows
CC simultaneous screening for many different diseases. This sequence
CC represents a peptide used to illustrate the method of the invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||

Db 1 DYKDDDDK 8
RESULT 93
AAV51938
ID AAV51938 standard; protein; 8 AA.
XX
AC AAV51938;
XX
DT 23-JUN-2000 (first entry)
XX
DE FLAP epitope.
XX
KM PRO201; human; NSP; SH2-containing protein; cytosolic; modulator;
KM Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;
KM cellular response; tumorigenesis; integrin stimulation; signalling.
XX
OS Homo sapiens.
XX
PN US6051403-A.
XX
PD 18-APR-2000.
XX
PF 04-AUG-1999; 99US-00369028.
XX
PR 23-APR-1998; 98US-00065275.
XX
PA (GETH) GENENTECH INC.
XX
PI Lu Y, Stewart TA;
XX
DR WPI; 2000-328246/28.
XX
PT New isolated nucleic acid molecules encoding novel Src Homology-2
PT containing proteins capable of modulating the activity of cellular
PT response to external signaling.
XX
PS Example 3; Col 71-72; 63pp; English.
XX
CC This invention describes the novel isolated Src Homology-2 (SH2)
CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309
CC (Nsp3), respectively which have cytosolic activity. (I) plays an
CC important role in modulating the cellular response to external stimuli.
CC (I) binds and affects e.g. block or modulate, an activity such as
CC regulation of tumorigenesis, response to stimulation by integrin
CC receptors, epidermal growth factor, insulin growth factor and through
CC other tyrosine receptor ligands, of cellular response to external
CC signaling. (I) is useful for producing antibodies, agonists and
CC antagonists to modulate the activity of cellular response to external
CC signalling. The encoding NSP nucleotides are useful as hybridization
CC probes in chromosome and gene mapping. In cDNA library and in the
CC generation of anti-sense RNA and DNA. They are also useful for preparing
CC the NSP proteins, for producing transgenic animals and for gene therapy.
CC NI are also useful for treating and diagnosing cells associated with cell
CC proliferative disorders. This sequence represents the FLAP epitope which
CC is used in the method of the invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||

DB 1 DYKDDDDK 8
|||||||

RESULT 94
AAB22877
ID AAB22877 standard; peptide; 8 AA.
XX
AC AAB22877;
XX

10-JAN-2001 (first entry)
 FLAG epitope, SEQ ID NO:36.
 Biotector protein; fusion protein; recognition site;
 cellular targeting sequence; cellular localisation; fluorescent protein;
 protease activity detection; toxin detection; cellular stress detection;
 drug discovery; cell based screening; epitope.
 Synthetic.
 WO200050872-A2.
 31-AUG-2000.
 25-FEB-2000; 2000MO-US004794.
 26-FEB-1999; 99US-0122152P.
 08-MAR-1999; 99US-0123399P.
 12-JUL-1999; 99US-0035217L.
 (CELL-) CELLONICS INC.
 Giuliano KA, Kapur R;
 WPI; 2000-594086/56.
 N-PESD; AAA93368.
 Automated cell-based characterization of toxin by contacting cells
 containing luminescent reporter molecules with test substance and
 analyzing optically.
 Example 11; Fig 29A; 336pp; English.
 The invention relates to systems, methods and reagents for cell-based
 screening or detection of compounds which affect particular biological
 functions. The methods of the invention utilise fluorescent biotector
 molecules which, when acted on by a compound of interest, cause an
 alteration in the cellular distribution of at least the fluorescent
 moiety. In one embodiment, the biosensors comprise heat shock proteins
 (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
 protein (GFP), or derivatives thereof). Such biosensors are located in
 the cytoplasm, but on stress activation translocate to the nucleus. In
 another embodiment biotector proteins can be used to detect protease
 activity. Such protease biotector fusion proteins comprise one or more
 fluorescent proteins; a recognition signal which is cleaved by the
 protease; and at least one cellular localisation signal. The latter two
 components may be components of a single protein which is acted upon by
 the protease, or may be from heterologous sources. Due to the
 localisation signal, the biotector protein is localised to a particular
 region of the cell. Once acted on by the protease of interest, the
 fluorescent protein is cleaved from the localisation sequence, and is
 free to migrate to other locations within the cell. The presence of a
 second localisation signal attached to the fluorescent protein enables
 the fluorescent protein to be directed to a different cellular
 compartment after cleavage of the protease recognition sequence. The
 change in distribution of the fluorescent protein can be detected using
 imaging methods with a high degree of spatial resolution. The methods and
 biosensors of the invention can be used to investigate a wide range of
 cellular activities and to screen compounds which modulate these
 activities. Biosensors containing a recognition site for caspase, for
 example, may be used for the screening of compounds which modulate
 apoptosis, while biosensors containing other protease recognition sites
 may be used for the detection of proteolytic toxins (such as anthrax
 lethal factor). The method provides improved target validation and
 candidate compound optimisation by combining many cell screening formats
 with fluorescence-based molecular reagents and computer-based feature
 extraction, data analysis and automation, resulting in increased quantity
 and speed of data collection and faster evaluation of drug candidates.
 Sequences ABB22877-B22880 represent epitope sequences that can be used in
 biosensor fusion proteins of the invention

```

SQ Sequence 8 AA;
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

RESULT 95
AAB26126
ID AAB26126 standard; protein; 8 AA.
AC AAB26126;
AD 30-JAN-2001 (first entry)
DE Human TGF-beta superfamily protein PCIGP recognition site.
KW Human; TGF-beta superfamily; prostate cancer-induced growth factor;
KW PCIGP; prostate disease; prostate cancer; benign prostatic hyperplasia;
KW prostatic; prostatic intraepithelial neoplasia; affinity purification.
OS Synthetic.
PN WO200056352-A2.
PD 28-SEP-2000.
PF 24-MAR-2000; 2000WO-US007945.
PR 25-MAR-1999; 99US-00276600.
PA (ABBO ) ABBOTT LAB.
PI Billing-Medel PA, Cohen M, Colpitts TL, Gordon J, Granados EN;
PI Russell JC, Stroupe SD;
PI WPI; 2000-628218/60.
DR
DX
DT
PT Novel prostate cancer induced growth factor derived polynucleotide useful
PT for detecting, diagnosing, prognosing, preventing or treating conditions
PT of the prostate, especially prostate cancer.
PS
PX
PY
SQ Example 11a; Page 78; 117pp; English.

The present sequence comprises the translated sequence of an affinity
purification recognition system site. It was inserted into a vector for
the human prostate cancer-induced growth factor (PCIGP). The protein is a
member of the TGF-beta superfamily. The 3' part of its gene has been
shown to be upregulated in prostate cancer, and thus can be used in the
diagnosis of the disease. It is also useful for the identification of
antagonists to the PCIGP protein which can be used to treat cancer. In
addition, benign prostatic hyperplasia, prostatitis and prostatic
intraepithelial neoplasia can be detected using the gene and protein

Sequence 8 AA;

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDDK 8
   |||||
Db 1 DYKDDDDK 8

RESULT 96
AAB28432
ID AAB28432 standard; peptide; 8 AA.
XX

```

```

AC  AAB28432;
XX
XX
DT  29-JAN-2001 (first entry)
XX
DE  FLAG epitope.
XX
XX  FLAG epitope; gene therapy; gene-trapping retrovirus; transgenic animal.
XX
OS  Unidentified.
XX
XX  WO20056874-A1.
XX
PD  28-SEP-2000.
XX
XX
PF  24-MAR-2000; 2000WO-US007841.
XX
XX
PR  25-MAR-1999; 99US-0126123P.
XX
XX  (MAST ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX  Hopkins N, Chen W, Burgess S, Amsterdam A;
XX
XX  WPI; 2000-628260/60.
XX
XX  Recombinant retrovirus for gene trapping, gene mutation and for
XX  transgenic animal production, comprises a branch point sequence,
XX  polypyrimidine tract, splice acceptor, splice donor and long-terminal
XX  repeats.
XX
XX  Disclosure; Page 13; 38pp; English.
XX
XX  The present sequence is the FLAG epitope, which may be incorporated into
XX  an artificial mini-exon used in a novel gene-trapping retrovirus. The
XX  retrovirus comprises a branch point sequence, a polypyrimidine tract, a
XX  splice acceptor, a splice donor and long-terminal repeats (LTRs). It is
XX  useful for introducing a mutation into a gene in a cell, for determining
XX  the expression pattern of a gene in a non-human animal, and for gene
XX  therapy. It is also useful for producing transgenic animals such as mice,
XX  zebrafish, pufferfish, medaka, frogs, flies, goats, sheep, cows, pigs and
XX  chickens. High-titre virus producer cell lines have been developed which
XX  permit efficient production of retroviral vectors for the construction of
XX  transgenic animals and for human gene therapy
XX
XX  Sequence 8 AA;
XX
XX  Query Match 100.0%; Score 47; DB 3; Length 8;
XX  Best Local Similarity 100.0%; Pred. No. 2.1e+06;
XX  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX  Qy 1 DYKDDDDK 8
XX  |||||||
XX  1 DYKDDDDK 8
XX
XX  Db
XX
XX  RESULT 97
XX  ID AAY95914
XX  AAY95914
XX  AAY95914;
XX
XX  20-NOV-2000 (first entry)
XX
XX  FLAG peptide.
XX
XX  FLAG; Goodpasture antigen binding protein; GPBP, autoimmune disease;
XX  apoptosis; cancer; tumour; diagnosis; therapy.
XX
XX  Synthetic.
XX
XX  WO200050607-A2.
XX
XX  31-AUG-2000.
XX
XX

```

PF	24-FEB-2000; 2000MO-IB000324.
XX	
PR	24-FEB-1999; 99US-0121483P.
XX	
PA	(SAUS/). SAUS J.
XX	
PI	Saus J;
XX	
XX	WPI; 2000-572094/53.
XX	
PT	Novel Goodpasture antigen binding proteins useful for diagnosing and
PT	treating autoimmune disorders, tumor, and preventing cell apoptosis.
XX	
PS	Example 1; Page 22; 158pp; English.
XX	
CC	The present sequence is that of FLAG peptide. FLAG was expressed at the N
CC	-terminus of recombinant human Goodpasture antigen binding protein (GPBP)
CC	constructs (see AA95907-11) of the invention to facilitate purification
CC	from host cells. GPBP (see AA95900) is a novel serine/threonine kinase
CC	that specifically binds to and phosphorylates the N-terminus of
CC	Goodpasture antigen. The invention provides nucleic acids (see AA950341-
CC	53) encoding GPBP, recombinant vectors, host cells, encoded polypeptides
CC	(see AA95900-11) and antibodies. It also provides methods for detecting
CC	the presence of an autoimmune condition or apoptosis by detecting an
CC	increase in GPBP expression, and methods for treating an autoimmune
CC	disorder, apoptosis or a tumor by modifying GPBP expression or activity
XX	
SQ	Sequence 8 AA;
XX	
Query Match	100.0%; Score 47; DB 3; Length 8;
Best Local Similarity	100.0%; Pred. No. 2.1e+06;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 DYKDDDDK 8
DB	1 DYKDDDDK 8
XX	
RESULT 98	
AA953260	
ID	AA953260 standard; peptide; 8 AA.
XX	
AC	AA953260;
XX	
DT	17-JUL-2000 (first entry)
XX	
DE	Mouse neurotactin FLAG epitope tag SEQ ID NO:14.
XX	
KW	Neurotactin; identification; characterisation; chemokine; inflammation;
KW	antiinflammatory; antiarteriosclerotic; chemotaxis inhibitor; brain;
KW	viral encephalitis; multiple sclerosis; meningitis; head trauma; stroke;
KW	neuro-degenerative disease; HIV encephalopathy; primary brain tumour;
KW	lupus associated cerebritis; inflammatory disease; atherosclerosis;
KW	respiratory infection; diagnosis; gene therapy.
XX	
OS	Mus musculus.
XX	
PN	US6043086-A.
XX	
XX	28-MAR-2000.
XX	
PF	28-AUG-1998; 98US-00143470.
XX	
PR	07-MAY-1996; 96US-00643798.
PR	05-MAY-1997; 97US-00851160.
PR	16-DEC-1997; 97US-00991426.
XX	
PA	(MILL-) MILLENIUM BIOTHERAPEUTICS INC.
XX	
PI	Pan Y;
XX	
DR	WPI; 2000-270344/23.
XX	

CC malignant cell growth. MLK3 which is also known as PTK1 was cloned by
 CC using degenerate primers derived from the highly conserved V1b and IX
 CC subdomains of PTK polypeptides. To obtain MLK3 the cDNA was cloned into a
 CC baculoviral expression vector pFB-FLAG. pFB-FLAG is derived from pFB and
 CC has the coding sequence for the FLAG epitope with a start codon added to
 CC the polylinker in the BamHI site
 XX

Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 |||||
 Db 1 DYKDDDDK 8

Search completed: June 29, 2006, 11:35:36
 Job time : 215 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:35:56 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDK 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 500 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	47	2	T10471
2	41	87.2	423	2	S59425
3	38	80.9	306	2	S32834
4	38	80.9	565	2	AC0184
5	38	80.9	1085	2	S55352
6	38	80.9	1277	2	S54451
7	38	80.9	2067	2	A42854
8	37	78.7	351	2	T10503
9	37	78.7	513	2	B96524
10	37	78.7	721	2	B96974
11	37	78.7	791	2	T20815
12	37	78.7	838	2	T05410
13	36	76.6	195	2	B70192
14	36	76.6	215	2	T31963
15	36	76.6	289	2	S39814
16	36	76.6	312	2	S39823
17	36	76.6	485	2	T49237
18	36	76.6	748	2	H84913
19	36	76.6	796	2	S56231
20	36	76.6	917	2	S07183
21	36	76.6	987	2	A88746
22	36	76.6	1076	2	S50536
23	36	76.6	1287	2	T30988
24	36	76.6	2295	2	B71621
25	36	76.6	2457	2	T18492
26	35	74.5	78	2	AF2345
27	35	74.5	151	2	A40592
28	35	74.5	151	2	G97355
29	35	74.5	287	2	T32029

30	35	74.5	288	2	A86384	unknown protein (i
31	35	74.5	306	2	D96708	unknown protein, p
32	35	74.5	338	2	PC4365	calcium-binding pr
33	35	74.5	374	2	T09106	gibberellin 20-oxi
34	35	74.5	410	2	T25165	hypothetical prote
35	35	74.5	430	2	S67161	hypothetical prote
36	35	74.5	451	2	S58653	hypothetical prote
37	35	74.5	472	2	S41720	intermediate filam
38	35	74.5	635	2	D84920	hypothetical prote
39	35	74.5	679	2	G71615	phospholipase A2-1
40	35	74.5	1010	2	T34314	hypothetical prote
41	35	74.5	1345	2	S46817	hypothetical prote
42	35	74.5	2452	1	RN202L	DNA-directed RNA p
43	35	74.5	2573	2	D71614	hypothetical prote
44	34	72.3	140	2	T32477	hypothetical prote
45	34	72.3	165	2	A36237	melanin-concentrat
46	34	72.3	177	1	R8BYG1	regulatory protein
47	34	72.3	197	2	T15725	hypothetical prote
48	34	72.3	259	1	S46286	RNA-binding protei
49	34	72.3	300	2	T52379	zinc finger protei
50	34	72.3	337	2	T48564	probable serine ri
51	34	72.3	362	2	T48564	hypothetical prote
52	34	72.3	381	2	S45766	hypothetical prote
53	34	72.3	386	2	T05781	hypothetical prote
54	34	72.3	396	2	T26987	hypothetical prote
55	34	72.3	430	2	T23899	hypothetical prote
56	34	72.3	467	2	A85363	probable calmoduli
57	34	72.3	484	2	S66713	hypothetical prote
58	34	72.3	502	2	S36494	E2 protein - human
59	34	72.3	609	2	T40660	hypothetical C2H2-
60	34	72.3	614	2	T10862	phaseolin G-box bi
61	34	72.3	734	2	T13674	hypothetical prote
62	34	72.3	743	2	T13673	hypothetical prote
63	34	72.3	860	2	A48433	hypothetical prote
64	34	72.3	936	2	E96508	hypothetical prote
65	34	72.3	984	2	A41996	NF-kappa-B p50 sub
66	34	72.3	1099	2	T18257	phospholipase C -
67	34	72.3	1157	2	C96761	hypothetical prote
68	34	72.3	1350	2	AF2005	RNA polymerase bet
69	34	72.3	1953	2	S63244	BNI protein - yea
70	34	72.3	4550	2	T18440	hypothetical prote
71	34	72.3	125	2	S76216	hypothetical prote
72	33	70.2	145	2	JX0313	E4 type molecule
73	33	70.2	147	1	B46315	hypothetical prote
74	33	70.2	151	2	E69077	hypothetical prote
75	33	70.2	175	2	S59766	translational elonga
76	33	70.2	188	2	A61442	conserved hypotet
77	33	70.2	190	2	T43013	FUN34 protein - ye
78	33	70.2	205	2	S36720	translation elonga
79	33	70.2	225	1	S25432	translational prote
80	33	70.2	225	2	S62693	hypothetical prote
81	33	70.2	235	2	G90525	hypothetical prote
82	33	70.2	258	2	H84905	homeodomain trans
83	33	70.2	262	2	A33470	fibroin light chai
84	33	70.2	267	2	S47137	homeotic protein A
85	33	70.2	270	2	B86486	protein P2839.7 li
86	33	70.2	280	2	T00737	myb-related protei
87	33	70.2	280	2	T51667	myb-related trans
88	33	70.2	299	2	S49469	glucose-1-phosphat
89	33	70.2	322	2	G95244	hypothetical prote
90	33	70.2	333	2	T20033	hypothetical prote
91	33	70.2	393	2	S16321	light-induced prot
92	33	70.2	436	2	AH1387	cell wall binding
93	33	70.2	450	2	T40337	probable saccharop
94	33	70.2	504	2	DB1224	catalase (EC 1.11.
95	33	70.2	517	1	S26606	myb-related protei
96	33	70.2	524	1	A48341	nucleocapsid prote
97	33	70.2	524	1	VANZT1	arginyl-tRNA synth
98	33	70.2	553	2	A89830	hypothetical prote
99	33	70.2	563	2	C71529	hypothetical prote
100	33	70.2	650	2	T06648	DNA topoisomerase
101	33	70.2	651	2	G64068	hypothetical prote
102	33	70.2	799	2	S65192	hypothetical prote

103	33	70.2	810	2	S67696	probable membrane	176	32	68.1	487	2	T51121	probable DNA photo
104	33	70.2	829	2	T32744	hypothetical prote	177	32	68.1	499	2	H86148	hypothetical prote
105	33	70.2	830	2	T18860	hypothetical prote	178	32	68.1	506	2	JC5678	minor core protein
106	33	70.2	836	1	S34399	dynamn 3 - fruit	179	32	68.1	524	1	VHNZSV	nucleocapsid prote
107	33	70.2	836	2	S17974	dynamn-like prote	180	32	68.1	537	2	T41631	hypothetical prote
108	33	70.2	836	2	S15413	dynamn-like prote	181	32	68.1	553	2	S19476	hypothetical prote
109	33	70.2	848	2	S15498	testicular dynam	182	32	68.1	581	2	T00979	hypothetical prote
110	33	70.2	849	2	A35791	pre-mRNA processi	183	32	68.1	594	2	T06467	phosphoinositide-s
111	33	70.2	851	2	B40671	dynamn, internal	184	32	68.1	601	2	S74239	secretogranin II p
112	33	70.2	851	2	S11508	d100 protein - rat	185	32	68.1	625	2	T37719	thymidylate syntha
113	33	70.2	854	2	S33558	unc-33 protein - C	186	32	68.1	632	2	T32454	hypothetical prote
114	33	70.2	864	2	A40671	dynamn, internal	187	32	68.1	641	2	E96612	probable transcrip
115	33	70.2	883	2	S16130	dynamn 4 - fruit	188	32	68.1	671	2	S61693	probable membrane
116	33	70.2	883	2	S17975	dynamn-like prote	189	32	68.1	680	2	S46308	initiator-binding
117	33	70.2	902	2	S33918	dynamn-like prote	190	32	68.1	685	2	S46309	hypothetical prote
118	33	70.2	902	2	T43523	cut17 protein - fi	191	32	68.1	699	2	T18426	hypothetical prote
119	33	70.2	1063	2	S18211	hypothetical prote	192	32	68.1	702	2	S40904	FUN2 protein - yea
120	33	70.2	1111	2	T01239	hypothetical prote	193	32	68.1	719	2	S55119	hypothetical prote
121	33	70.2	1193	2	G71605	hypothetical prote	194	32	68.1	735	2	T19065	probable protein k
122	33	70.2	1230	2	T42735	TBP-interacting pr	195	32	68.1	752	2	T27276	hypothetical prote
123	33	70.2	1325	2	T25753	hypothetical prote	196	32	68.1	776	2	T02702	hypothetical prote
124	33	70.2	1329	2	T33136	hypothetical prote	197	32	68.1	778	2	D87965	protein Y63D3A.6b
125	33	70.2	1802	2	G71616	hypothetical prote	198	32	68.1	781	2	A56244	DNA repair/recombi
126	33	70.2	1880	2	T18531	tractin - medicina	199	32	68.1	788	2	S75209	dnak protein - Syn
127	33	70.2	2206	2	JC5280	voltage-dependent	200	32	68.1	788	2	G86273	hypothetical prote
128	33	70.2	2437	2	T18482	hypothetical prote	201	32	68.1	790	2	T05576	probable transpor
129	33	70.2	2829	2	A42771	reticulocyte-bindi	202	32	68.1	837	2	C84546	penicillin-binding
130	32	68.1	49	2	B26815	peptide pyr-amide	203	32	68.1	844	1	ZPECPB	peptidoglycan synt
131	32	68.1	153	2	T09405	conserved hypochet	204	32	68.1	844	2	A85499	peptidoglycan synt
132	32	68.1	200	2	F85020	hypothetical prote	205	32	68.1	844	2	A99648	hypothetical prote
133	32	68.1	213	2	D71669	adenylate kinase (206	32	68.1	853	2	H70470	alanyl-L-CRNA synthe
134	32	68.1	220	2	T02014	hypothetical prote	207	32	68.1	890	2	F75289	transforming prote
135	32	68.1	221	2	A84638	hypothetical prote	208	32	68.1	896	2	B43817	hypothetical prote
136	32	68.1	224	2	T45992	hypothetical prote	209	32	68.1	900	2	F71426	hypothetical prote
137	32	68.1	222	2	T22698	hypothetical prote	210	32	68.1	906	2	S03313	hypothetical prote
138	32	68.1	240	2	S11293	SAB5-1.2 protein -	211	32	68.1	906	2	A43817	transforming prote
139	32	68.1	250	2	T16728	hypothetical prote	212	32	68.1	959	2	E85276	hypothetical prote
140	32	68.1	289	2	C96778	hypothetical prote	213	32	68.1	1043	2	AH1906	hypothetical prote
141	32	68.1	298	2	T37251	homeobox protein c	214	32	68.1	1051	2	T51904	hypothetical prote
142	32	68.1	303	2	A69542	conserved hypochet	215	32	68.1	1056	2	S56039	RIC1 protein - Yea
143	32	68.1	306	2	T26126	hypothetical prote	216	32	68.1	1132	2	S37932	hypothetical prote
144	32	68.1	321	2	A86857	ribose-phosphate d	217	32	68.1	1150	2	S49956	probable membrane
145	32	68.1	324	2	T10518	fruit bromelain (E	218	32	68.1	1154	2	A39577	protein-tyrosine k
146	32	68.1	332	2	A81675	conserved hypochet	219	32	68.1	1208	2	T23467	hypothetical prote
147	32	68.1	335	2	E71140	hypothetical prote	220	32	68.1	1212	2	T44236	hypothetical prote
148	32	68.1	340	2	T10516	fruit bromelain (E	221	32	68.1	1212	2	T44051	hypothetical prote
149	32	68.1	344	2	T48827	hypothetical prote	222	32	68.1	1222	2	T22490	hypothetical prote
150	32	68.1	345	2	T07839	ananain (EC 3.4.22	223	32	68.1	1260	2	T14022	reverse transcript
151	32	68.1	349	2	T29256	hypothetical prote	224	32	68.1	1335	2	T30211	autolysin E - Stap
152	32	68.1	352	2	T10501	fruit bromelain (E	225	32	68.1	1338	2	T18416	hypothetical prote
153	32	68.1	352	2	AD0927	major capsid prote	226	32	68.1	1400	2	T52359	hypothetical prote
154	32	68.1	356	2	T07840	ananain (EC 3.4.22	227	32	68.1	1417	2	A57570	Bloom's syndrome r
155	32	68.1	356	2	T10514	probable stem brom	228	32	68.1	1491	2	T28048	hypothetical prote
156	32	68.1	357	2	T07851	ananain (EC 3.4.22	229	32	68.1	1510	2	T33100	hypothetical prote
157	32	68.1	363	2	F87754	conserved C43B11.1	230	32	68.1	1526	2	T13823	frizzled gene prot
158	32	68.1	381	2	D89922	conserved hypochet	231	32	68.1	1589	1	RGBYC5	cell division cont
159	32	68.1	391	1	VFXRIB	major inner capsid	232	32	68.1	1703	2	S15047	SNF2 protein - Yea
160	32	68.1	398	2	S06324	dnab protein homol	233	32	68.1	2148	2	A56011	transcription fact
161	32	68.1	401	2	A34856	49K photoreceptor	234	32	68.1	2268	2	T29999	hypothetical prote
162	32	68.1	401	2	S11566	arrestin homolog -	235	32	68.1	2288	2	VFIHBI	FI protein - avian
163	32	68.1	401	2	B55081	arrestin 2 - blueb	236	32	68.1	3951	1	F82885	hypothetical prote
164	32	68.1	401	2	T48495	hypothetical prote	237	31	66.0	37	2	S21665	S-layer protein -
165	32	68.1	421	2	B82023	probable periplasm	238	31	66.0	131	1	TRI8PUL	minor tail protein
166	32	68.1	421	2	F81244	conserved hypochet	239	31	66.0	131	2	G90833	minor tail protein
167	32	68.1	429	2	T23152	hypothetical prote	240	31	66.0	131	2	A85691	probable tail comp
168	32	68.1	432	2	T00949	hypothetical prote	241	31	66.0	138	2	AE1060	conserved hypochet
169	32	68.1	440	2	T51278	hypothetical prote	242	31	66.0	138	2	S34360	hypothetical prote
170	32	68.1	451	2	A37386	dnab protein homol	243	31	66.0	155	2	T03087	conserved hypochet
171	32	68.1	451	2	S01921	dnab protein homol	244	31	66.0	164	2	T28547	hypothetical prote
172	32	68.1	458	2	S53936	hypothetical prote	245	31	66.0	164	2	C72164	hypothetical prote
173	32	68.1	461	2	T01825	hypothetical prote	246	31	66.0	164	2	F36848	ASR protein - vari
174	32	68.1	469	2	C82495	glycerol-3-phospha	247	31	66.0	165	2	D64141	hypothetical prote
175	32	68.1	474	2	A81732	glycogen synthase	248	31	66.0	175	2	PH0261	hypothetical 17.8K

249	31	66.0	177	2	T32856	hypothetical prote
250	31	66.0	178	2	S26481	calcium-binding pr
251	31	66.0	183	1	R5B932	ribosomal protein
252	31	66.0	185	1	WZVZSW	Swf8a protein - sw
253	31	66.0	201	2	A34146	hypothetical prote
254	31	66.0	205	2	UC4964	beta-B2-crystallin
255	31	66.0	205	2	S05015	beta-crystallin B2
256	31	66.0	205	2	A10967	conserved hypotet
257	31	66.0	207	2	A39757	beta-crystallin B2
258	31	66.0	210	2	T40719	hypothetical prote
259	31	66.0	210	2	T28771	hypothetical prote
260	31	66.0	211	2	T25911	hypothetical prote
261	31	66.0	218	2	T30415	hoat range factor
262	31	66.0	219	2	T19897	hypothetical prote
263	31	66.0	224	2	JH0456	tumor rejection an
264	31	66.0	227	2	E97719	ribonuclease III (
265	31	66.0	237	2	D89990	hypothetical prote
266	31	66.0	243	2	H70227	antigen, P35 homol
267	31	66.0	253	2	B29653	aspartic acid-rich
268	31	66.0	253	2	A75252	conserved hypotet
269	31	66.0	264	2	T10155	hypothetical prote
270	31	66.0	269	2	B84849	hypothetical prote
271	31	66.0	283	2	B10668	hypothetical prote
272	31	66.0	283	2	C85912	hypothetical prote
273	31	66.0	294	1	A37818	osteopontin precu
274	31	66.0	300	2	E96585	hypothetical prote
275	31	66.0	301	1	S12361	heat shock transcr
276	31	66.0	301	2	JC5811	osteopontin - rat
277	31	66.0	309	2	D57126	cRNA delta(2) - Isop
278	31	66.0	317	1	A25917	osteopontin precu
279	31	66.0	319	2	AF0406	transcription regu
280	31	66.0	319	2	A47499	thiamine diphospho
281	31	66.0	334	2	A29561	prostatic spermine
282	31	66.0	335	2	T38175	hypothetical prote
283	31	66.0	345	2	T38894	hypothetical colle
284	31	66.0	350	2	A40459	nuclear phosphopro
285	31	66.0	366	2	B84265	hypothetical prote
286	31	66.0	374	2	D81937	probable ribosomal
287	31	66.0	374	2	A81168	ribosomal large ch
288	31	66.0	374	2	A37282	52K active chromac
289	31	66.0	379	2	C84577	probable nucleosom
290	31	66.0	387	2	C86133	hypothetical prote
291	31	66.0	387	2	A98292	hypothetical prote
292	31	66.0	389	2	T03691	calreticulin - com
293	31	66.0	390	2	T51197	hypothetical prote
294	31	66.0	395	2	T25651	hypothetical prote
295	31	66.0	400	2	T45919	hypothetical prote
296	31	66.0	401	2	D87368	imidazolepropion
297	31	66.0	406	2	S59296	probable finger pr
298	31	66.0	407	2	T26127	hypothetical prote
299	31	66.0	409	2	S70119	hypothetical prote
300	31	66.0	412	2	T40155	mannose-6-phosphat
301	31	66.0	416	1	S06763	calreticulin precu
302	31	66.0	416	2	T16968	calreticulin cal1
303	31	66.0	421	2	E96522	DnaJ-like protein
304	31	66.0	423	2	T09338	histidine-tRNA lig
305	31	66.0	424	2	A10821	biphenyl dioxygena
306	31	66.0	426	2	T31278	3-phosphoshikimate
307	31	66.0	432	2	H89924	probable tyrosine
308	31	66.0	434	2	S55155	hypothetical prote
309	31	66.0	440	2	S60423	hypothetical prote
310	31	66.0	449	2	G96992	metaxin homolog -
311	31	66.0	450	2	T40446	RNA helicase RH5
312	31	66.0	451	2	T51143	hypothetical prote
313	31	66.0	455	2	T38517	hypothetical prote
314	31	66.0	460	2	B82549	hypothetical prote
315	31	66.0	466	2	T46054	26S proteasome reg
316	31	66.0	467	2	S34354	serine/threonine p
317	31	66.0	467	2	H84441	lipoprotein (impor
318	31	66.0	467	2	S35782	RNA helicase-like
319	31	66.0	493	2	D90587	ribosome releasing
320	31	66.0	496	2	T46157	
321	31	66.0	498	2	D71616	
322	31	66.0	500	2	T26067	hypothetical prote
323	31	66.0	504	2	G84251	hypothetical prote
324	31	66.0	512	2	T41955	probable proteinase
325	31	66.0	514	2	G84724	probable ARI-like
326	31	66.0	528	2	D97270	ATP-dependent RNA
327	31	66.0	530	2	F96491	hypothetical prote
328	31	66.0	537	2	T04944	hypothetical prote
329	31	66.0	538	2	E72561	probable thesmosa
330	31	66.0	552	2	S50313	iron transport pro
331	31	66.0	558	2	F75382	probable propionyl
332	31	66.0	572	2	T52520	hypothetical prote
333	31	66.0	572	2	S42866	serine/threonine p
334	31	66.0	600	2	S30153	low-temperature-in
335	31	66.0	645	2	D88022	protein W07E6.1 [1
336	31	66.0	645	2	T33803	hypothetical prote
337	31	66.0	657	2	E83660	cell-division proc
338	31	66.0	667	2	T6136	hypothetical prote
339	31	66.0	677	2	T45921	serine/threonine-s
340	31	66.0	683	2	T34103	hypothetical prote
341	31	66.0	690	2	H82923	conserved hypotet
342	31	66.0	710	2	S40934	hypothetical prote
343	31	66.0	735	2	T49622	hypothetical prote
344	31	66.0	744	2	AG1382	transport protein
345	31	66.0	744	2	AH1751	transport protein
346	31	66.0	746	2	T01536	hypothetical prote
347	31	66.0	746	2	G02838	enhancer-of-reste
348	31	66.0	762	2	A34355	cell surface prote
349	31	66.0	813	2	A40601	ferrityoverdine re
350	31	66.0	815	2	H83345	ferrityoverdine re
351	31	66.0	841	2	A86188	hypothetical prote
352	31	66.0	844	2	C91212	probable outer mem
353	31	66.0	844	2	C86058	probable fibrillar
354	31	66.0	848	2	B85087	hypothetical prote
355	31	66.0	849	2	C87740	protein H26D21.2 [
356	31	66.0	849	2	T15190	hypothetical prote
357	31	66.0	871	2	T48502	hypothetical prote
358	31	66.0	891	2	T22560	hypothetical prote
359	31	66.0	904	2	T15400	hypothetical prote
360	31	66.0	909	2	JN0665	nitrate reductase
361	31	66.0	913	2	D82885	multiple banded an
362	31	66.0	959	2	A55913	transcyclois- assoc
363	31	66.0	960	2	T07680	VP541 protein homo
364	31	66.0	970	2	T28234	ORF MSV076 probab
365	31	66.0	1016	2	T19006	ankyrin related pr
366	31	66.0	1018	2	T40253	hypothetical prote
367	31	66.0	1019	2	S53694	DNA topoisomerase
368	31	66.0	1029	2	F86210	hypothetical prote
369	31	66.0	1031	2	T38411	probable GTPase ac
370	31	66.0	1036	2	H96553	unknown protein, 2
371	31	66.0	1051	2	T05426	hypothetical prote
372	31	66.0	1058	2	S50295	hypothetical prote
373	31	66.0	1063	2	E96662	hypothetical prote
374	31	66.0	1066	2	T30903	arachidonate 8-lip
375	31	66.0	1076	2	C70007	hypothetical prote
376	31	66.0	1112	2	T47784	hypothetical prote
377	31	66.0	1129	2	T43674	Edi-27 protein - C
378	31	66.0	1151	2	T33777	hypothetical prote
379	31	66.0	1154	2	T15963	hypothetical prote
380	31	66.0	1178	2	S57535	probable membrane
381	31	66.0	1195	2	E96615	hypothetical prote
382	31	66.0	1268	2	B88209	protein K02A2.6 [1
383	31	66.0	1313	2	T29193	hypothetical prote
384	31	66.0	1341	2	S66835	probable membrane
385	31	66.0	1359	2	S49883	nuclear protein ST
386	31	66.0	1360	2	T06699	zinc finger protei
387	31	66.0	1466	2	A36426	SPA2 protein - yea
388	31	66.0	1468	1	S30818	hypothetical prote
389	31	66.0	1491	1	S43793	copper-transporin
390	31	66.0	1500	2	S36149	copper-transporin
391	31	66.0	1846	2	A59289	myr 6, unconventio
392	31	66.0	2197	2	B71600	variant-specific s
393	31	66.0	2269	2	T18472	hypothetical prote
394	31	66.0	2325	2	T15566	hypothetical prote

395	31	66.0	2391	2	T18410	carbamoyl-phosphat
396	31	66.0	5170	2	T15348	hypothetical prote
397	30.5	64.9	48	2	D64614	hypothetical prote
398	30.5	64.9	48	2	E71501	hypothetical prote
399	30.5	64.9	258	1	SNBY3	proteasome endope
400	30.5	64.9	367	2	T22653	hypothetical prote
401	30.5	64.9	786	2	T26811	hypothetical prote
402	30.5	64.9	1092	2	T18305	replication factor
403	30.5	64.9	1092	2	T18306	replication factor
404	30	63.8	67	2	E95089	hypothetical prote
405	30	63.8	73	2	H97956	hypothetical prote
406	30	63.8	73	2	AC2049	hypothetical prote
407	30	63.8	78	2	QJ1781	Salfer 8.8K protei
408	30	63.8	79	2	AF1065	hypothetical prote
409	30	63.8	81	2	AF2998	hypothetical prote
410	30	63.8	95	2	T46086	hypothetical prote
411	30	63.8	101	2	T09662	multicatalytic end
412	30	63.8	111	2	A69932	hypothetical prote
413	30	63.8	111	2	T05198	hypothetical prote
414	30	63.8	112	2	C91216	hypothetical prote
415	30	63.8	112	2	D86062	hypothetical prote
416	30	63.8	112	2	G65179	hypothetical prote
417	30	63.8	112	2	AE0475	conserved hypochet
418	30	63.8	121	1	A40157	androgen-regulated
419	30	63.8	122	2	A43644	sarcocystatin A pr
420	30	63.8	128	2	H97101	uncharacterized pr
421	30	63.8	128	2	H97354	hypothetical prote
422	30	63.8	130	4	S58337	hypothetical prote
423	30	63.8	132	2	T13098	probable minor tal
424	30	63.8	132	2	T17907	hypothetical prote
425	30	63.8	133	2	T15449	hypothetical prote
426	30	63.8	135	2	T06681	hypothetical prote
427	30	63.8	137	2	B82998	hypothetical prote
428	30	63.8	144	2	T23275	hypothetical prote
429	30	63.8	145	2	D84458	probable translati
430	30	63.8	145	2	T49102	hypothetical prote
431	30	63.8	147	2	A33675	beta-crystallin BC
432	30	63.8	149	1	WMVZK7	K7 protein 28R - v
433	30	63.8	152	2	T31054	hypothetical prote
434	30	63.8	155	2	T15930	hypothetical prote
435	30	63.8	157	2	F69368	carbon monoxide de
436	30	63.8	164	2	G84068	transcription regu
437	30	63.8	166	2	F64693	hypothetical prote
438	30	63.8	170	2	AH3318	hypothetical cytos
439	30	63.8	173	2	T41773	LSF-6 ortf28 - Bomb
440	30	63.8	181	1	B64167	cytochrome c bioge
441	30	63.8	187	2	H71819	hypothetical prote
442	30	63.8	193	2	E59095	hypothetical prote
443	30	63.8	194	2	H84771	probable AP2 domai
444	30	63.8	194	2	D87357	hypothetical prote
445	30	63.8	194	2	G83696	hypothetical prote
446	30	63.8	199	2	D64482	hypothetical prote
447	30	63.8	200	2	T25406	hypothetical prote
448	30	63.8	202	2	D84013	hypothetical prote
449	30	63.8	205	2	JC2009	beta-crystallin B2
450	30	63.8	205	2	JC4528	beta-crystallin B2
451	30	63.8	206	2	S63180	hypothetical prote
452	30	63.8	214	2	T10681	hypothetical prote
453	30	63.8	217	2	T46225	alpha MNC-like pro
454	30	63.8	217	2	T28343	hypothetical prote
455	30	63.8	223	2	T05755	hypothetical prote
456	30	63.8	226	2	S33024	hypothetical prote
457	30	63.8	233	2	A84745	hypothetical prote
458	30	63.8	235	2	A82667	conserved hypochet
459	30	63.8	237	2	B83728	phosphoribosylamin
460	30	63.8	239	2	E64699	hypothetical prote
461	30	63.8	240	2	T37432	probable 27.6K pro
462	30	63.8	240	2	JQ1784	Salfer protein - v
463	30	63.8	240	2	E72170	A56R protein - vari
464	30	63.8	240	2	T28591	21R protein - vari
465	30	63.8	240	2	H36853	A52R protein - vari
466	30	63.8	240	2	E84390	24-seirol C-methyl
467	30	63.8	250	2	T09160	proteasome subunit

468	30	63.8	250	2	T51969	20S proteasome sub
469	30	63.8	253	2	F89836	ABC transporter AT
470	30	63.8	255	2	TG0179	superoxide dismuta
471	30	63.8	261	2	B82462	hypothetical prote
472	30	63.8	263	1	A26147	egg-laying hormone
473	30	63.8	263	1	B85076	hypothetical prote
474	30	63.8	265	1	MNVV4	nonstructural prot
475	30	63.8	269	2	S11400	phosphotransferase
476	30	63.8	271	1	JX0316	phosphatidylinosic
477	30	63.8	271	2	S64615	hypothetical prote
478	30	63.8	286	2	T02641	probable C2H2-type
479	30	63.8	288	2	D64694	hypothetical prote
480	30	63.8	288	2	B40722	homeotic protein 1
481	30	63.8	290	2	G71623	11fin PFB0065w - m
482	30	63.8	292	2	T41772	IAP1 ortf27 - Bomby
483	30	63.8	293	2	H64158	hypothetical prote
484	30	63.8	295	2	B86571	hypothetical prote
485	30	63.8	295	2	A41241	ubiquitin-conjugat
486	30	63.8	297	2	A89582	protein C18A11.3 l
487	30	63.8	298	2	T52117	zinc finger protei
488	30	63.8	300	2	T32133	hypothetical prote
489	30	63.8	301	2	JC7882	esterase (EC 3.1.1
490	30	63.8	308	2	D30315	methyl viologen-re
491	30	63.8	308	2	C30315	coenzyme-M-7-merca
492	30	63.8	315	2	T45099	methenyltetrahydro
493	30	63.8	315	2	T00528	hypothetical prote
494	30	63.8	317	2	H70566	hypothetical prote
495	30	63.8	320	2	S50716	hypothetical prote
496	30	63.8	320	2	E84681	probable bHLH tran
497	30	63.8	321	2	F98318	hypothetical prote
498	30	63.8	321	2	AG2964	fibrinogen binding
499	30	63.8	324	2	A84295	probable DNA helic
500	30	63.8	328	2	T07610	MS176 protein - ri

ALIGNMENTS

RESULT 1

potassium channel-blocking toxin K-alpha - Pandinus imperator (fragment)

C:Species: Pandinus imperator

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T10471

R:Rogowski, R.S.; Collins, J.H.; O'Neill, T.J.; Gustafson, T.A.; Werhman, T.R.; Rogawsk

Mol.Pharmacol. 50, 1167-1177, 1996

A>Title: Three new coxins from the scorpion Pandinus imperator selectively block certai

A:Reference number: Z17036; PMID:9707422; PMID:8913348

A:Accession: T10471

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-47 <ROG>

A:Cross-references: UNIPROT:P55927; UNIPARC:UPI0000135658; EMBL:U79579; NID:q1945405; P

C:Gene: PTX-1

C:Superfamily: Kallitoxin

C:Keywords: neurotoxin; potassium channel inhibitor; venom

Query Match 100.0%; Score 47; DB 2; Length 47;

Best Local Similarity 100.0%; Pred.No. 0.14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
 |||||
 Db 5 DYKDDDK 12

RESULT 2

S59425

SPR28 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YD934.03c; protein YDR218c

C:Species: Saccharomyces cerevisiae

C>Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

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C;Accession: S59425
R;Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59425
A;Molecule type: DNA
A;Residues: 1-423 <MOR>
A;Cross-references: UNIPROT:Q04921; UNIPARC:UPI000006C4F5; EMBL:Z48612; NID:G728671; PID
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:SPR28
A;Cross-references: SGD:S0002626; MIPS:YDR218c
A;Map position: 4R
C;Superfamily: Saccharomyces cerevisiae cell division control protein CDC10

Query Match      87.2%; Score 41; DB 2; Length 423;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 62 DYDDDDDK 69

RESULT 3
S32834
Methylviologen-reducing hydrogenase chain vhcG [similarity] - Methanococcus voltae
C;Species: Methanococcus voltae
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: S32834; S16726
R;Klein, A.
Submitted to the EMBL Data Library, August 1991
A;Reference number: S32833
A;Accession: S32834
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <KDE>
A;Cross-references: UNIPROT:Q00406; UNIPARC:UPI00000625CA; EMBL:X61203; NID:G296614; PID
R;Halboch, S.; Klein, A.
Submitted to the EMBL Data Library, August 1991
A;Description: Methanococcus voltae harbors two gene groups each of homologous (NiFe) - a
A;Reference number: S16721
A;Accession: S16726
A;Molecule type: DNA
A;Residues: 1-99, 'TA', '102-107', 'P', '126', '129-306' <HAL>
A;Cross-references: UNIPARC:UPI0000174FEO; EMBL:X61203
A;Note: the sequence is revised in GenBank entry X61203, release 117, (PIDN:CAA43505.1)
R;Halboch, S.; Klein, A.
Mol. Gen. Genet. 233, 217-224, 1992
A;Title: Methanococcus voltae harbors four gene clusters potentially encoding two [NiFe]
A;Reference number: A59304; MUID:92293118; PMID:1603063
A;Contents: annotation
C;Genetics:
A;Gene: vhcG
C;Superfamily: methyl viologen-reducing hydrogenase gamma chain

Query Match      80.9%; Score 38; DB 2; Length 306;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 260 DYKVDKDK 267

RESULT 4
AC0184
malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38) [imported] - Yersinia
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C;Accession: AC0184
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

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11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0184
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <KUR>
A;Cross-references: UNIPROT:Q82G09; UNIPARC:UPI00000DC2B; GB:AL590842; PIDN:CAK90334.1
C;Genetics:
A;Gene: stcA
C;Superfamily: malic enzyme
C;Keywords: oxidoreductase

Query Match      80.9%; Score 38; DB 2; Length 565;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 66 DFKVDKDK 73

RESULT 5
S53352
IFH1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L8083.9; protein YLR223c; RRP3 protein
C;Species: Saccharomyces cerevisiae
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S53352; S51446; S47477
R;Cherel, I.; Thuriaux, P.
Yeast 11, 261-270, 1995
A;Title: The IFH1 gene product interacts with a fork head protein in Saccharomyces cere
A;Reference number: S53352; MUID:95304839; PMID:7785326
A;Accession: S53352
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1085 <CHE>
A;Cross-references: UNIPROT:P39520; UNIPARC:UPI000012D3D6; EMBL:Z29488; NID:G531491; PI
R;Hallsworth, K.
Submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmid 8083.
A;Reference number: S51443
A;Accession: S51446
A;Molecule type: DNA
A;Residues: 1-1085 <HAL>
A;Cross-references: UNIPARC:UPI000012D3D6; EMBL:U19027; NID:G609363; PID:G609372; MIPS:
C;Genetics:
A;Gene: SGD:IFH1; RRP3
A;Cross-references: SGD:S0004213; MIPS:YLR223c
A;Map position: 12R

Query Match      80.9%; Score 38; DB 2; Length 1085;
Best Local Similarity 85.7%; Pred. No. 1,2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 7
Db 612 DYEDDD 618

RESULT 6
S54451
hypothetical protein YMR076c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YMR076c; hypothetical protein YMR076c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: S54451; S52836
R;Gentile, S.; Bowman, S.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S54451
A;Accession: S54451
A;Molecule type: DNA

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A;Residues: 1-682 <GEN>
A;Cross-references: UNIPROT:Q04264; UNIPARC:UPI0000168AB1; EMBL:Z49259; NID:9807956; PID
A;Experimental source: strain AB972
R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, April 1995
A;Reference number: S52814
A;Accession: S52836
A;Molecule type: DNA
A;Residues: 659-1277 <PEA>
A;Cross-references: UNIPARC:UPI0000168AC7; EMBL:Z48952; NID:9763008; PID:CAA88801.1; PI
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:PDS5
A;Cross-references: SGD:S0004681; MIPS:YMR076C
A;Map position: 13R

Query Match 80.9%; Score 38; DB 2; Length 1277;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 1265 DYKDDDD 1271

RESULT 7
A42854
probable spindle pole body component bimB - *Emicella nidulans*
NAlternate names: cell division-associated protein bimB
C;Species: *Emicella nidulans*, *Aspergillus nidulans*
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42854; S27411
R;May, G.S.; McGoldrick, C.A.; Holt, C.L.; Denison, S.H.
J. Biol. Chem. 267, 15737-15743, 1992
A;Title: The bimB mutation of *Aspergillus nidulans* uncouples DNA replication from the C
A;Reference number: A42854; M0ID:9234836; PMID:1639810
A;Accession: A42854
A;Molecule type: mRNA
A;Residues: 1-2067 <MAV>
A;Cross-references: UNIPROT:P33144; UNIPARC:UPI000012693F
A;Note: Sequence extracted from NCBI backbone (NCBIN:112444, NCBI:P.112445)
R;May, G.S.; McGoldrick, C.A.; Denison, S.H.; Holt, C.L.
submitted to the EMBL Data Library, February 1992
A;Description: The bimB mutation of *Aspergillus nidulans* uncouples DNA replication from
A;Reference number: S27411
A;Accession: S27411
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2010; 'PLSIG', 2016 <MA2>
A;Cross-references: UNIPARC:UPI00001688E9; EMBL:M83232; NID:9168020; PID:9168021
A;Note: this sequence differs by a frameshift after residue 2010
C;Keywords: nucleus

Query Match 80.9%; Score 38; DB 2; Length 2067;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 899 DYKDDDD 905

RESULT 8
T10503
fruit bromelain (EC 3.4.22.33) FB18 precursor - pineapple
C;Species: *Ananas comosus* (pineapple)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10503
R;Muta, E.; Aramaki, H.; Takata, Y.; Kono, A.; Okamoto, Y.; Ota, S.
submitted to the EMBL Data Library, January 1993
A;Description: Cloning and sequencing of fruit bromelain.
A;Reference number: Z17060
A;Accession: T10503

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-351 <MTU>
A;Cross-references: UNIPROT:Q23791; UNIPARC:UPI0000044EB5; EMBL:D14059
A;Experimental source: cv. N67-10; nearly mature fruit
C;Function:
A;Description: hydrolases proteins; cysteine proteinase
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-121/Domain: amino-terminal propeptide #status predicted <PRO>
F;122-339/Product: fruit bromelain #status predicted <MTU>
F;340-351/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;147,279,300/Active site: Cys, His, Asn #status predicted

Query Match 78.7%; Score 37; DB 2; Length 351;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
DB 48 YKDDDDK 54

RESULT 9
B96524
hypothetical protein F11A17.5 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B96524
R;Theologos, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.P.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiz, R.; Marziani
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: A86141; M0ID:21016719; PMID:11130712
A;Accession: B96524
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-513 <STO>
A;Cross-references: UNIPROT:Q9SX72; UNIPARC:UPI00000A3573; GB:AE005173; NID:95733869; P
C;Genetics:
A;Gene: F11A17.5
A;Map position: 1
C;Superfamily: *Arabidopsis thaliana* hypothetical protein F11A17.30

Query Match 78.7%; Score 37; DB 2; Length 513;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 282 DYKDDDD 288

RESULT 10
B96974
superfamily I DNA and RNA helicase [imported] - *Clostridium acetobutylicum*
C;Species: *Clostridium acetobutylicum*
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96974
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
A;Reference number: A96900; M0ID:21359325; PMID:21359325
A;Accession: B96974
A;Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-721 <KUR>
 A:Cross-references: UNIPROT:Q97LF8; UNIPARC:UPI00000C9F00; GB:AE001437; PIDD:AAK78581.1;
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0603
 C:Superfamily: Bacillus subtilis hypothetical protein yvgs

Query Match 78.7%; Score 37; DB 2; Length 721;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 67 DYADDEDK 74

RESULT 11

hypothetical protein F26D2.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T20815; T21409

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19327

A:Accession: T20815

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <WIL>

A:Cross-references: UNIPROT:Q8WUP4; UNIPARC:UPI0000060F93; EMBL:Z93377; PIDD:CA807581.1;

A:Experimental source: clone F1A7

R:McMurray, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19418

A:Accession: T21409

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-791 <WIL>

A:Cross-references: UNIPARC:UPI0000060F93; EMBL:Z81513; PIDD:CA804186.1; GSEDB:GN00023;

A:Experimental source: clone F26D2

C:Genetics:

A:Gene: CESP:F26D2.2

A:Map position: 5

A:Introns: 28/3; 194/2; 195/3; 299/2; 404/1; 462/3; 500/1; 670/3; 698/3

Query Match 78.7%; Score 37; DB 2; Length 791;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 DB 274 DYNDDD 280

RESULT 12

T05410

hypothetical protein F10M6.180 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999

C:Accession: T05410

R:Bevan, M.; Weichselgartner, M.; Fairmann, B.; Grandpré, K.; Dauner, D.; Herzl, A.;

submitted to the Protein Sequence Database, February 1998

A:Reference number: Z15414

A:Accession: T05410

A:Molecule type: DNA

A:Residues: 1-838 <BEV>

A:Cross-references: UNIPARC:UPI000016DADA; EMBL:AL021811

C:Experimental source: cultivar Columbia; BAC clone F10M6

C:Genetics:

A:Map position: 4

A:Introns: 86/1; 158/1; 175/3; 214/3; 254/3; 286/2; 317/3; 361/3; 399/2; 463/3; 533/2; 5

Query Match 78.7%; Score 37; DB 2; Length 838;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 99 DYSNDDK 106

RESULT 13

B70192

hypothetical protein BB0739 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: B70192

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whi

son, D.; Peterson, J.; Kurlavsky, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vug

bowman, C.; Garland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: B70192

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-195 <KLE>

A:Cross-references: UNIPROT:O51681; UNIPARC:UPI00000575C8; GB:AE001174; GB:AE000783; N

C:Superfamily: Borrelia burgdorferi hypothetical protein BB0739

Query Match 76.6%; Score 36; DB 2; Length 195;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 7
 DB 129 YKDDDD 134

RESULT 14

T31963

hypothetical protein C33C12.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004

C:Accession: T31963

R:Gatung, S.; Schneet, P.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid C33C12.

A:Reference number: Z21105

A:Accession: T31963

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-215 <GAT>

A:Cross-references: UNIPROT:O16579; UNIPARC:UPI0000078124; EMBL:AF016662; PIDD:AB66052

A:Experimental source: strain Bristol N2; clone C33C12

C:Genetics:

A:Gene: CESP:C33C12.7

A:Map position: 2

A:Introns: 63/3; 94/3; 124/2; 168/2

Query Match 76.6%; Score 36; DB 2; Length 215;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 182 DYKDDDK 189

RESULT 15

S39814

DNA polymerase homolog pol-r - rye mitochondrion (strain Halo)

C/Species: mitochondrion Secale cereale (rye)
A/Variety: strain Halo
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S39814
R/Dohmen, G.; Tudzynski, P.
Curr. Genet. 25, 59-65, 1994
A/Title: A DNA-polymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.
A/Reference number: S39814; MUID:94363738; PMID:8082167
A/Accession: S39814
A/Molecule type: DNA
A/Residues: 1-289 <DOH>
A/Cross-references: UNIPROT:Q36545; UNIPARC:UPI000008F158; EMBL:X74132; NID:G439279; PII
A/Experimental source: strain Halo; etiolated shoots
C/Genetics:
A/Status: pol-r
A/Genome: mitochondrion
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 289;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
|:|||||
Db 252 DHKSDDDK 259

RESULT 16
S39823
DNA polymerase homolog pol-r - rye mitochondrion (strain B-P2)
C/Species: mitochondrion Secale cereale (rye)
A/Variety: strain B-P2
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S39823
R/Dohmen, G.; Tudzynski, P.
Curr. Genet. 25, 59-65, 1994
A/Title: A DNA-polymerase-related reading frame (pol-r) in the mtDNA of Secale cereale.
A/Reference number: S39814; MUID:94363738; PMID:8082167
A/Accession: S39823
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-312 <DOH>
A/Cross-references: UNIPROT:Q36546; UNIPARC:UPI0000096B6D; EMBL:X74133; NID:G439281; PII
A/Experimental source: strain B-P2; etiolated shoots
C/Genetics:
A/Status: pol-r
A/Genome: mitochondrion
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 312;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
|:|||||
Db 252 DHKSDDDK 259

RESULT 17
T49237
hypothetical protein F7K15.80 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: T49237
R/Obernatter, B.; Ottenwaelter, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Lem
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z25019
A/Accession: T49237
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-485 <OBE>
A/Cross-references: UNIPROT:Q9LXL1; UNIPARC:UPI00000A1EFC; EMBL:AL353871; GSPDB:GN00061;

A/Experimental source: cultivar Columbia; BAC clone F7K15
C/Genetics:
A/Status: ATPS:F7K15.80
A/Map position: 3
A/Insertions: 292/3; 359/3; 425/1

Query Match 76.6%; Score 36; DB 2; Length 485;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 22 DYDDDD 28

RESULT 18
H84913
probable ATP-dependent RNA helicase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: H84913
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84913
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-748 <STO>
A/Cross-references: UNIPROT:Q22907; UNIPARC:UPI000017A71E; CB:AE02093; NID:G2275211; P
C/Genetics:
A/Status: At2g47330
A/Map position: 2

Query Match 76.6%; Score 36; DB 2; Length 748;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 7
|:|||||
Db 107 YKDDDD 112

RESULT 19
S56231
hypothetical protein YFL023w - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C/Accession: S56231
R/Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasan
submitted to the EMBL Data Library, May 1995
A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces c
A/Reference number: S56186
A/Accession: S56231
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-796 <MOR>
A/Cross-references: UNIPROT:P43573; UNIPARC:UPI000013ADF2; EMBL:D50617; NID:G836685; PII
A/Genetics:
A/Status: SGD:FYV11
A/Cross-references: SGD:S0001871
A/Map position: 6L

Query Match 76.6%; Score 36; DB 2; Length 796;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 583 DYDDDD 589

RESULT 20

S07183
hypothetical protein 3 - maize mitochondrion plasmid S-1
C:Species: mitochondrion Zea mays (maize)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
C/Accession: S07183
R:Pallard, M.; Sederoff, R.R.; Levine III, C.S.
EMBO J. 4, 1125-1128, 1985
A:Title: Nucleotide sequence of the S-1 mitochondrial DNA from the S cytoplasm of maize.
A:Reference number: S07183
A/Accession: S07183
A:Status: translation not shown
A/Molecule type: DNA
A:Residues: 1-917 <PAT>
A/Cross-references: UNIPROT:Q9MJC4; UNIPARC:UPI0000178E85; EMBL:X02451
C/Genetics:
A:Genome: mitochondrion
C/Superfamily: DNA polymerase, mitochondrial plasmid type
C/Keywords: mitochondrion

Query Match 76.6%; Score 36; DB 2; Length 917;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYKDDDD 7
Db 443 YKDDDD 448

RESULT 21

A88746
protein C18F3.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: A88746
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: A88746
A:Status: preliminary
A/Molecule type: DNA
A:Residues: 1-987 <STO>
A/Cross-references: UNIPROT:Q18100; UNIPARC:UPI000017A61F; GB:chr_IV; PIDN:AAA93439.1; F
C/Genetics:
A:Gene: C18F3.2
A/Map position: 4

Query Match 76.6%; Score 36; DB 2; Length 987;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 8
Db 922 DYKDDDD 929

RESULT 22

S50536
hypothetical protein YER033c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C/Accession: S50536
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9379, 9501, and lambda clone 4678.
A/Reference number: S50432
A/Accession: S50536
A/Molecule type: DNA
A:Residues: 1-1076 <DIE>

A/Cross-references: UNIPROT:P40021; UNIPARC:UPI000013AC6F; EMBL:U18796; NID:G603265; P
C/Genetics:
A:Gene: SGD:ZRG8; MIPS:YER033c
A/Cross-references: SGD:S0000835
A/Map position: 5R

Query Match 76.6%; Score 36; DB 2; Length 1076;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 7
Db 436 DYKDDDD 442

RESULT 23

T30988
hypothetical protein C18F3.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30988
R:Du, Z.; Gattung, S.
submitted to the EMBL Data Library, August 1999
A:Description: The sequence of C. elegans cosmid C18F3.
A/Reference number: Z20953
A/Accession: T30988
A:Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A:Residues: 1-1287 <DUZ>
A/Cross-references: UNIPROT:Q18100; UNIPARC:UPI0000081960; EMBL:U50067; PIDN:AAA93439.2
A/Experimental source: strain Bristol N2
C/Genetics:
A/Map position: IV
A:Insertions: 34/3; 72/1; 131/2; 157/1; 254/3; 303/1; 400/1; 495/1; 592/1; 681/3; 950/1; 1
A/Note: C18F3.2
C/Superfamily: neural cell adhesion molecule 11; fibronectin type III repeat homology;

Query Match 76.6%; Score 36; DB 2; Length 1287;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDD 8
Db 1222 DYKDDDD 1229

RESULT 24

B71621
probable membrane associated protein PFB0190C - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C/Accession: B71621
R:Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.C
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551
A/Accession: B71621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A:Residues: 1-2295 <GAR>
A/Cross-references: UNIPROT:Q9TY98; UNIPARC:UPI000007C03B; GB:AE001379; GB:AE001362; N
A/Experimental source: clone 3D7
C/Genetics:
A:Gene: PFB0190C

Query Match 76.6%; Score 36; DB 2; Length 2295;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDD 6
Db 1504 DYKDD 1509

RESULT 25
T18492
hypothetical protein C0805w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18492
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18492
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2457 <LAW>
A:Cross-references: UNIPROT:O77375; UNIPARC:UPI00000829FD; EMBL:Z98551; PIDN:CAB1131.1
C:Genetics:
A:Map position: 3
A:Note: C0805w
C:Superfamily: Plasmodium DNA-directed RNA polymerase II large chain

Query Match 76.5%; Score 36; DB 2; Length 2457;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 1264 DYDDDD 1270

RESULT 26
AF2345
hypothetical protein asl4317 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2345
R:Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <KUR>
A:Cross-references: UNIPROT:Q8YF82; UNIPARC:UPI000000C8AB9; GB:BA000019; PIDN:BA876016.1
C:Genetics:
A:Gene: asl4317

Query Match 74.5%; Score 35; DB 2; Length 78;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 64 DYDDDD 70

RESULT 27
A40592
heat shock protein hsp18 - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: A40592; S25534
R:Sauer, U.; Duetre, P.
J. Bacteriol. 175, 3394-3400, 1993
A:Title: Sequence and molecular characterization of a DNA region encoding a small heat shock
A:Reference number: A40592; MUID:93273706; PMID:8501044
A:Accession: A40592
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-151 <SAN>
A:Cross-references: UNIPROT:Q03928; UNIPARC:UPI000012CC00; EMBL:X65276; NID:g40362; PIDN:BA876016.1
C:Superfamily: alpha-crystallin-related small heat shock protein

Query Match 74.5%; Score 35; DB 2; Length 151;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 48 DYEKDDK 55

RESULT 28
G97355
molecular chaperone (small heat shock protein), Hsp18 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97355
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G97355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: UNIPROT:Q03928; UNIPARC:UPI000012CC00; GB:AE001437; PIDN:AAK61634.1
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3714
C:Superfamily: alpha-crystallin-related small heat shock protein

Query Match 74.5%; Score 35; DB 2; Length 151;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 48 DYEKDDK 55

RESULT 29
T32029
hypothetical protein C03H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32029
R:Rohlfing, T.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C03H5.
A:Reference number: Z21114
A:Accession: T32029
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-287 <ROH>
A:Cross-references: UNIPROT:O16657; UNIPARC:UPI0000077A6F; EMBL:AF016674; PIDN:AAB66130
A:Experimental source: strain Bristol NZ; clone C03H5
C:Genetics:
A:Gene: CESP:C03H5.3
A:Map position: 2
A:Introns: 2/1; 15/3; 234/2

Query Match 74.5%; Score 35; DB 2; Length 287;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 106 DFEKDDDE 113

RESULT 30
A86384
unknown protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86384
R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <STO>
A:Cross-references: UNIPROT:Q9C6L0; UNIPARC:UPI000005EAA4; GB:AE005172; NID:g10092327; F C:Genetics:
A:Map position: 1

Query Match 74.5%; Score 35; DB 2; Length 288;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDD 8
DB 128 YHDDDDK 134

RESULT 31
D96708
unknown protein, 9003-8083 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D96708
R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96708
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <STO>
A:Cross-references: UNIPROT:Q9M9C9; UNIPARC:UPI00000A11A6; GB:AE005173; NID:g6714347; P C:Genetics:
A:Gene: T2E12.1
A:Map position: 1

Query Match 74.5%; Score 35; DB 2; Length 306;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 137 DYDDDD 143

RESULT 32
PC4365
calcium-binding protein - tapeworm (Echinococcus granulosus) (fragment)
C:Species: Echinococcus granulosus

C>Date: 15-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: PC4365
R:Rodrigues, J.J.S.; Ferreira, H.B.; Farias, S.E.; Zaha, A.
Biochem. Biophys. Res. Commun. 237, 451-456, 1997
A>Title: A protein with a novel calcium-binding domain associated with calcareous corpi
A:Reference number: PC4365; MUID:97415820; PMID:9268732
A:Accession: PC4365
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-338 <ROD>
A:Cross-references: UNIPROT:Q24795; UNIPARC:UPI0000755B8; GB:I33817; NID:g499140; PID F:1-7,8-20,21-33,34-45,46-89,90-103,104-116,117-129,130-141,142-155,156-169,170-182,18

Query Match 74.5%; Score 35; DB 2; Length 338;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 3 DYDDDD 9

RESULT 33
T09106
gibberellin 20-oxidase (EC 1.14.11.-) - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09106
R:Wu, K.; Li, L.; Gage, D.A.; Zeevart, J.A.D.
Plant Physiol. 110, 547-554, 1996
A>Title: Cloning and photoperiod-regulated expression of gibberellin 20-oxidase from c
A:Reference number: 216564; MUID:96351185; PMID:8742334
A:Accession: T09106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-374 <WU>
A:Cross-references: UNIPROT:Q41366; UNIPARC:UPI0000A09D6; EMBL:U33330; NID:g1144389; F C:Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C:Keywords: oxidoreductase

Query Match 74.5%; Score 35; DB 2; Length 374;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDD 8
DB 150 YDDDDDK 156

RESULT 34
T25165
hypothetical protein T23D8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25165
R:Mild, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: 219989
A:Accession: T25165
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-410 <WIL>
A:Cross-references: UNIPROT:O02327; UNIPARC:UPI000078796; EMBL:Z81128; PIDN:CAB03401.1 A:Experimental source: clone T23D8
C:Genetics:
A:Gene: CESP:T23D8.3
A:Map position: 1
A:Introns: 61/3; 208/3; 247/3; 396/3

Query Match 74.5%; Score 35; DB 2; Length 410;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 338 DMEDDDDK 345

RESULT 35

S67161

hypothetical protein YOR264w - yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein O5375

C/Species: *Saccharomyces cerevisiae*

C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004

C/Accession: S67161

R/Jauniaux, J.C.; Poirey, R.

submitted to the Protein Sequence Database, July 1996

A/Reference number: S67143

A/Accession: S67161

A/Molecule type: DNA

A/Residues: 1-430 <NU>

A/Cross-references: UNIPROT:Q08729; UNIPARC:UPI00006A307; EMBL:Z75171; NID:G1420592; PI

C/Genetics:

A/Gene: MIPS:YOR264w

A/Cross-references: SGD:S0005790

A/Map position: 15R

Query Match 74.5%; Score 35; DB 2; Length 430;

Best Local Similarity 62.5%; Pred. No. 1.5e+02;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 38 DFEDDDDK 45

RESULT 36

S58653

hypothetical protein YFR024c-a - yeast (*Saccharomyces cerevisiae*)C/Species: *Saccharomyces cerevisiae*

C/Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 15-Mar-2004

C/Accession: S58653

R/Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanna, S.I.; Sasana

submitted to the EMBL Data Library, May 1995

A/Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces ce*

A/Reference number: S56186

A/Accession: S58653

A/Molecule type: DNA

A/Residues: 1-451 <MUR>

A/Cross-references: UNIPARC:UPI000053060; EMBL:D50617; GSPDB:GN00006; MIPS:YFR024c-a

C/Genetics:

A/Gene: MIPS:YFR024c-a

A/Map position: 6R

A/Intons: 16/2

F/399-448/Domain: SH3 homology <SH3>

Query Match 74.5%; Score 35; DB 2; Length 451;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 226 DYYDDDD 232

RESULT 37

S41720

intermediate filament - goldfish

C/Species: *Carassius auratus* (goldfish)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S41720

R/Glasgow, E.; Druger, R.K.; Fuchs, C.; Lane, W.S.; Schechter, N.

EMBO J. 13, 297-305, 1994

A/Title: Molecular cloning of gefitin (ON11): serial expression of two new neurofilam
A/Reference number: S41720; MID:94147974; PMID:8313874
A/Accession: S41720
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-472 <GLA>
A/Cross-references: UNIPROT:Q07962; UNIPARC:UPI00000FB57F; EMBL:L19595; NID:G304478; PI
C/Superfamily: cytoskeletal keratin

Query Match 74.5%; Score 35; DB 2; Length 472;

Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 430 EVKDDDDK 437

RESULT 38

D84920

hypothetical protein At2g47860 [imported] - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: D84920

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A/Reference number: A84420; MID:20083487; PMID:10617197

A/Accession: D84920

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-635 <STO>

A/Cross-references: UNIPROT:Q82253; UNIPARC:UPI00000A0189; GB:AE002093; NID:G3738298; P

C/Genetics:

A/Gene: At2g47860

A/Map position: 2

A/Superfamily: *Arabidopsis* hypothetical protein F19F18.80Query Match 74.5%; Score 35; DB 2; Length 635;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 358 EYRDDDD 364

RESULT 39

G71615

phospholipase A2-like a/b fold hydrolase PFB0410C - malaria parasite (*Plasmodium falcip*C/Species: *Plasmodium falciparum*

C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C/Accession: G71615

R/Gardner, M.J.; Tectelin, H.; Carucci, D.J.; Cummings, L.M.; Atavind, L.; Koonin, E.V.

; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O

Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A/Reference number: A71600; MID:99021743; PMID:9804531

A/Accession: G71615

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-679 <GAR>

A/Cross-references: UNIPROT:O96176; UNIPARC:UPI0000077A97; GB:AE001393; GB:AE001362; NI

A/Experimental source: clone 3D7

C/Genetics:

A/Gene: PFB0410C

Query Match 74.5%; Score 35; DB 2; Length 679;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
 |||||
 DB 251 YDDDDK 257

RESULT 40

T34314
 hypothetical protein F59G1.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T34314
 R/Lacelle, P.
 submitted to the EMBL Data Library, April 1996
 A/Description: The sequence of C. elegans cosmid F59G1.
 A/Reference number: 221504
 A/Accession: T34314
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1010 <LMT>
 A/Cross-references: UNIPARC:UPI000017BA5D; EMBL:U53332; PIDN:AAC71155.1; GSPDB:GN00020;
 A/Experimental source: strain Bristol N2; clone F59G1
 C/Genetics:
 A/Gene: CESP:F59G1.3
 A/Map position: 2
 A/Intons: 13/3; 65/1; 113/1; 149/3; 188/2; 224/3; 255/1; 297/2; 593/2; 714/3; 793/3; 94

Query Match 74.5% Score 35; DB 2; Length 1010;
 Best Local Similarity 75.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 |||||
 DB 751 DMKDEDDK 758

RESULT 41

S46817
 hypothetical protein YHR080C - Yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
 C/Accession: S46817
 R/Favell, T.
 submitted to the EMBL Data Library, June 1994
 A/Description: The sequence of S. cerevisiae cosmid 9205.
 A/Reference number: S46795
 A/Accession: S46817
 A/Molecule type: DNA
 A/Residues: 1-1345 <FAV>
 A/Cross-references: UNIPROT:P38800; UNIPARC:UPI000013B2B1; EMBL:U10556; NID:G500825; PIR
 C/Genetics:
 A/Cross-references: SGD:S0001122
 A/Map position: 8R
 C/Superfamily: uncharacterized conserved protein
 C/Keywords: transmembrane protein

Query Match 74.5% Score 35; DB 2; Length 1345;
 Best Local Similarity 85.7%; Pred. No. 5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 |||||
 DB 691 DYGDddd 697

RESULT 42

RN202L
 DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - malaria parasite (Plasmodium f
 C/Species: Plasmodium falciparum
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: S07485
 R/Li, W.B.; Bzik, D.J.; Gu, H.; Tanaka, M.; Fox, B.A.; Inselburg, J.
 Nucleic Acids Res. 17, 9621-9636, 1989
 A/Title: An enlarged largest subunit of Plasmodium falciparum RNA polymerase II defines

A/Reference number: S07485; MUID:90098832; PMID:2690004
 A/Accession: S07485
 A/Molecule type: DNA
 A/Residues: 1-2452 <LMT>
 A/Cross-references: UNIPROT:P14248; UNIPARC:UPI00001345CB; EMBL:X16561; NID:G9942; PIDN
 C/Genetics:
 A/Map position: 3
 C/Superfamily: Plasmodium DNA-directed RNA polymerase II large chain
 C/Keywords: DNA binding; nucleic acid transferase; phosphoprotein; tandem repeat; transcr
 F/68-94/Region: zinc finger CCH motif
 F/2247-2384/Region: 7-residue repeats
 F/376/Binding site: ATP/GMP (Lys) #status predicted

Query Match 74.5% Score 35; DB 1; Length 2452;
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 |||||
 DB 1264 DYVDDDD 1270

RESULT 43

D71614
 hypothetical protein PFB0460C - malaria parasite (Plasmodium falciparum)
 C/Species: Plasmodium falciparum
 C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 C/Accession: D71614
 R/Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V
 ; Petre, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.C
 Science 282, 1126-1132, 1998
 A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A/Reference number: A71600; MUID:95021743; PMID:9804551
 A/Accession: D71614
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-2573 <GAR>
 A/Cross-references: UNIPROT:O96185; UNIPARC:UPI0000079076; GB:AE001396; GB:AE001362; N
 A/Experimental source: clone 3D7
 C/Genetics:
 A/Gene: PFB0460C

Query Match 74.5% Score 35; DB 2; Length 2573;
 Best Local Similarity 85.7%; Pred. No. 9.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 |||||
 DB 1331 DYVDDDD 1337

RESULT 44

T32477
 hypothetical protein F52H2.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T32477
 R/Chisoe, S.; Hawkins, J.
 submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid F52H2.
 A/Reference number: 221175
 A/Accession: T32477
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-140 <CHI>
 A/Cross-references: UNIPROT:O17393; UNIPARC:UPI0000074F66; EMBL:AF026214; PIDN:AA071313
 A/Experimental source: strain Bristol N2; clone F52H2
 C/Genetics:
 A/Gene: CESP:F52H2.3
 A/Map position: X
 A/Intons: 45/3; 88/2

Query Match 72.3% Score 34; DB 2; Length 140;

Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8
Db 124 KDDDDK 129

RESULT 45

A:Residues: 1-177 <DOB>
A:Cross-references: UNIPARC:UPI0000125DF0; EMBL:Z48502; NID:G695715; PIDN:CAA8408.1; P

C:Species: Rattus norvegicus (Norway rat)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C:Accession: A36237; A37407; A37406

R:Thompson, R.C.; Watson, S.J.

DNA Cell Biol. 9, 637-645, 1990

A:Title: Nucleotide sequence and tissue-specific expression of the rat melanin concentra

A:Reference number: A36237; PMID:91083836; PMID:2261081

A:Accession: A36237

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-165 <THO>

A:Cross-references: UNIPROT:P14200; UNIPARC:UPI000012F1D6; GB:M62641; NID:G205329; PIDN:

R:Mahon, J.L.; Presse, F.; Bittencourt, J.C.; Sawchenko, P.E.; Vale, W.

Endocrinology 125, 2056-2065, 1989

A:Title: The rat melanin-concentrating hormone messenger ribonucleic acid encodes multi

A:Reference number: A37407; PMID:90005146; PMID:2477226

A:Accession: A37407

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-165 <NH>

A:Cross-references: UNIPARC:UPI000012F1D6; GB:M29712; NID:G205327; PIDN:AAA41580.1; PID:

R:Vaughan, J.M.; Fischer, W.H.; Hoeger, C.; Rivier, J.; Vale, W.

Endocrinology 125, 1660-1665, 1989

A:Title: Characterization of melanin-concentrating hormone from rat hypothalamus.

A:Reference number: A37406; PMID:8938286; PMID:2759038

A:Accession: A37406

A:Status: preliminary

A:Molecule type: protein

A:Residues: 147-165 <VAU>

A:Cross-references: UNIPARC:UPI0000037310

C:Superfamily: melanin-concentrating hormone

Query Match

Best Local Similarity 100.0%; Pred. No. 80;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8
Db 75 KDDDDK 80

RESULT 46

A:Residues: 1-177 <DOB>
A:Cross-references: UNIPARC:UPI0000125DF0; EMBL:X05327; NID:G3373; PIDN:

C:Species: Saccharomyces cerevisiae

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: S05822; S52891

R:Dubois, E.; Bercy, J.; Messenguy, F.

Mol. Gen. Genet. 207, 142-148, 1987

A:Title: Characterization of two genes, ARG1 and ARG11 required for specific regulat

A:Reference number: S05822; PMID:87257286; PMID:3298999

A:Accession: S05822

A:Molecule type: DNA

A:Residues: 1-177 <DOB>

A:Cross-references: UNIPROT:P07249; UNIPARC:UPI0000125DF0; EMBL:X05327; NID:G3373; PIDN:

R:Odell, C.; Bowman, S.

submitted to the EMBL Data Library, February 1995

A:Reference number: S52885

A:Accession: S52891

A:Molecule type: DNA

A:Residues: 1-177 <DOB>

A:Cross-references: UNIPARC:UPI0000125DF0; EMBL:Z48502; NID:G695715; PIDN:CAA8408.1; P

C:Species:

A:Gene: SGD:ARG80; ARG1; MIPS:YMR042W

A:Cross-references: SGD:S0004645; MIPS:YMR042W

A:Map position: 13R

C:Function:

A:Description: required for arginine-dependent activation of CAR1

C:Superfamily: regulatory protein ARG1; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; nucleus; transcription regulation

F:79-134/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match

Best Local Similarity 75.0%; Pred. No. 86;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 47 DEEDDDK 54

RESULT 47

A:Residues: 1-197 <LFT>
A:Cross-references: UNIPARC:Q18337; UNIPARC:UPI0000077BCA; EMBL:U42848; NID:G1125817; P

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004

C:Accession: T15725

R:Je, T.

submitted to the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid C31H1.

A:Reference number: Z18395

A:Accession: T15725

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197 <LFT>

A:Cross-references: UNIPROT:Q18337; UNIPARC:UPI0000077BCA; EMBL:U42848; NID:G1125817; P

A:Gene: CESP:C31H1.2

A:Introns: 21/1; 98/3; 130/3; 143/1; 178/3

Query Match

Best Local Similarity 71.4%; Pred. No. 97;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 7
Db 185 EYQDDDD 191

RESULT 48

A:Residues: 1-259 <HR>
A:Cross-references: UNIPARC:UPI00000A96B4; GB:D26182; NID:G575607; PIDN:

C:Species: Nicotiana sylvestris (wood tobacco)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S46286

R:Hirose, T.; Sugita, M.; Sugitara, M.

Mol. Gen. Genet. 244, 360-366, 1994

A:Title: Characterization of a cDNA encoding a novel type of RNA-binding protein in tob

A:Reference number: S46286; PMID:94359458; PMID:8078461

A:Accession: S46286

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-259 <HR>

A:Cross-references: UNIPROT:Q40436; UNIPARC:UPI00000A96B4; GB:D26182; NID:G575607; PIDN:

C:Superfamily: wood tobacco RNA-binding protein; ribonucleoprotein repeat homology

F:41-108/Domain: ribonucleoprotein repeat homology <RNP1>

Query Match

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 1 KDDDDK 8

Db 244 YRDDDE 250

RESULT 49

T52379

zinc finger protein ZPT3-3 [imported] - garden petunia

C/Species: Petunia x hybrida (garden petunia)

C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C/Accession: T52379

R/Kibo, K.; Sakamoto, A.; Kobayashi, A.; Rybka, Z.; Kanno, Y.; Nakagawa, H.; Nishino, T.

Nucleic Acids Res. 26, 608-615, 1998

A/Title: Cys2/His2 zinc-finger protein family of petunia: evolution and general mechanisms

A/Reference number: Z26061

A/Accession: T52379

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-300 <KDB>

A/Cross-references: UNIPROT:O22090; UNIPARC:UPI00000ACAC2C; EMBL:AB006605; PIDN:BAA21927.

A/Experimental source: strain Mitchell diploid

C/Superfamily: Arabidopsis thaliana hypothetical protein F12E4.290

Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 300;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 141 DYSDDE 148

RESULT 50

T24387

probable cysteine proteinase (EC 3.4.22.-) T03E6.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T24387

R/Lloyd, C.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z19885

A/Accession: T24387

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-337 <WLI>

A/Cross-references: UNIPROT:O45734; UNIPARC:UPI000007623; EMBL:Z52812; PIDN:CAB07275.1;

A/Experimental source: clone T03E6

C/Genetics:

A/Gene: CESP.T03E6.7

A/Map position: 5

A/Intons: 86/3; 119/3; 269/1

C/Superfamily: papain

C/Keywords: cysteine proteinase; hydrolase

F,144,283,304/Active site: Cys, His, Asn #status predicted

Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 337;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 34 DYKEDFDK 41

RESULT 51

T48564

probable serine rich protein - Arabidopsis thaliana

N/Alternate names: protein F14F18.220

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T48564

R/Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A/Reference number: Z24490

A/Accession: T48564

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-362 <BEV>

A/Cross-references: UNIPROT:Q9LYH0; UNIPARC:UPI000009E7C1; EMBL:AL163812

A/Experimental source: cultivar Columbia; BAC clone F14F18

C/Genetics:

A/Map position: 5

A/Note: F14F18.220

Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 362;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 7

Db 310 DYEDDE 316

RESULT 52

S45766

hypothetical protein YBL032w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YBL0418

C/Species: Saccharomyces cerevisiae

C/Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C/Accession: S45766; S50299

R/Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45745

A/Accession: S45766

A/Molecule type: DNA

A/Residues: 1-381 <GOF>

A/Cross-references: UNIPROT:P38199; UNIPARC:UPI000005318E; EMBL:Z35793; NID:G536038; PI

A/Experimental source: strain S288C

R/van Dyck, L.; Jonniaux, J.L.; de Melo Barreiros, T.; Kleine, K.; Goffeau, A.

Yeast 10, 1663-1673, 1994

A/Title: Analysis of a 17.4 kb DNA segment of yeast chromosome II encompassing the ribc

human proliferation-associated p120 antigen.

A/Reference number: S50299; MUID:95242843; PMID:7725803

A/Accession: S50299

A/Molecule type: DNA

A/Residues: 1-381 <VAN>

A/Cross-references: UNIPARC:UPI000005318E; EMBL:X77291; NID:G602888; PIDN:CAA54496.1; F

A/Experimental source: strain S288C

C/Genetics:

A/Cross-references: SGD:S0000128

A/Map position: ZL

Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 381;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8

Db 297 KDDDDK 302

RESULT 53

T05781

hypothetical protein M4E13.160 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T05781

R/Bevan, M.; Purnelle, B.; Boutry, M.; Goffeau, A.; Hohnsels, J.; Mewes, H.W.; Mayer, K

submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15451

A/Accession: T05781

A/Molecule type: DNA

A/Residues: 1-386 <BEV>

A/Cross-references: UNIPROT:O49617; UNIPARC:UPI00000AC134; EMBL:AL022023

A/Experimental source: cultivar Columbia; BAC clone M4E13

A/Map position: 4

A/Intons: 42/1; 140/3

A>Note: M4E13.160

Query Match 72.3%; Score 34; DB 2; Length 386;

Best Local Similarity 62.5%; Pred. No. 2e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|:|||||
Db 185 DFSDDDDE 192

RESULT 54

T26987

hypothetical protein Y48A6B.13 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T26987

R/Gardner, A.

submitted to the EMBL Data Library, June 1998

A/Reference number: Z20295

A/Accession: T26987

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-396 <WIL>

A/Cross-references: UNIPROT:Q9XXC7; UNIPARC:UPI000007A333; EMBL:AL023844; PIDN:CAA19534.

A/Experimental source: clone Y48A6B

C/Genetics:

A/Gene: CSP:Y48A6B.13

A/Map position: 3

A/Introns: 11/2; 48/3; 224/3; 298/1; 387/1

Query Match 72.3%; Score 34; DB 2; Length 396;

Best Local Similarity 71.4%; Pred. No. 2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 71 NYRDDDD 77

RESULT 55

T23899

hypothetical protein R04D3.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T23899

R/Swinburne, J.

submitted to the EMBL Data Library, March 1996

A/Reference number: Z19815

A/Accession: T23899

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1430 <WIL>

A/Cross-references: UNIPROT:Q21713; UNIPARC:UPI000007D6C1; EMBL:Z70212; PIDN:CAA94163.1;

A/Experimental source: clone R04D3

C/Genetics:

A/Gene: CSP:R04D3.3

A/Map position: X

A/Introns: 108/3; 296/3; 352/3

Query Match 72.3%; Score 34; DB 2; Length 430;

Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 339 DYEDDD 345

RESULT 56

A85363

probable calmodulin-binding protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004

C/Accession: A85363

C/Anonymous: The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr.

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A/Accession: A85363

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-467 <SNO>

A/Cross-references: UNIPROT:O65550; UNIPARC:UPI00000AB646; GB:NC_001268; NID:G7270002;

A/Genetics:

A/Gene: AT4g31000

A/Map position: 4

C/Superfamily: Calmodulin-binding protein

Query Match 72.3%; Score 34; DB 2; Length 467;

Best Local Similarity 62.5%; Pred. No. 2.4e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|:|||||
Db 55 DFNDEDDK 62

RESULT 57

S66713

hypothetical protein YOL030w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein O2145

C/Species: Saccharomyces cerevisiae

C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004

C/Accession: S66713

R/Habib, B.; Hattenhorst, U.; Hollenberg, C.P.; Ramezani Rad, M.

submitted to the Protein Sequence Database, July 1996

A/Reference number: S66703

A/Accession: S66713

A/Molecule type: DNA

A/Residues: 1-484 <HAB>

A/Cross-references: UNIPROT:Q08193; UNIPARC:UPI000013BC67; EMBL:Z74772; NID:G1419818; P

A/Experimental source: strain S288C

C/Genetics:

A/Gene: MIPS:YOL030w

A/Cross-references: SGD:S0005390

A/Map position: 15L

C/Superfamily: glycopospholipid-anchored surface glycoprotein GAS1

Query Match 72.3%; Score 34; DB 2; Length 484;

Best Local Similarity 75.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|:|||||
Db 392 DAKDDDE 399

RESULT 58

S36494

E2 protein - human papillomavirus type 25

C/Species: human papillomavirus type 25

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36494

R/Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36494

A/Molecule type: DNA

A/Residues: 1-502

A/Cross-references: UNIPROT:P36787; UNIPARC:UPI0000138340; EMBL:X74471; NID:G396948; PI

C/Superfamily: papillomavirus E2 protein; transcription regulation

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 72.3%; Score 34; DB 2; Length 502;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 YKDDDDK 8
DB 139 YVDDDDK 145

RESULT 59

T10660
hypothetical C2H2-type zinc-finger protein - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T10660

R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, W.
submitted to the EMBL Data Library, November 1998

A/Reference number: Z21889

A/Accession: T10660

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-609 <L>N>

A/Cross-references: UNIPROT:O94326; UNIPARC:UPI000006C388; EMBL:AL034352; PIDN:CAA22180.

A/Experimental source: strain 972h-; cosmid c725

C/Genetics:

A/Map position: 2

A/Intons: 22/1; 58/1; 68/2

C/Superfamily: Schizosaccharomyces hypothetical C2H2-type zinc-finger protein

Query Match
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8
DB 359 KDDDDK 364

RESULT 60

T10862

phaseolin G-box binding protein pg2 - kidney bean (fragment)

C/Species: Phaseolus vulgaris (kidney bean)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004

C/Accession: T10862

R/Kawagoe, Y.; Murai, N.
Plant Physiol. 117, 720, 1998

A/Title: FBP2, a second bHLH protein binding to the E-box motif of the bean seed-storage

A/Reference number: Z17191

A/Accession: T10862

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-614 <K>W>

A/Cross-references: UNIPROT:Q41102; UNIPARC:UPI00000A8095; EMBL:U18349; NID:G1142620; PI

A/Experimental source: strain Contender

C/Genetics:

A/Status: PG2

A/Function:

A/Description: transcription factor

C/Superfamily: BHLH containing MYC-related DNA binding protein

Query Match
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 YKDDDDK 8
DB 43 YKDDDDK 49

RESULT 61

T13674

hypothetical protein EG0002.1 - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T13674
R/Bolsakov, V.; Borkova, D.; Minna, B.; Kafatos, F.
submitted to the EMBL Data Library, September 1998

A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A/Reference number: Z17698

A/Accession: T13674

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-734 L>

A/Cross-references: UNIPROT:O77282; UNIPARC:UPI0000075017; EMBL:AL031130; PIDN:CAA20015

C/Genetics:

A/Map position: 2

A/Intons: 18/3; 46/1; 122/2

A/Note: EG:EG0002.1

C/Superfamily: peptide transport protein PEPT1

Query Match
Best Local Similarity 72.3%; Score 34; DB 2; Length 734;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 681 DFEDDDD 687

RESULT 62
T13673
hypothetical protein EG0002.1 - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T13673

R/Bolsakov, V.; Borkova, D.; Minna, B.; Kafatos, F.
submitted to the EMBL Data Library, September 1998

A/Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A/Reference number: Z17698

A/Accession: T13673

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-743 L>

A/Cross-references: UNIPROT:Q9W4P7; UNIPARC:UPI000016BB3A; EMBL:AL031130; PIDN:CAA20014

C/Genetics:

A/Map position: 2

A/Intons: 27/3; 55/1; 131/2

A/Note: EG:EG0002.1

C/Superfamily: peptide transport protein PEPT1

C/Keywords: alternative splicing

Query Match
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDD 7
DB 690 DFEDDDD 696

RESULT 63

A84833

hypothetical protein At2g40720 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: A84833

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyam, L.; Tallon, L.
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, .
Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; NID:20083487; PMID:1061197

A/Accession: A84833

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-860 <S>T>O>

A/Cross-references: UNIPROT:Q7XJN6; UNIPARC:UPI00001623FA; GB:AE002093; NID:g4895221; P
C/Species: Arabidopsis thaliana (mouse-ear cross)
A:Gene: At2g940720
A:Map position: 2

Query Match 72.3%; Score 34; DB 2; Length 860;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 464 DMKDDDD 470

RESULT 64
E96508
hypothetical protein T12C22.19 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: E96508
R/Theologus, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: E96508
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-936 <STO>
A/Cross-references: UNIPROT:Q9LPD9; UNIPARC:UPI00000AA9E4; GB:AE005173; NID:g8656002; P
C/Species: Arabidopsis thaliana (mouse-ear cross)
A:Gene: T12C22.19
A:Map position: 1
C/Superfamily: replication licensing factor MCM2; MCM homology

Query Match 72.3%; Score 34; DB 2; Length 936;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 183 DYDDEDD 189

RESULT 65
A41996
NF-kappa-B p50 subunit precursor p105 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C/Accession: A41996
R/Capobianco, A.J.; Chang, D.; Mostoslav, G.; Gilmore, T.D.
J. Virol. 66, 3758-3767, 1992
A>Title: p105, the NF-kappa-B p50 precursor protein, is one of the cellular proteins com
A/Reference number: A41996; MUID:92260650; PMID:11533881
A/Accession: A41996
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-984 <CMP>
A/Cross-references: UNIPROT:Q04861; UNIPARC:UPI000012DC52; GB:M66930; NID:g212525; P1DN
C/Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel hom
C/Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation
F/47-371/Domain: rel homology <REL>
F/366-370/Region: nuclear location signal
F/342/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 72.3%; Score 34; DB 2; Length 984;
Best Local Similarity 85.7%; Pred. No. 5.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 757 DYKDDDD 763

RESULT 66
T18257
phospholipase C - yeast (Candida albicans)
C/Species: Candida albicans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18257
R/Bennett, D.E.; McCreary, C.E.; Coleman, D.C.
Microbiology 144, 55-72, 1998
A>Title: Genetic characterization of a phospholipase C gene from Candida albicans: pres
A/Reference number: Z18844; MUID:98129081; PMID:9467900
A/Accession: T18257
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1099 <BER>
A/Cross-references: UNIPROT:O13433; UNIPARC:UPI000013BCA; EMBL:Y13975; NID:g2462981; P
C/Species: Candida albicans
A:Gene: PUC1
F/566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X h

Query Match 72.3%; Score 34; DB 2; Length 1099;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KDDDDK 8
Db 628 KDDDDK 633

RESULT 67
C96761
hypothetical protein T9L24.35 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C96761
R/Theologus, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: C96761
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1157 <STO>
A/Cross-references: UNIPROT:Q9FX39; UNIPARC:UPI000009E7EF; GB:AE005173; NID:g11120792;
C/Species: Arabidopsis thaliana (mouse-ear cross)
A:Gene: T9L24.35
A:Map position: 1

Query Match 72.3%; Score 34; DB 2; Length 1157;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 421 EYEDDD 427

RESULT 68
AF2005
RNA polymerase beta prime chain [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2005
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Accession: AF2005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1150 <KOR>
A:Cross-references: UNIPROT:P22705; UNIPARC:UPI00001655C2; GB:BA000019; PIDN:BAW77962.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: rpoC2
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain

Query Match 72.3%; Score 34; DB 2; Length 1350;
Best Local Similarity 71.4%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDD 7
|||:|
Db 1337 DYEDDDE 1343

RESULT 69
S63244
BNI1 protein - yeast (Saccharomyces cerevisiae)
A:Alternate names: protein N0646; protein YNL271C
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C:Accession: S63244; S63245; S48523; S60909; S65111
R:Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63235
A:Accession: S63244
A:Molecule type: DNA
A:Residues: 1-1553 <SEN>
A:Cross-references: UNIPROT:P41632; UNIPARC:UPI0000168B2A; EMBL:Z71547; MIPS:YNL271C
A:Experimental source: strain S288C
R:Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B.; Pierard, A.; Glanville, N.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63245
A:Accession: S63245
A:Molecule type: DNA
A:Residues: 987-1953 <MES>
A:Cross-references: UNIPARC:UPI000017B262; EMBL:Z71547; MIPS:YNL271C
A:Experimental source: strain S288C
R:Fares, H.F.; Pringle, J.R.
submitted to the EMBL Data Library, April 1994
A:Description: Synthetic lethals of CDC12.
A:Reference number: S48524
A:Accession: S48523
A:Molecule type: DNA
A:Residues: 1-937, 'A', 939-1429, 'C', 1431-1953 <FAR>
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:G1045236; PIDN:AAA4455.1; PI
R:Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV fr
A:Reference number: S60909
A:Accession: S60909
A:Molecule type: DNA
A:Residues: 1-1553 <SE2>
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:G1045236; PIDN:CAA63225.1; B
Yeast 12, 505-514, 1996
A:Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from SA
A:Reference number: S65111; MUID:96310631; PMID:8740425
A:Accession: S65111
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-1553 <SEN>
A:Cross-references: UNIPARC:UPI0000168B2A; EMBL:X92494; NID:G1045236; PIDN:CAA63225.1;
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: SGD:BNI1; SHE5; SYL39
A:Cross-references: SGD:S0005215; MIPS:YNL271C
A:Map position: 14L

Query Match 72.3%; Score 34; DB 2; Length 1953;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||:|
Db 849 DYKDDSK 856

RESULT 70
T18440
hypothetical protein C0425w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18440
R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z18935
A:Accession: T18440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4550 <LAW>
A:Cross-references: UNIPROT:O77336; UNIPARC:UPI0000110116; EMBL:Z98547; NID:el325376; I
C:Genetics:
A:Map position: 3
A:Note: C0425w

Query Match 72.3%; Score 34; DB 2; Length 4550;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||:|
Db 3543 DYKDDNDK 3550

RESULT 71
S76216
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76216
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A:Reference number: S74322, MUID:97061201; PMID:8905231
A:Accession: S76216
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-125 <KAN>
A:Cross-references: UNIPROT:P74379; UNIPARC:UPI00000C0B6F; EMBL:D90914; GB:AB001339; NI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

Query Match 70.2%; Score 33; DB 2; Length 125;
Best Local Similarity 62.5%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||:|

Db 44 DYQDDHDR 51

RESULT 72

JK0313

dnak-type molecular chaperone mag29 - house-dust mite (Dermatophagoides farinae)

N/Alternate names: mite allergen mag 29 protein

C/Species: Dermatophagoides farinae

C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 31-Dec-2004

C/Accession: JK0313; PC2125

R/Aki, T.; Fujikawa, A.; Wada, T.; Uyo, T.; Shigeta, S.; Murooka, Y.; Oka, S.; Ono, K.

J. Biochem. 115, 435-440, 1994

A/Title: Cloning and expression of cDNA coding for a new allergen from the house dust mite.

A/Reference number: JK0313; MUID:94334283; PMID:8056755

A/Accession: JK0313

A/Molecule type: mRNA

A/Residues: 1-145 <AKI1>

A/Cross-references: UNIPROT:P39674; UNIPARC:UPI000012EAE8; DDBJ:D17676; NID:9642918; PID

A/Note: the nucleotide sequence for this amino acid sequence is inconsistent with that of

A/Accession: PC2125

A/Molecule type: protein

A/Residues: 1-17 <AK2>

A/Cross-references: UNIPARC:UPI0000177D21

C/Genetics:

A/Gene: mag29

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: bcr protein

C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match

Best Local Similarity 70.2%; Score 33; DB 2; Length 145;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8

Db 14 YKEDDDK 20

RESULT 73

B46315

E4 protein - human papillomavirus type 4

C/Species: human papillomavirus type 4

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C/Accession: B46315

R/Doordat, J.; Comeran, I.; Gallimore, P.H.

Virology 172, 51-62, 1989

A/Title: Sequence divergence yet conserved physical characteristics among the E4 protein

A/Reference number: A46315; MUID:89370332; PMID:2549722

A/Accession: B46315

A/Molecule type: DNA

A/Residues: 1-147 <DOO>

A/Cross-references: UNIPARC:UPI00000F4EFO; GB:M28744; NID:9333136; PIDN:AAA47015.1; PID:

C/Superfamily: papillomavirus type 4 E4 protein

C/Keywords: early protein

Query Match

Best Local Similarity 70.2%; Score 33; DB 1; Length 147;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 78 DYEDDDK 85

RESULT 74

E69077

hypothetical protein MTH1578 - Methanobacterium thermoautotrophicum (strain Delta H)

C/Species: Methanobacterium thermoautotrophicum

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: E69077

R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

A/Reference number: A69000; MUID:98037514; PMID:9371463

A/Accession: E69077

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-151 <MTH>

A/Cross-references: UNIPROT:Q27619; UNIPARC:UPI000062BDE; GB:AE000918; GB:AE000666; NI

A/Experimental source: strain Delta H

C/Genetics:

A/Gene: MTH1578

Query Match

Best Local Similarity 70.2%; Score 33; DB 2; Length 151;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 6

Db 69 DYRDDDD 74

RESULT 75

S59766

hypothetical protein YPR101w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein P8283.11

C/Species: Saccharomyces cerevisiae

C/Date: 11-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C/Accession: S59766

R/Nelson, J.

submitted to the EMBL Data Library, July 1995

A/Description: The sequence of S. cerevisiae cosmid 8283.

A/Reference number: S59764

A/Accession: S59766

A/Molecule type: DNA

A/Residues: 1-175 <NEL>

A/Cross-references: UNIPROT:Q06091; UNIPARC:UPI0000531F2; EMBL:U32445; NID:9914969; PI

C/Superfamily: Saccharomyces cerevisiae hypothetical protein YPR101w

Query Match

Best Local Similarity 70.2%; Score 33; DB 2; Length 175;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 78 DFNDDDD 84

RESULT 76

A61442

translation elongation factor eEF-1 beta chain - pig (fragments)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: A61442

R/Ammons, R.; Schipper, A.; van Damme, H.; Kriek, J.; Moeller, W.

J. Protein Chem. 11, 404, 1992

A/Title: The primary structure of elongation factor 1beta from pig liver.

A/Reference number: A61442

A/Accession: A61442

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-188 <AMO>

A/Cross-references: UNIPROT:Q7M397; UNIPARC:UPI00001782A2

C/Superfamily: translation elongation factor eEF-1 beta chain; translation elongation f

QY	1	DKDDDD	7
Db	88	DSKDDDD	94

RESULT 77
T42013

conserved hypotheical protein SPPC645.03c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43013, T41520
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe CDVs.
A:Reference number: Z17323, MUID:99162722, PMID:9501991
A:Accession: T43013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <YOS>
A:Cross-references: UNIPROT:P78859; UNIPARC:UPI000013A6A4; EMBL:D89209; NID:g1749625; P
A:Experimental source: strain PR745
R:Wood, V.; Rejandream, M.A.; Barrell, B.G.; Rieger, M.
Submitted to the EMBL Data Library, March 1999
A:Reference number: Z22000
A:Accession: T41520
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-190 <WOO>
A:Cross-references: UNIPARC:UPI000013A6A4; EMBL:AL049498; PIDD:CA33899.1; GSPDB:GN00066
A:Experimental source: strain 972h-, cosmid c645
C:Genetics:
A:Gene: SPPC645.03c
A:Map position: 3
;Introns: 85/3

Query Match	70.2%;	Score 33;	DB 2;	Length 190;
Best Local Similarity	83.3%;	Pred. NO. 1.4e+02;		
Matches	5;	Conservative	1;	Mismatches 0;
				Indels

QY	1	DYKDD	6
		:	
Db	159	DYRDD	164

RESULT 78

FUN34 protein yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YAL014c
 C:Species: Saccharomyces cerevisiae
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: S36720
 R:Ouellete, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
 submitted to the EMBL Data Library, January 1993
 A:Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
 A:Reference number: S36711
 A:Accession: S36720
 A:Molecule type: DNA
 A:Residues: 1-205 <OE>
 A:Cross-references: UNIPROT:P31377; UNIPARC:UPI000013A006; EMBL:L05146; NID:g171851; PIR
 C:Genetics:
 A:Cross-references: MIPS:YAL014c
 A:Cross-references: SGD:S0000012
 ;Map position: 1L

Query Match	70.2%	Score 33;	DB 2;	Length 205;
Best Local Similarity	71.4%	Pred. No.	1.5e+02;	
Matches	5;	Conservative	2;	Mismatches 0;
				Gaps 0;

Qy	2	YKDDDK	8
		:	
Db	1.13	YKDDDEQ	1.15

RESULT 79
S25A37

translational elongation factor eEF-1 beta chain - human
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S25432; J01038; B61013; S15689
R.Sanders, J.; Maassen, J.A.; Amons, R.; Moeller, W.
Nucleic Acids Res. 19, 4551, 1991
A.Title: Nucleotide sequence of human elongation factor-1-beta cDNA.
A.Reference number: S25432; UID:91360360; PMID:1886777
A.Accession: S25432

A1:Residues: 1-225 <SNAP>
A1:Cross-references: UNIPROT:P24534, UNIPARC:UPI000000068; EMBL:660489; NID:g31099; PDB:1VON (from Kammer, H.; Klaudiny, J.; Zimmer, M.; Scheit, K.H. Biochem. Biophys. Res. Commun. 177, 312-317, 1991)
A1Title: Human elongation factor 1beta: cDNA and derived amino acid sequence.
A1Reference number: J01038, MUID:91254293; PMID:1710449
A1Accession: J01038

A:Residues: 1525 <NON>
A:Cross-references: UNIPARC:UPI00000000C68; GB:X60656; NID:g31134; PIDN:CMA43063.1; PID:
A:Experimental source: ovarian granulosa cells
A:Barw, G.; Kasmuss, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Geeser, B.;
Electrophoresis 11, 526-536, 1990
A:Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing
A:Reference number: A61002; MUID:91031404; PMID:1659755

A:Structure: preliminary
A:Molecule type: protein
A:Residues: 2-6, 'X', 'X', '56-60 <BAU>
A:Cross-references: UNIPARC:UPI0000174808; UNIPARC:UPI0000174805
C:Genetics: -----

A:Gene: GDB:ESF1B2
A:Cross-references: GDB:682589
A:Map position: 2pter-2qter
C:Superfamily: translation elongation factor eEF-1 beta chain; translation elongation factor F
C:Keywords: phosphoprotein; protein biosynthesis
F:2-225/Product: translation elongation factor eEF-1 beta chain #status predicted <MT>

Query Match	70.2%	Score	NC	DB	1	Length	225
Best Local Similarity	85.7%	Pred.	NC	1.5e+02			
Matches	6	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

QY	1	DYKDDDD	7
Db	94	DSKDDDD	100

RESULT 80

Translation elongation factor eEF-1 beta chain - rabbit
C/Species: *Oryctolagus cuniculus* (domestic rabbit)
C/Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #ext_change 09-Jul-2004
C/Accession: S62693; S62688; S37087
R/Chen, C.J., Traugh, J.A.,
Biochim. Biophys. Acta 1864, 303-311, 1995
A/Title: Expression of recombinant elongation factor 1 beta from rabbit in *Escherichia*
A/Reference number: S62688; MUID:96138552; PMID:8547218
A/Accession: S62693
A/Molecule type: mRNA
A/Residues: 1-225 <CH>
A/Cross-references: UNIPROT:P34826; UNIPARC:UPI0000178226; EMBL:X74728
A/Accession: S62688
A/Molecule type: protein
A/Residues: 80-91 <CHP>
A/Cross-references: UNIPARC:UPI00001782A7
R/Chen, C.J.
submitted to the EMBL Data Library, August 1993
A/Reference number: S37087
A/Accession: S37087

A:Molecule type: mRNA
A:Residues: 1-77, 'T', 79-225 <CHW>
A:Cross-references: UNIPARC:UPI000016C566; EMBL:X174728; NID:g398394; P1DN:CAAS2741.1; P1
C:Gene: EF1B
C:Function:
A:Pathway: protein biosynthesis
C:Superfamily: translation elongation factor eEF-1 beta chain; translation elongation fa
C:Keywords: GTP exchange; phosphoprotein
F:2-225/Product: translation elongation factor eEF-1 beta chain #status predicted <MAT>
F:97-105/Region: beta, beta and delta chain signature
F:106/Binding site: phosphate (Ser) (covalent) (by unidentified kinase) #status predicted

Query Match 70.2%; Score 33; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 94 DSKDDDD 100

RESULT 81
G90525
hypothetical protein MYPU 1110 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90525
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A9512; MUID:21267165; PMID:11353084
A:Accession: G90525
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <KIR>
A:Cross-references: UNIPROT:Q98R99; UNIPARC:UPI00000CTFF8; GB:AL445566; PID:g14089524; F
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU_1110
A:Genetic code: SGCS

Query Match 70.2%; Score 33; DB 2; Length 235;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 39 DYKDDDD 45

RESULT 82
H84905
homodomain transcription factor (ATHB-7) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
C:Accession: H84905
R:Lin, X.; Kail, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84905
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: UNIPROT:P46897; UNIPARC:UPI0000126233; GB:AB002093; NID:g3831442; P1
C:Genetics:
A:Gene: AT2g46680
A:Map position: 2
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 70.2%; Score 33; DB 2; Length 258;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 189 DYKDDDD 195

RESULT 83
A33470
fibroin light chain precursor - silkworm
C:Species: Bombyx mori (silkworm)
C>Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C:Accession: A33470; JH0580; S4145; S4146; S10622
R:Yamaguchi, K.; Kikuchi, Y.; Takagi, T.; Kikuchi, A.; Oyama, F.; Shimura, K.; Mizuno,
J. Mol. Biol. 210, 127-139, 1989
A>Title: Primary structure of the silk fibroin light chain determined by cDNA sequencin
A:Reference number: A33470; MUID:90064541; PMID:2585514
A:Accession: A33470
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-262 <YAM>
A:Cross-references: UNIPROT:P21828; UNIPARC:UPI000012A56D; GB:X17291; NID:g5920; P1DN:C
R:Kikuchi, Y.; Mori, K.; Suzuki, S.; Yamaguchi, K.; Mizuno, S.
Gene 110, 151-158, 1992
A>Title: Structure of the Bombyx mori fibroin light-chain-encoding gene: upstream sequen
A:Reference number: JH0580; MUID:92165053; PMID:1147033
A:Accession: JH0580
A:Molecule type: DNA
A:Residues: 1-45, 'R', 47-262 <KIK>
A:Cross-references: UNIPARC:UPI000016B892; GB:M76430; NID:g289362; P1DN:AAA27840.1; PID
A:Experimental source: strain J-139
A>Note: the authors translated the codon CGA for residue 46 as Ala
R:Mori, K.; Kikuchi, Y.; Honma-Waga, M.; Waga, S.; Mizuno, S.
submitted to the EMBL Data Library, October 1993
A:Description: Production of a chimeric fibroin light-chain polypeptide as a consequenc
A:Reference number: S41445
A:Accession: S41445
A:Molecule type: mRNA
A:Residues: 1-105, 'SMGSVTSLSLPANVYKIQDNIDGHTKRI', 'FTLVNLIARAYKNTAHVPSITKDFYRKI', 'TA
YKRMCE' <MORI>
A:Cross-references: UNIPARC:UPI0000077132; EMBL:Z26884; NID:g452377; P1DN:CAA81529.1; P
A:Experimental source: Nd-s mutant
A:Accession: S41446
A:Molecule type: mRNA
A:Residues: 1-105, 'SMGSVTSLSLPANVYKIQDNIDGHTKRI', 'FTLVNLIARAYKNTAHVPSITKDFYRKI', 'TA
YKRMCE' <MORI>
A:Cross-references: UNIPARC:UPI00007794F; EMBL:Z26885; NID:g452391; P1DN:CAA81530.1; P
A:Experimental source: Nd-sb mutant
R:Hui, C.; Suzuki, Y.; Kikuchi, Y.; Mizuno, S.
J. Mol. Biol. 213, 395-398, 1990
A>Title: Homodomain binding sites in the 5' flanking region of the Bombyx mori silk fi
A:Reference number: S10622; MUID:90278949; PMID:1972197
A:Accession: S10622
A:Molecule type: DNA
A:Residues: 1-12 <HUI>
A:Cross-references: UNIPARC:UPI0000178C89; GB:X53319; NID:g10893
A>Note: the complete translation is not shown
C:Comment: Silk fibroin is secreted from the posterior silk gland.
C:Genetics:
A:Insertions: 12/3; 40/2; 105/3; 153/3; 183/2; 231/3
C:Superfamily: fibroin light chain
C:Keywords: extracellular protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-26/Product: fibroin light chain #status predicted <MAT>

Query Match 70.2%; Score 33; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
Db 111 DSKDDDD 111

Db 48 DYVDDTK 55

RESULT 84

S47137
homeotic protein Atchb-7 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C/Accession: S47137; S52653
R/Soderman, E.; Mattsson, J.; Svensson, M.; Borklind, C.; Engstrom, P.
submitted to the EMBL Data Library, June 1992
A/Reference number: S47135
A/Accession: S47137
A/Molecule type: mRNA
A/Residues: 1-267 <SOE>
A/Cross-references: UNIPARC:UPI000016DA98; EMBL:X67032; NID:g493163; PIDD:CAA47425.1; PIR/Soderman, E.; Mattsson, J.; Svensson, M.; Borklind, C.; Engstrom, P.
Plant Mol. Biol. 26, 145-154, 1994
A/Title: Expression patterns of novel genes encoding homeodomain leucine-zipper proteins
A/Reference number: S52651; MUID:95035986; PMID:7948864
A/Accession: S52653
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 37-45, 'N', 47-133 <SOE>
A/Cross-references: UNIPARC:UPI000017A2CA; EMBL:X67032
C/Keywords: DNA binding; homeobox; leucine zipper; nucleus; transcription regulation
F/39-95/Domain: homeobox homology <HOX>

Query Match 70.2%; Score 33; DB 2; Length 267;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 198 DYEDDDN 204

RESULT 85

B86486
protein F2809.7 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B86486
R/Theologian, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: B86486
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-270 <STO>
A/Cross-references: UNIPROT:Q9S9S2; UNIPARC:UPI00000A508D; GB:AE005172; NID:96272376; PIR/C/Genetics:
A/Gene: F2809.7
A/Map position: 1

Query Match 70.2%; Score 33; DB 2; Length 270;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 257 FKDDDE 263

RESULT 86

T00737

myb-related protein F22013.32 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004
C/Accession: T00737
R/Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Cologian, A.; Becker, J.R.
submitted to the EMBL Data Library, April 1998
A/Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A/Reference number: Z14200
A/Accession: T00737
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-280 <SHI>
A/Cross-references: UNIPROT:O8GYP5; UNIPARC:UPI000000C547; EMBL:AC003981; NID:g3063438
A/Experimental source: cultivar Columbia
C/Genetics:
A/Gene: ATSP:F22013.32
A/Map position: 1
A/Introns: 45/1; 88/2
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
F/9-61/Domain: myb DNA-binding repeat homology <MYB1>
F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 70.2%; Score 33; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 236 DHEDDDD 242

RESULT 87

T51667
myb-related transcription factor MYB60 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C/Accession: T51667
R/Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A/Title: Towards functional characterisation of the members of the R2R3-MYB gene family
A/Reference number: Z14349; MUID:9839469; PMID:9839469
A/Accession: T51667
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-280 <KTA>
A/Cross-references: UNIPROT:Q9S8G0; UNIPARC:UPI000009EF40; EMBL:AF062895; PIDD:ACB8361;
A/Experimental source: cultivar Columbia
C/Genetics:
A/Gene: MYB60
A/Map position: 1
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C/Keywords: transcription factor

Query Match 70.2%; Score 33; DB 2; Length 280;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 236 DHEDDDD 242

RESULT 88

S49469
glucose-1-phosphate cytidyllyltransferase (EC 2.7.7.33) strQ - Streptomyces glaucescens
C/Species: Streptomyces glaucescens
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S49469
R/Beyer, S.; Mayer, G.M.; Piepersberg, W.
submitted to the EMBL Data Library, October 1994

A:Reference number: S49469
 A:Accession: S49469
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-299 <BBY>
 A:Cross-references: UNIPROT:Q54266; UNIPARC:UPI000008A7DC; EMBL:X82177; NID:G902359; PTD
 C:Superfamily: glucose-1-phosphate cytidyltransferase
 C:Keywords: nucleotidyltransferase

Query Match 70.2%; Score 33; DB 2; Length 299;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 DB 206 DYKDDDK 213

RESULT 89
 G95244
 hypothetical protein SP2093 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95244
 R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 nson, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G95244
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-322 <KUR>
 A:Cross-references: UNIPROT:Q97NF0; UNIPARC:UPI0000051AFB; GB:AE005672; PIDN:AAK76152.1;
 A:Experimental source: strain TIGR4
 C:Genetics:

A:Gene: SP2093

Query Match 70.2%; Score 33; DB 2; Length 322;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 DB 127 DYKDDDK 134

RESULT 90
 T20033
 hypothetical protein CATG2.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20033
 R:Palmer, S.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: Z19213
 A:Accession: T20033
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-333 <WIL>
 A:Cross-references: UNIPROT:Q18694; UNIPARC:UPI0000080191; EMBL:Z49125; PIDN:CAA88935.1;
 A:Experimental source: clone CATG2
 C:Genetics:

A:Gene: CBSP:C47G2.2
 A:Map position: 2
 A:Introns: 113/2; 222/2

Query Match 70.2%; Score 33; DB 2; Length 333;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 7
 DB 101 DAKDDDD 107

RESULT 91
 S16321
 light-induced protein CPR-2 - parsley
 C:Species: Petroselinum crispum (parsley)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
 C:Accession: S16321
 R:Weishaar, B.; Armstrong, G.A.; Block, A.; da Costa e Silva, O.; Hahlbrock, K.
 EMB J. 10, 1777-1786, 1991
 A:Title: Light-inducible and constitutively expressed DNA-binding proteins recognizing
 A:Reference number: S16320; MUID:91266906; PMID:2050115
 A:Accession: S16321
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-393 <WEI>
 A:Cross-references: UNIPROT:Q99090; UNIPARC:UPI00001794P2; EMBL:X58577
 C:Superfamily: BZIP protein; fos/jun DNA-binding domain homology
 C:Keywords: DNA binding; nucleus; transcription regulation
 F:185-225/Domain: fos/jun DNA-binding domain homology <FID>

Query Match 70.2%; Score 33; DB 2; Length 393;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 DB 168 DHSDDDE 175

RESULT 92
 AH1387
 cell wall binding proteins homolog lmo2504 [imported] - Listeria monocytogenes (strain
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AH1387
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fath, H
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuzepkat, G.; Madueno, E.; Maitournam, A.; M
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AH1387
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-436 <GLA>
 A:Cross-references: UNIPROT:Q6Y4E2; UNIPARC:UPI0000055221; GB:NC_003210; PIDN:CAD00582.
 A:Experimental source: strain EGD-e
 C:Genetics:

A:Gene: lmo2504

Query Match 70.2%; Score 33; DB 2; Length 436;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 DB 168 DQKDDDK 175

RESULT 93
 T40337
 probable saccharopine dehydrogenase (NADP, L-glutamate-forming) (EC 1.5.1.10) [similari
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40337
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.; Pohl, T.
 submitted to the EMBL Data Library, March 1998

A:Reference number: Z21921
A:Accession: T40337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-450 <LVN>
A:Cross-references: UNIPROT:O59711; UNIPARC:UPI0000069880; EMBL:AL022244; PIDN:CAA18292.
A:Experimental source: strain 972h-; cosmid G3B8
C:Genetics:
A:Gene: SPDB:SPBC388.03
A:Map position: 2
C:Keywords: oxidoreductase

Query Match 70.2%; Score 33; DB 2; Length 450;
Best Local Similarity 71.4%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YKDDDDK 8
Db 308 FKEDDDK 314

RESULT 94
D81224
Cataloge (BC 1.11.1.6) NMA0050 [similarity] - Neisseria meningitidis (strain MCS8 serogr
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81224; C81996
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizze, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81224
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-504 <TER>
A:Cross-references: UNIPROT:Q9URF5; UNIPARC:UPI00000C4PD7; GB:AE002379; GB:AE002098; NID
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: C81996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-504 <PAR>
A:Cross-references: UNIPARC:UPI00000C4AD7; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: katA; NMB0216; NMA0050
C:Superfamily: catalase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:59,99,133/Active site: His, Thr, Asn #status predicted
F:342/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 70.2%; Score 33; DB 2; Length 504;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
Db 416 DYKDDDD 422

RESULT 95
S26606
myb-related protein 3 - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C:Date: 25-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S26606

R:Avila, J.; Nieto, C.; Canas, L.; Benito, M.; Paz-Ares, J.
submitted to the EMBL data library, July 1992
A:Description: Petunia hybrida genes related to the maize regulatory C1 gene and to an
A:Reference number: S26604
A:Accession: S26606
A:Molecule type: DNA
A:Residues: 1-517 <AVI>
A:Cross-references: UNIPROT:Q02994; UNIPARC:UPI000009D660; EMBL:Z13998; NID:G20564; PIL
A:Experimental source: strain v26, developing flowers
C:Superfamily: petunia myb-related protein 3; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:25-77/Domain: myb DNA-binding repeat homology <MYB1>
F:78-126/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 70.2%; Score 33; DB 1; Length 517;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YKDDDDK 8
Db 457 YEDEDK 463

RESULT 96
A48341
nucleocapsid protein - parainfluenza virus type 1 (strains A1426, 86-315, 62M-753)
N:Alternate names: nucleoprotein
C:Species: parainfluenza virus type 1
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A48341
R:Myahara, K.; Kitada, S.; Yoshimoto, M.; Matsumura, H.; Kawano, M.; Komada, H.; Tsu
Arch. Virol. 124, 255-268, 1992
A:Title: Molecular evolution of human paramyxoviruses. Nucleotide sequence analyses of
human paramyxoviruses.
A:Reference number: A48341; MUID:92296894; PMID:1605738
A:Accession: A48341
A:Molecule type: genomic RNA
A:Residues: 1-524 <MY>
A:Cross-references: UNIPROT:P36354; UNIPARC:UPI000012PDPD; GB:S38060; NID:G250340; PIDN
A>Note: Sequence extracted from NCBI backbone (NCBIN:106078, NCBI:P106079)
C:Genetics:
A:Gene: NP
C:Superfamily: paramyxovirus nucleocapsid protein
C:Keywords: nucleocapsid; nucleoprotein

Query Match 70.2%; Score 33; DB 1; Length 524;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
Db 508 DYENDDD 514

RESULT 97
VHNZT1
nucleocapsid protein - parainfluenza virus type 1
N:Alternate names: nucleoprotein
C:Species: parainfluenza virus type 1
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A38401
R:Lyn, D.; Gill, D.S.; Scroggs, R.A.; Portner, A.
J. Gen. Virol. 72, 983-987, 1991
A:Title: The nucleoproteins of human parainfluenza virus type 1 and Sendai virus share
A:Reference number: A38401; MUID:91202138; PMID:11707951
A:Accession: A38401
A:Molecule type: mRNA
A:Residues: 1-524 <LVN>
A:Cross-references: UNIPROT:P26590; UNIPARC:UPI000012PDPF; GB:D01070; NID:G222271; PIDN
C:Superfamily: paramyxovirus nucleocapsid protein
C:Keywords: nucleocapsid; nucleoprotein

Query Match 70.2%; Score 33; DB 1; Length 524;

Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 508 DYENDD 514

RESULT 98

A89830
arginyl-tRNA synthetase [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: A89830
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Itoh, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; PMID:21311952; PMID:11418146
A/Accession: A89830
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-553 <KUR>
A/Cross-references: UNIPROT:Q99W05; UNIPARC:UPI0000030ADB; GB:BA000018; PTD:913700499; F
A/Experimental source: strain N315
C/Genetics:
A/Gene: argS
C/Superfamily: Bacillus arginine-tRNA ligase

Query Match 70.2%; Score 33; DB 2; Length 553;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|:|||||
Db 296 DFKDDKDR 303

RESULT 99

C71529
hypothetical protein CT326 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: C71529
R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A/Reference number: A71570; PMID:9900809; PMID:9784136
A/Accession: C71529
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-563 <ARN>
A/Cross-references: UNIPROT:O84328; UNIPARC:UPI00000C0B2F; GB:AE001305; GB:AE001273; NIT
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: CT326

Query Match 70.2%; Score 33; DB 2; Length 563;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 30 DFKDDDD 36

RESULT 100

T06648
hypothetical protein T6G15.10 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06648

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15791

A/Accession: T06648
A/Molecule type: DNA
A/Residues: 1-650 <BEV>
A/Cross-references: UNIPROT:Q9T0G7; UNIPARC:UPI00000A733C; EMBL:AL049656; GSPDB:GN00062
A/Experimental source: cultivar Columbia; BAC clone T6G15
C/Genetics:
A/Gene: ATSP:T6G15.10
A/Map position: 4

Query Match 70.2%; Score 33; DB 2; Length 650;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
|:|||||
Db 259 YEDDDQ 265

Search completed: June 29, 2006, 11:41:16
Job time : 54 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:32:11 ; Search time 295 Seconds
(without alignments)
25.085 Million cell updates/sec

Title: US-10-671-054-2
Perfect score: 47
Sequence: 1 DYKDDDK 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 500 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	47	1	SCKA_PANIN
2	47	100.0	319	2	Q8NF66_HUMAN
3	43	91.5	246	2	Q36046_MARBY
4	42	89.4	154	2	Q4X9J6_PLACH
5	42	89.4	284	2	Q7Y283_PLACH
6	42	89.4	586	2	Q6FN57_PLACH
7	42	89.4	603	2	Q2PEW5_TRIPR
8	42	89.4	1385	2	Q6FK24_CANGA
9	41	87.2	399	2	Q91BJ4_NPVST
10	41	87.2	423	1	SPR28_YEAST
11	41	87.2	452	2	Q21WZ5_RHOPA
12	40	85.1	1767	2	Q6VZM2_CNPV
13	39	83.0	322	2	Q8JJK5_VIRIR
14	39	83.0	432	2	Q4N797_THERPA
15	39	83.0	506	2	Q7U0Z7_RHOBA
16	39	83.0	561	1	CWC25_YARLI
17	39	83.0	648	1	Q54DA4_DICDI
18	39	83.0	706	2	Q8XMT9_CLOPE
19	39	83.0	1254	2	Q54UV0_DICDI
20	38	80.9	110	2	Q46VH5_RALEJ
21	38	80.9	125	2	Q5C0A2_CRYPV
22	38	80.9	154	2	Q9FM73_ARATH
23	38	80.9	171	2	Q8D4G1_VIBUV
24	38	80.9	235	2	Q76542_DICDI
25	38	80.9	242	2	Q8L7V6_ARATH
26	38	80.9	265	2	Q4X8B5_PLACH
27	38	80.9	294	2	Q9LJY8_ARATH
28	38	80.9	301	2	Q54VA8_DICDI
29	38	80.9	306	2	VHCG_METVO
30	38	80.9	332	2	Q5AF51_CANAL
31	38	80.9	369	2	Q4XYM1_PLACH

32	38	80.9	416	2	Q5F360_CHICK	Q5F360_gallus gall
33	38	80.9	418	2	Q5ZKN5_CHICK	Q5ZKN5_gallus gall
34	38	80.9	418	2	Q8OHJ7_CHICK	Q8OHJ7_gallus gall
35	38	80.9	475	2	Q4X0E6_PLACH	Q4X0E6_plasmidium
36	38	80.9	565	1	MAOI_YERPE	Q82909_yersinia pe
37	38	80.9	565	1	MAOI_YERPE	Q66C80_yersinia ps
38	38	80.9	587	1	DEH2_KLULA	Q6C890_kluyveromyc
39	38	80.9	588	2	Q55CB4_DICDI	Q55CB4_dictyosteli
40	38	80.9	590	2	Q6BYD0_DEBHA	Q6BYD0_debaryomyce
41	38	80.9	629	2	Q2UGP9_ASFOR	Q2UGP9_aspergillus
42	38	80.9	782	2	Q2UF79_ASFOR	Q2UF79_aspergillus
43	38	80.9	804	2	Q3QT20_RHOB	Q3QT20_silicibacte
44	38	80.9	823	2	Q96505_DROME	Q96505_drosophila
45	38	80.9	823	2	Q9VK34_DROME	Q9VK34_drosophila
46	38	80.9	862	2	Q4Y0Z6_PLACH	Q4Y0Z6_plasmidium
47	38	80.9	926	2	Q6CG65_YARLI	Q6CG65_yarrowia li
48	38	80.9	1018	2	Q41609_GIBZE	Q41609_gibberella
49	38	80.9	1085	1	IFH1_YEAST	Q35520_saccharomyc
50	38	80.9	1212	2	Q4P6M8_USTMA	Q4P6M8_ustilago ma
51	38	80.9	1228	2	Q7MXW4_PORGI	Q7MXW4_porphyromon
52	38	80.9	1267	2	Q81LD1_PLAF7	Q81LD1_plasmidium
53	38	80.9	1277	1	PDS5_YEAST	Q04264_saccharomyc
54	38	80.9	1305	2	Q6FNZ8_CANGA	Q6FNZ8_candida gla
55	38	80.9	1523	2	Q813B1_PLAF7	Q813B1_plasmidium
56	38	80.9	1687	2	Q81BA8_PLAF7	Q81BA8_plasmidium
57	38	80.9	1818	2	Q4XUN1_PLACH	Q4XUN1_plasmidium
58	38	80.9	1921	2	Q4URC4_THEAN	Q4URC4_thelateria a
59	38	80.9	2051	2	Q5ASE7_EMENT	Q5ASE7_aspergillus
60	38	80.9	2067	1	B1MB_EMENT	Q5ASE7_aspergillus
61	38	80.9	2226	2	Q97225_PLAF7	P33144_emicellia
62	38	80.9	2384	2	Q5KID7_CRYNE	Q5KID7_cryptococcu
63	38	80.9	2432	2	Q55U02_CRYNE	Q55U02_cryptococcu
64	38	80.9	2577	2	Q81AM1_PLAF7	Q81AM1_plasmidium
65	37	78.7	119	2	Q8ST86_PLAF7	Q8ST86_plasmidium
66	37	78.7	132	2	Q6S8S9_PLAF7	Q6S8S9_plasmidium
67	37	78.7	136	2	Q7RB94_PLAYO	Q7RB94_plasmidium
68	37	78.7	142	2	Q4Y0T6_PLACH	Q4Y0T6_plasmidium
69	37	78.7	164	2	Q5TKF1_ORYSA	Q5TKF1_oryza sativ
70	37	78.7	168	2	Q4Y3M3_PLACH	Q4Y3M3_plasmidium
71	37	78.7	179	2	Q2ZAB1_GGAMM	Q2ZAB1_sheawellia
72	37	78.7	179	2	Q35Y65_GGAMM	Q35Y65_sheawellia
73	37	78.7	179	2	Q8EFW6_SHEON	Q8EFW6_sheawellia
74	37	78.7	179	2	Q366F4_GGAMM	Q366F4_sheawellia
75	37	78.7	197	2	Q2M3Y9_PHYIN	Q2M3Y9_phytophthor
76	37	78.7	225	2	Q4Z415_PLABE	Q4Z415_plasmidium
77	37	78.7	259	2	Q5CEP3_CRYPV	Q5CEP3_cryptospori
78	37	78.7	268	2	Q74H22_LACDO	Q74H22_lactobacilli
79	37	78.7	299	2	Q54U43_DICDI	Q54U43_dictyosteli
80	37	78.7	335	2	Q38DT4_9TRYR	Q38DT4_rypanosoma
81	37	78.7	341	2	Q6C9S5_YARLI	Q6C9S5_yarrowia li
82	37	78.7	351	1	BROMI_TANCO	Q023791_ananas como
83	37	78.7	364	1	BAMT_ANTWA	Q91Y29_antirrhinum
84	37	78.7	451	2	Q53LKL_ORYSA	Q53LKL_oryza sativ
85	37	78.7	452	1	TIG_RHOBA	Q65112_rhodospseudo
86	37	78.7	485	2	Q2R949_ORYSA	Q2R949_oryza sativ
87	37	78.7	487	2	Q6BVV5_DEBHA	Q6BVV5_debaryomyce
88	37	78.7	487	2	Q56XW8_ARATH	Q56XW8_arabidopsis
89	37	78.7	497	1	VE2_HP20	Q56XW8_arabidopsis
90	37	78.7	513	2	Q9SX72_ARATH	Q9SX72_human papil
91	37	78.7	524	2	Q59NM9_CANAL	Q59NM9_candida alb
92	37	78.7	554	2	Q8IEG8_PLAF7	Q8IEG8_plasmidium
93	37	78.7	567	2	Q5UIJ8_ORYSA	Q5UIJ8_oryza sativ
94	37	78.7	664	2	Q61OD3_CABER	Q61OD3_cenochadai
95	37	78.7	690	2	Q5AAB5_CANAL	Q5AAB5_candida alb
96	37	78.7	690	2	Q6VZ25_CNPV	Q6VZ25_canarypok v
97	37	78.7	691	2	Q5AAZ7_CANAL	Q5AAZ7_candida alb
98	37	78.7	697	2	Q54D84_DICDI	Q54D84_dictyosteli
99	37	78.7	700	2	Q5A932_CANAL	Q5A932_candida alb
100	37	78.7	702	2	Q4N9L1_THERPA	Q4N9L1_thelateria p
101	37	78.7	720	2	Q55WAB_CRYNE	Q55WAB_cryptococcu
102	37	78.7	721	2	Q97LFB_CLOAB	Q97LFB_clostridium
103	37	78.7	723	2	Q3YTB6_EHRCZ	Q3YTB6_ericthia c
104	37	78.7	724	2	Q5KJZ0_CRYNE	Q5KJZ0_cryptococcu

105	37	78.7	741	1	PL0D3_MOUSE	Q9r0e1	mus	musculu	178	36	76.6	334	2	Q9L1V4_ORYSA	Q9L1V4	oryza	sativ
106	37	78.7	741	2	O542E0_MOUSE	O542E0	m 2 days ne		179	36	76.6	357	2	O5BLI6_BRARE	O5BLI6	brachydanio	
107	37	78.7	783	2	O2V3C9_ARATH	O2V3C9	arabidopsis		180	36	76.6	366	2	O3BR73_ORYSA	O3BR73	trypanosoma	
108	37	78.7	824	2	O55BX2_DICDI	O55BX2	dicystosell		181	36	76.6	370	2	O7R9U0_PLAYO	O7R9U0	plasmodium	
109	37	78.7	827	2	Q7Q0Z9_ARATH	Q7Q0Z9	anopheles g		182	36	76.6	378	2	O55G67_DICDI	O55G67	dicystosell	
110	37	78.7	859	2	Q4DLMO_TRYCR	Q4dlm0	trypanosoma		183	36	76.6	383	2	O6C5D9_YARLI	O6C5D9	yarrowia 11	
111	37	78.7	869	2	O528F2_ORYSA	O528F2	oryza sativ		184	36	76.6	393	2	O9VDD0_DROME	O9VDD0	trypanosoma	
112	37	78.7	870	1	PANK2_ARATH	PANK2	arabidopsis		185	36	76.6	411	2	O6ZIK7_ORYSA	O6ZIK7	oryza sativ	
113	37	78.7	871	2	O6LPR8_ARATH	O6LPR8	arabidopsis		186	36	76.6	419	2	O2S776_PLAFA	O2S776	plasmodium	
114	37	78.7	885	2	O6CFR2_YARLI	O6CFR2	yarrowia 11		187	36	76.6	420	2	O2ZDS3_CALSA	O2ZDS3	caldicellul	
115	37	78.7	894	2	O8I5I1_PLAFA	O8I5I1	plasmodium		188	36	76.6	421	2	O3B2K1_9TRYP	O3B2K1	trypanosoma	
116	37	78.7	906	2	O97262_PLAFA	O97262	homarus ame		189	36	76.6	422	2	O86AN7_DICDI	O86AN7	dicystosell	
117	37	78.7	936	2	O95VU2_HOMAM	O95VU2	homarus ame		190	36	76.6	427	2	O54YR3_DICDI	O54YR3	dicystosell	
118	37	78.7	942	2	O9FMJ7_ARATH	O9fmj7	arabidopsis		191	36	76.6	434	2	O4QAI2_LEIMA	O4QAI2	leishmania	
119	37	78.7	970	2	O2OV65_ORYSA	O2OV65	oryza sativ		192	36	76.6	442	2	O5JLE4_ORYSA	O5JLE4	oryza sativ	
120	37	78.7	985	2	O8B9I7_NPVRO	O8b9i7	rachiplusia		193	36	76.6	446	2	O753Y9_ASHGO	O753Y9	ashbya goss	
121	37	78.7	1038	2	O54UJ3_DICDI	O54UJ3	dicystosell		194	36	76.6	452	2	O7ZXV8_XENLA	O7ZXV8	xenopus lae	
122	37	78.7	1088	2	O4PIJ4_USTMA	O4pij4	ustiliago ma		195	36	76.6	453	2	O6P368_XENTR	O6P368	xenopus tro	
123	37	78.7	1137	2	O4I9I7_GIBZE	O4I9I7	gibberella		196	36	76.6	458	2	O9W4D3_DROME	O9W4D3	trypanosoma	
124	37	78.7	1159	2	O5CS80_CRYPV	O5CS80	cryptospori		197	36	76.6	463	2	O5CST6_CRYPV	O5CST6	cryptospori	
125	37	78.7	1169	2	O5CJY3_CRYHO	O5CJY3	cryptospori		198	36	76.6	464	2	O2OXZ5_ORYSA	O2OXZ5	oryza sativ	
126	37	78.7	1210	2	O5YWM4_CANAL	O5YWM4	candida alb		199	36	76.6	472	2	O6BID3_DEBHA	O6BID3	debaromyce	
127	37	78.7	1287	2	O7RMJ4_PLAYO	O7rmj4	plasmodium		200	36	76.6	475	2	O5SGI8_DICDI	O5SGI8	dicystosell	
128	37	78.7	1299	2	O4P8T6_USTMA	O4P8T6	ustiliago ma		201	36	76.6	479	2	O5STK6_CRYNE	O5STK6	cryptococcu	
129	37	78.7	1313	2	O8IB25_PLAFA	O8IB25	plasmodium		202	36	76.6	479	2	O5KIT9_CRYNE	O5KIT9	cryptococcu	
130	37	78.7	1377	2	O54WG7_DICDI	O54WG7	dicystosell		203	36	76.6	485	2	O9LXL1_ARATH	O9LXL1	arabidopsis	
131	37	78.7	1382	2	O4IOG4_GIBZE	O4IOG4	gibberella		204	36	76.6	486	2	O8LGB1_ARATH	O8LGB1	arabidopsis	
132	37	78.7	1468	2	O8GU85_ORYSA	O8GU85	oryza sativ		205	36	76.6	493	2	O9FHI9_ARATH	O9FHI9	arabidopsis	
133	37	78.7	1482	2	O8I4X9_PLAFA	O8I4X9	plasmodium		206	36	76.6	495	2	O6K1I4_PICHO	O6K1I4	picophyllus	
134	37	78.7	1482	2	O8H7L0_ORYSA	O8H7L0	oryza sativ		207	36	76.6	496	2	O4DFK6_TRYCR	O4DFK6	trypanosoma	
135	37	78.7	1618	2	O8I5I3_PLAFA	O8I5I3	plasmodium		208	36	76.6	519	2	O5ALV8_CANAL	O5ALV8	candida alb	
136	37	78.7	2200	2	O54MP8_DICDI	O54MP8	dicystosell		209	36	76.6	521	2	O4I3V7_GIBZE	O4I3V7	gibberella	
137	37	78.7	2221	2	O8I2S9_PLAFA	O8I2S9	plasmodium		210	36	76.6	521	2	O9CUB8_MOUSE	O9CUB8	mus musculu	
138	37	78.7	2491	2	O4YNO6_PLAFA	O4YNO6	plasmodium		211	36	76.6	523	2	O772J8_DROME	O772J8	drosophila	
139	37	78.7	2598	2	O7RNO6_PLAYO	O7rno6	plasmodium		212	36	76.6	533	2	O6S6E1_ORYSA	O6S6E1	oryza sativ	
140	37	78.7	2605	2	O8ID88_PLAFA	O8ID88	plasmodium		213	36	76.6	537	2	O5SGO0_DICDI	O5SGO0	dicystosell	
141	36	76.6	24	2	O6KY77_PICHO	O6ky77	picophyllus		214	36	76.6	567	2	O3U7D5_MOUSE	O3U7D5	mus musculu	
142	36	76.6	77	2	O9ZTN5_PETHY	O9ZTN5	petunia hyb		215	36	76.6	572	2	O54A06_DICDI	O54A06	candida alb	
143	36	76.6	116	2	O16579_CABEL	O16579	caenorhabdi		216	36	76.6	573	2	O54R06_DICDI	O54R06	dicystosell	
144	36	76.6	122	2	O3BGE1_PLAFA	O3BGE1	plasmodium		217	36	76.6	577	2	O54WX8_DICDI	O54WX8	dicystosell	
145	36	76.6	122	2	O3BGE9_PLAFA	O3BGE9	plasmodium		218	36	76.6	591	2	O7S883_NEUCR	O7S883	neutrospora	
146	36	76.6	122	2	O3BIT2_PLAFA	O3BIT2	plasmodium		219	36	76.6	596	2	O3J7B6_ORYSA	O3J7B6	oryza sativ	
147	36	76.6	122	2	O3BJR0_PLAFA	O3BJR0	plasmodium		220	36	76.6	616	2	O5APB5_CANAL	O5APB5	candida alb	
148	36	76.6	145	2	O922Q2_MOUSE	O922Q2	mus musculu		221	36	76.6	633	2	O54IL9_DICDI	O54IL9	dicystosell	
149	36	76.6	156	2	O7XEA8_ORYSA	O7XEA8	oryza sativ		222	36	76.6	634	2	O569P4_BRAAE	O569P4	brachydanio	
150	36	76.6	177	1	SIVA_RAT	P59692	rattus norv		223	36	76.6	636	2	O2MOM9_DROS	O2MOM9	drosophila	
151	36	76.6	194	2	O6OF49_ORYSA	O6OF49	oryza sativ		224	36	76.6	638	2	O2UFL4_ASPPR	O2UFL4	aspepgillus	
152	36	76.6	195	2	O5I6B1_BOREU	O5I6B1	borrelia bu		225	36	76.6	644	2	O6LSV3_PHOFR	O6LSV3	photobacter	
153	36	76.6	197	2	O2RYO5_9SPHI	O2RYO5	salinibacte		226	36	76.6	653	2	O86KR4_DICDI	O86KR4	dicystosell	
154	36	76.6	202	2	O5NFD0_FRATY	O5NFD0	franciseila		227	36	76.6	660	2	O5AEE0_CANAL	O5AEE0	candida alb	
155	36	76.6	203	2	O54CW8_DICDI	O54CW8	dicystosell		228	36	76.6	670	2	O8MTJ1_DROME	O8MTJ1	drosophila	
156	36	76.6	206	2	O6DGA7_BRARE	O6DGA7	brachydanio		229	36	76.6	675	2	O9VTX7_DROME	O9VTX7	drosophila	
157	36	76.6	210	2	O6FTC6_CANCA	O6FTC6	candida gla		230	36	76.6	699	2	O5BHV4_DROME	O5BHV4	drosophila	
158	36	76.6	211	2	O5OMG9_ENTHI	O5OMG9	entamoeba h		231	36	76.6	699	2	O2LYT2_DROS	O2LYT2	drosophila	
159	36	76.6	211	2	O5ONP8_ENTHI	O5ONP8	entamoeba h		232	36	76.6	713	2	O8ID82_PLAFA	O8ID82	plasmodium	
160	36	76.6	214	2	O7PJZ7_ANOGA	O7PJZ7	anopheles g		233	36	76.6	734	2	O6R3N8_MAIZE	O6R3N8	rattus norv	
161	36	76.6	222	2	O6MY92_ASPTU	O6MY92	aspepgillus		234	36	76.6	734	2	O6R3N8_MAIZE	O6R3N8	zea mays (m	
162	36	76.6	227	2	O8IL59_PLAFA	O8IL59	plasmodium		235	36	76.6	738	1	PIOD3_HUMAN	PIOD3	homo sapien	
163	36	76.6	229	2	O4BSH6_LISMO	O4BSH6	listeria mo		236	36	76.6	738	2	PIOD3_PONPY	PIOD3	pongy pygma	
164	36	76.6	232	2	O5ASB3_EMENT	O5ASB3	aspergillus		237	36	76.6	741	1	O5R8K5_PONPY	O5R8K5	pongy pygma	
165	36	76.6	236	2	O2XR60_PLAFA	O2XR60	plasmodium		238	36	76.6	750	2	O9YOJ3_9ALPH	O9YOJ3	suid herpes	
166	36	76.6	278	2	O7SGQ0_NEUCR	O7SGQ0	neutrospora		239	36	76.6	752	2	O6LKL3_PHOFR	O6LKL3	photobacter	
167	36	76.6	289	2	O36S45_SECCR	O36S45	seccale cere		240	36	76.6	760	2	O22907_ARATH	O22907	arabidopsis	
168	36	76.6	290	2	O8T4S9_AEDAE	O8T4S9	aedes aegypt		241	36	76.6	788	2	O7RAU2_PLAFA	O7RAU2	plasmodium	
169	36	76.6	290	2	O8T4T0_AEDAE	O8T4T0	aedes aegypt		242	36	76.6	789	2	O6BKX0_DEBHA	O6BKX0	debaromyce	
170	36	76.6	290	2	O8T4T1_AEDAE	O8T4T1	aedes aegypt		243	36	76.6	796	2	O6BKX0_DEBHA	O6BKX0	debaromyce	
171	36	76.6	290	2	O8T4T2_AEDAE	O8T4T2	aedes aegypt		244	36	76.6	796	1	BUD27_YEAST	BUD27	saccharomyc	
172	36	76.6	290	2	O95P61_AEDAE	O95P61	aedes aegypt		245	36	76.6	801	2	O8NC87_HUMAN	O8NC87	homo sapien	
173	36	76.6	290	2	O9BJW8_AEDAE	O9BJW8	aedes aegypt		246	36	76.6	804	2	O59ZG4_CANAL	O59ZG4	candida alb	
174	36	76.6	300	2	O4E0O5_TRYCR	O4E0O5	trypanosoma		247	36	76.6	804	2	O59ZM8_CANAL	O59ZM8	candida alb	
175	36	76.6	312	2	O36S46_SECCR	O36S46	seccale cere		248	36	76.6	819	2	O54TR9_DICDI	O54TR9	dicystosell	
176	36	76.6	314	2	O4DCF4_TRYCR	O4DCF4	trypanosoma		249	36	76.6	822	2	O7XCT3_ORYSA	O7XCT3	oryza sativ	
177	36	76.6	318	2	O5ALF1_CANAL	O5ALF1	candida alb		250	36	76.6	822	2	O94HZ3_ORYSA	O94HZ3	oryza sativ	

251	36	76.6	825	2	Q6D1Y4_ERWCT	Q6d1y4 erwinia car	324	35	74.5	151	1	HSP18_CLOAB	003928_clostridium
252	36	76.6	844	2	Q6BT18_DEBHA	Q6bt18 debaryomyce	325	35	74.5	156	2	OSX233_BORSA	05x233 borrelia ga
253	36	76.6	853	2	Q59V55_CANAL	Q59v55 candida alb	326	35	74.5	163	2	Q8MZM8_TRESO	Q8mzm8 taenia soli
254	36	76.6	865	2	Q54G58_DICDI	Q54g58 dictyosteli	327	35	74.5	175	2	Q4XAS8_PLACH	Q4xas8 plasmodium
255	36	76.6	894	2	Q54Y56_DICDI	Q54y56 dictyosteli	328	35	74.5	181	2	Q3E122_ACTSC	Q3e122 actinobacill
256	36	76.6	899	2	Q81BN8_PLAF7	Q81bn8 plasmodium	329	35	74.5	192	2	Q5XV07_ARATH	Q5xv07 arabidopsis
257	36	76.6	912	2	Q4CP12_TRYCR	Q4cp12 trypanosoma	330	35	74.5	193	2	Q9FK94_ARATH	Q9fk94 arabidopsis
258	36	76.6	917	2	Q5SB17_MAIZE	Q5sb17 zea mays (m	331	35	74.5	204	2	Q93Z27_ARATH	Q93z27 arabidopsis
259	36	76.6	919	2	Q4DJL9_TRYCR	Q4djl9 trypanosoma	332	35	74.5	204	2	Q91J01_ORYSA	Q91j01 oryza sativ
260	36	76.6	923	2	Q4DDH2_TRYCR	Q4ddh2 trypanosoma	333	35	74.5	207	2	Q8B399_ORYSA	Q8b399 aspergillus
261	36	76.6	929	1	DPOM_MAIZE	P10582 zea mays (m	334	35	74.5	236	2	Q6NLCS_ARATH	Q6nlcs arabidopsis
262	36	76.6	929	1	Q9MJC4_MAIZE	Q9mj4 zea mays (m	335	35	74.5	245	2	Q5BB45_EMENT	Q5bb45 aspergillus
263	36	76.6	997	2	Q7R191_PLASMO	Q7r191 plasmodium	336	35	74.5	247	2	Q4RV32_TETNG	Q4rv32 tetradon n
264	36	76.6	1052	2	Q6BMH0_DEBHA	Q6bmh0 debaryomyce	337	35	74.5	269	1	IL1B_TRYIVU	Q94tH9 trypanosom
265	36	76.6	1055	2	Q59X70_CANAL	Q59x70 candida alb	338	35	74.5	277	2	Q51H20_ENTHI	Q51h20 entamoeba h
266	36	76.6	1055	2	Q59XHB_CANAL	Q59xhb candida alb	339	35	74.5	279	2	Q51H20_ENTHI	Q51h20 entamoeba h
267	36	76.6	1076	1	YEM3_YEAST	P40021 saccharomyc	340	35	74.5	281	2	Q8F1L6_PLAF7	Q8f1l6 plasmodium
268	36	76.6	1100	2	Q5B316_EMENT	Q5b316 aspergillus	341	35	74.5	281	2	Q8FQC2_COREF	Q8fqc2 corynebacte
269	36	76.6	1144	2	Q18100_CAEEL	Q18100 caenorhabdi	342	35	74.5	287	2	Q6B2T8_YARLI	Q6bzt8 yarrowia li
270	36	76.6	1147	2	Q53U86_CAEEL	Q53u86 caenorhabdi	343	35	74.5	287	2	Q16657_CAEEL	Q16657 caenorhabdi
271	36	76.6	1177	2	Q2UKW0_ASPOR	Q2ukw0 aspergillus	344	35	74.5	288	2	Q9C6L0_ARATH	Q9c6l0 arabidopsis
272	36	76.6	1210	2	Q3E9P3_ARATH	Q3e9f3 arabidopsis	345	35	74.5	293	2	Q861W3_DICDI	Q861w3 dictyosteli
273	36	76.6	1239	2	Q81AN4_PLAF7	Q81an4 plasmodium	346	35	74.5	300	2	Q6L207_METMP	Q6l207 methanococc
274	36	76.6	1241	2	Q54DG6_DICDI	Q54dg6 dictyosteli	347	35	74.5	306	2	Q54CU2_DICDI	Q54cu2 dictyosteli
275	36	76.6	1250	2	Q624U4_CAEER	Q624j4 caenorhabdi	348	35	74.5	306	2	Q9M9C9_ARATH	Q9m9c9 arabidopsis
276	36	76.6	1257	2	Q4SKRF_DROVI	Q4skrf drosophila	349	35	74.5	325	2	Q7OSH9_GITALA	Q7osh9 giardia lam
277	36	76.6	1267	2	Q54D51_DICDI	Q54d51 dictyosteli	350	35	74.5	338	2	Q24795_ECHGR	Q24795 echinococcu
278	36	76.6	1292	2	Q6C889_YARLI	Q6c889 yarrowia li	351	35	74.5	342	2	Q7X826_ORYSA	Q7x826 oryza sativ
279	36	76.6	1295	2	Q2RIQ3_ORYSA	Q2r1q3 oryza sativ	352	35	74.5	352	2	Q6BMW3_DEBHA	Q6bmw3 debaryomyce
280	36	76.6	1303	2	Q86KP3_DICDI	Q86kp3 dictyosteli	353	35	74.5	362	2	Q3S3B1_RHILE	Q3s3b1 rhizobium l
281	36	76.6	1310	2	Q7RHN1_PLAYO	Q7rhn1 plasmodium	354	35	74.5	362	2	Q5MB41_BORHE	Q5mb41 borrelia he
282	36	76.6	1310	2	Q86IX0_DICDI	Q86ix0 dictyosteli	355	35	74.5	365	2	Q55G49_DICDI	Q55g49 dictyosteli
283	36	76.6	1328	2	Q4PIU9_CAEEL	Q4piu9 caenorhabdi	356	35	74.5	366	2	Q461U4_ENTCL	Q461u4 enticloplusi
284	36	76.6	1331	2	Q53U87_CAEEL	Q53u87 caenorhabdi	357	35	74.5	368	2	Q2KDH0_RHLET	Q2kdh0 rhizobium e
285	36	76.6	1351	2	Q7RFV8_PLAYO	Q7rfv8 plasmodium	358	35	74.5	371	2	Q6NSB1_HUMAN	Q6nsb1 homo sapien
286	36	76.6	1357	2	Q556A3_DICDI	Q556a3 dictyosteli	359	35	74.5	374	2	Q41366_SPIOL	Q41366 spincella ol
287	36	76.6	1363	2	Q81AM5_PLAF7	Q81am5 plasmodium	360	35	74.5	391	2	Q3CRV5_ALUTAT	Q3crv5 pseudalter
288	36	76.6	1369	2	Q69Z18_MOUSE	Q69z18 mus musculu	361	35	74.5	396	2	Q5KG90_CRYNE	Q5kg90 crypococcu
289	36	76.6	1419	2	Q54HA0_DICDI	Q54ha0 dictyosteli	362	35	74.5	410	2	Q02327_CAEEL	Q02327 caenorhabdi
290	36	76.6	1427	2	Q6FK39_CANGA	Q6fk39 candida gla	363	35	74.5	412	2	Q88X29_IACPL	Q88x29 lactobacilli
291	36	76.6	1448	2	Q557G1_DICDI	Q557g1 dictyosteli	364	35	74.5	413	2	Q6B056_DEBHA	Q6bq56 debaryomyce
292	36	76.6	1476	2	Q4DE53_TRYCR	Q4de53 trypanosoma	365	35	74.5	416	2	Q55RT7_CRYNE	Q55rt7 crypococcu
293	36	76.6	1484	2	Q4D8L4_TRYCR	Q4d8l4 trypanosoma	366	35	74.5	416	2	Q5KG91_CRYNE	Q5kg91 crypococcu
294	36	76.6	1570	2	Q389Q3_9TRYR	Q389q3 trypanosoma	367	35	74.5	420	2	Q4HYO2_GIBRE	Q4hyo2 gibbrellia
295	36	76.6	1571	2	Q81JF5_PLAF7	Q81jf5 plasmodium	368	35	74.5	422	2	Q9RCX6_ARATH	Q9rcx6 arabidopsis
296	36	76.6	1590	2	Q67WV4_ORYSA	Q67wv4 oryza sativ	369	35	74.5	423	2	Q9FW47_ARATH	Q9fw47 arabidopsis
297	36	76.6	1641	2	Q54BH0_DICDI	Q54bh0 dictyosteli	370	35	74.5	427	2	Q2M184_DROPS	Q2m184 drosophila
298	36	76.6	1657	2	Q51C65_ENTHI	Q51c65 entamoeba h	371	35	74.5	430	2	Q08729_YEAST	Q08729 saeccharomyc
299	36	76.6	1943	2	Q54G63_DICDI	Q54g63 dictyosteli	372	35	74.5	439	2	Q3LIB9_HUMAN	Q3lib9 homo sapien
300	36	76.6	1972	1	BAZ2B_HUMAN	Q9uif8 homo sapien	373	35	74.5	445	2	Q96OP3_DROME	Q96op3 drosophila
301	36	76.6	1973	2	Q7NP45_GLOVI	Q7np45 gloeobacter	374	35	74.5	447	2	Q61X96_CAEER	Q61x96 caenorhabdi
302	36	76.6	2130	1	BAZ2B_CHICK	Q9del1 gallus galli	375	35	74.5	451	1	LSB3_YEAST	P43603 saeccharomyc
303	36	76.6	2249	2	Q811Y8_PLAF7	Q811y8 plasmodium	376	35	74.5	455	2	Q4UIB5_THENM	Q4uib5 theileria a
304	36	76.6	2295	2	Q81ER2_PLAF7	Q81er2 plasmodium	377	35	74.5	460	2	Q9VF39_DROME	Q9vf39 drosophila
305	36	76.6	2295	2	Q9TY98_PLAF7	Q9ty98 plasmodium	378	35	74.5	464	2	Q3ECN7_ARATH	Q3ecn7 arabidopsis
306	36	76.6	2379	2	Q81JQ2_PLAF7	Q81jq2 plasmodium	379	35	74.5	469	2	Q5B8H1_BRARE	Q5b8h1 brachydanio
307	36	76.6	2457	2	Q77375_PLAF7	Q77375 plasmodium	380	35	74.5	471	2	P87360_BRARE	P87360 brachydanio
308	36	76.6	2706	2	Q97292_PLAF7	Q97292 plasmodium	381	35	74.5	472	2	Q07962_CARUV	Q07962 carassius a
309	36	76.6	2773	2	Q81BR4_PLAF7	Q81br4 plasmodium	382	35	74.5	506	2	Q43HK4_9CHUB	Q43hk4 chlorobium
310	36	76.6	2814	2	Q81CI5_PLAF7	Q81ci5 plasmodium	383	35	74.5	517	2	Q3EBB5_ARATH	Q3ebb5 arabidopsis
311	36	76.6	2864	2	Q4QDV7_LEIMA	Q4qdv7 leishmania	384	35	74.5	523	2	Q7RME4_PLAYO	Q7rme4 plasmodium
312	36	76.6	2994	2	Q95ZG5_DICDI	Q95z5 dictyosteli	385	35	74.5	550	2	Q4YR25_PLABE	Q4yr25 plasmodium
313	36	76.6	3328	2	Q81JG6_PLAF7	Q81jg6 plasmodium	386	35	74.5	575	2	Q4XX79_PLACH	Q4xx79 plasmodium
314	36	76.6	5910	2	Q81AP1_PLAF7	Q81ap1 plasmodium	387	35	74.5	581	2	Q59UG5_CANAL	Q59ug5 candida alb
315	35	74.5	78	2	Q3MDP4_ANAVT	Q3mdp4 anabena va	388	35	74.5	585	2	Q59UL8_CANAL	Q59ul8 candida alb
316	35	74.5	78	2	Q8YPR2_ANASP	Q8ypr2 anabena sp	389	35	74.5	592	2	Q4RRD5_TETNG	Q4rrd5 tetradon n
317	35	74.5	82	2	Q4OD67_9RHOB	Q4od67 jannaschia	390	35	74.5	617	2	Q5B4Q0_EMENT	Q5b4q0 aspergillus
318	35	74.5	87	2	Q6J3Q8_CANFA	Q6j3q8 canis famli	391	35	74.5	635	2	Q82253_ARATH	Q82253 arabidopsis
319	35	74.5	97	2	Q4XC35_PLACH	Q4xc35 plasmodium	392	35	74.5	647	2	Q4FW53_LEIMA	Q4fw53 leishmania
320	35	74.5	97	2	Q4B995_BURVI	Q4b995 burkholderi	393	35	74.5	658	2	Q5NVJ2_FONYF	Q5nvj2 pongo pygma
321	35	74.5	117	2	Q9LJEL_ARATH	Q9ljei arabidopsis	394	35	74.5	664	2	Q4E4V1_TRYCR	Q4e4v1 trypanosoma
322	35	74.5	136	2	Q45UK5_GHIV1	Q45uk5 human immun	395	35	74.5	679	2	Q96176_PLAF7	Q96176 plasmodium
323	35	74.5	150	2	Q2U900_ASPOR	Q2u900 aspergillus	396	35	74.5	680	1	PIT_DROME	Q9v451 drosophila

397	35	74.5	681	2	06A809_PROAC	06A809 propionibac	470	34	72.3	125	2	09NH0_PLAFA	Q9nh0 plasmodium
398	35	74.5	682	2	05TR26_9TRYP	05TR26 trypanosoma	471	34	72.3	131	2	08STF4_PLAFA	Q8stf4 plasmodium
399	35	74.5	685	2	07ZMF4_BRARE	07ZMF4 brachydanio	472	34	72.3	132	2	08AA71_BACTN	Q8aa71 bacteroides
400	35	74.5	715	2	0690A4_ORISA	0690A4 oryza sativ	473	34	72.3	134	2	0868X1_PLAFA	Q868x1 plasmodium
401	35	74.5	716	2	066HD4_DICDI	066hd4 dictyostell	474	34	72.3	135	2	05M0X9_STRT1	Q5m0x9 streptococc
402	35	74.5	724	2	06MWT1_NEUCR	06mwt1 neurospora	475	34	72.3	135	2	05M5G6_STRT2	Q5m5g6 streptococc
403	35	74.5	724	2	02MNX3_CLOBE	02mnx3 clostridium	476	34	72.3	136	2	0590Y2_CANAL	Q590y2 candida alb
404	35	74.5	724	2	03IPF3_PSEHT	03ipf3 pseudalter	477	34	72.3	136	2	071177_PLAFA	Q71177 plasmodium
405	35	74.5	734	2	06ZTV1_ORYSA	06ztv1 oryza sativ	478	34	72.3	136	2	03BHK9_PLAFA	Q3bhk9 plasmodium
406	35	74.5	738	2	05XK08_9MONO	05xk08 sudan ebola	479	34	72.3	136	2	03BTL6_PLAFA	Q3btl6 plasmodium
407	35	74.5	774	2	094170_PNECA	094170 pneumocysti	480	34	72.3	137	2	03BPS8_PLAFA	Q3bps8 plasmodium
408	35	74.5	791	2	09VTC1_DROME	09vtc1 drosophila	481	34	72.3	137	2	08TF53_PLAFA	Q8tf53 plasmodium
409	35	74.5	793	2	0210S3_CAEBL	0210s3 caenorhabdi	482	34	72.3	138	2	03BFG7_PLAFA	Q3bfg7 plasmodium
410	35	74.5	798	2	08SSP3_DICDI	08ssp3 dictyostell	483	34	72.3	138	2	03B132_PLAFA	Q3b132 plasmodium
411	35	74.5	810	2	07SC92_NEUCR	07sc92 neurospora	484	34	72.3	139	2	03B465_PLAFA	Q3b465 plasmodium
412	35	74.5	812	2	02LXK7_DROPS	02lxk7 drosophila	485	34	72.3	139	2	09NHM4_PLAFA	Q9nhm4 plasmodium
413	35	74.5	813	2	0584Y5_9TRYP	0584y5 trypanosoma	486	34	72.3	139	2	02ZV45_STRSU	Q2zv45 streptococc
414	35	74.5	816	2	05M1X1_STRT1	05m1x1 streptococc	487	34	72.3	140	2	017393_CABEL	Q17393 caenorhabdi
415	35	74.5	816	2	05M6G1_STRT2	05m6g1 streptococc	488	34	72.3	144	2	0330E3_9GAMM	Q330e3 shewanella
416	35	74.5	825	2	055CM6_DICDI	055cm6 dictyostell	489	34	72.3	147	2	06FVN4_CANGA	Q6fyn4 candida gla
417	35	74.5	833	1	SPBI_XLUTA	06cvt2 kluyveromyc	490	34	72.3	148	2	060TC3_CAEBR	Q60tc3 caenorhabdi
418	35	74.5	844	2	0553N1_DICDI	0553n1 dictyostell	491	34	72.3	151	2	05ANM5_CANAL	Q5anm5 candida alb
419	35	74.5	845	1	SPBI_ASHGO	0751u1 ashya goss	492	34	72.3	153	2	03CFH0_THRET	Q3cfh0 thermoaer
420	35	74.5	873	2	04PGS2_USTMA	04pgs2 ustilago ma	493	34	72.3	162	2	03TLL4_MOUSE	Q3tll4 mus muscula
421	35	74.5	888	2	07RXL7_NEUCR	07rxl7 neurospora	494	34	72.3	163	2	093VF4_ARATH	Q93vf4 arabidopsis
422	35	74.5	960	2	09V5L1_DROME	09v5l1 drosophila	495	34	72.3	165	1	MCH_RAT	P14200 rattus norv
423	35	74.5	962	2	04Z8K6_DROME	04z8k6 drosophila	496	34	72.3	165	2	0816F7_BACCR	Q816f7 bacillus ce
424	35	74.5	972	2	054F86_DICDI	054f86 dictyostell	497	34	72.3	168	2	03ERM0_BACTI	Q3erm0 bacillus th
425	35	74.5	986	2	04DITD3_TRYCR	04ditd3 trypanosoma	498	34	72.3	169	2	075HG1_ORYSA	Q75hg1 oryza sativ
426	35	74.5	1006	2	08EMF6_MYCPE	08emf6 mycoplasma	499	34	72.3	177	1	ARGRI_YEAST	P07449 saccharomyc
427	35	74.5	1018	2	07S706_NEUCR	07s706 neurospora	500	34	72.3	212	2	0541N9_DICDI	Q541n9 dictyostell
428	35	74.5	1026	2	086B03_DICDI	086b03 dictyostell							
429	35	74.5	1037	2	05CG08_CRYHO	05cgg8 cryptospori							
430	35	74.5	1038	2	09PAC6_PICPA	09pac6 picchia past							
431	35	74.5	1040	2	05CSD0_CRYPV	05csd0 cryptospori							
432	35	74.5	1046	2	054118_DICDI	054118 dictyostell							
433	35	74.5	1047	2	07RPJ9_PLAFO	07rpj9 plasmodium							
434	35	74.5	1054	2	04D0T2_TRYCR	04d0t2 trypanosoma							
435	35	74.5	1055	2	0556G5_DICDI	0556g5 dictyostell							
436	35	74.5	1172	2	07SS92_NEUCR	07ss92 neurospora							
437	35	74.5	1199	2	054Q41_DICDI	054q41 dictyostell							
438	35	74.5	1345	1	YH00_YEAST	P38800 saccharomyc							
439	35	74.5	1349	2	06RCM0_ENTHI	06rcm0 entamoeba h							
440	35	74.5	1349	2	06RCM0_ENTHI	06rcm0 entamoeba h							
441	35	74.5	1442	2	0815V9_PLA7	0815v9 plasmodium							
442	35	74.5	1469	2	05SVU9_CRYNE	05svu9 cryptococcu							
443	35	74.5	1469	2	05KX00_CRYNE	05kx00 cryptococcu							
444	35	74.5	1559	2	08IDC3_PLA7	08idc3 plasmodium							
445	35	74.5	1671	2	054M02_DICDI	054m02 dictyostell							
446	35	74.5	1726	1	SPTE6I_BRARE	08buv2 brachydanio							
447	35	74.5	2039	2	0658K1_HUMAN	0658k1 homo sapien							
448	35	74.5	2062	1	ANR12_HUMAN	06ub98 homo sapien							
449	35	74.5	2122	2	054E43_DICDI	054e43 dictyostell							
450	35	74.5	2169	2	097312_PLA7	097312 plasmodium							
451	35	74.5	2452	1	RPBI_PLA7	P14248 plasmodium							
452	35	74.5	2461	2	03AR75_CHLCH	03ar75 chlorobium							
453	35	74.5	2573	2	096185_PLA7	096185 plasmodium							
454	35	74.5	2594	2	07RJ44_PLA7	07rj44 plasmodium							
455	35	74.5	4507	2	07RF07_PLA7	07rf07 plasmodium							
456	35	74.5	4805	2	07RRN5_PLA7	07rrn5 plasmodium							
457	34	72.3	61	2	031TV8_NATPD	Q31tv8 nationomona							
458	34	72.3	69	2	07XPY4_ORYSA	Q7xpy4 oryza sativ							
459	34	72.3	74	2	04YEG5_PLA8B	Q4yeg5 plasmodium							
460	34	72.3	85	2	08DP28_YIBVU	Q8df28 vibrio vuln							
461	34	72.3	101	2	04NCK5_5MITC	Q4ncx5 arthrobacte							
462	34	72.3	104	2	09XG51_LYC8S	Q9xg51 lycoperisico							
463	34	72.3	113	2	041VW3_DESHA	Q41vw3 desulficoba							
464	34	72.3	114	2	086HP6_DICDI	Q86hp6 dictyostell							
465	34	72.3	115	2	03BHE1_PLA7A	Q3bhe1 plasmodium							
466	34	72.3	123	2	095W71_PLA7A	Q95w71 plasmodium							
467	34	72.3	124	2	081G20_BACCR	Q81g20 bacillus ce							
468	34	72.3	125	2	03BGW5_PLA7A	Q3bgw5 plasmodium							
469	34	72.3	125	2	095V2_PLA7A	Q95v2 plasmodium							

ALIGNMENTS

RESULT 1	SCKA_PANIM	STANDARD;	PRT;	47 AA.
AC	P55977;			
DT	01-NOV-1997, integrated into UniProtKB/Swiss-Prot.			
DT	15-DEC-1998, sequence version 2.			
DT	07-FEB-2006, entry version 47.			
DE	Potassium channel-blocking toxin PiTX-K-alpha precursor (Pandinotoxin			
DE	alpha) (Potassium channel-blocking toxin 2) (Pi2) (Pi-2) (Alpha-KTx			
DE	7.1) (Fragment).			
GN	Name=PTX-1;			
OS	Pandinus imperator (Emperor scorpion).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;			
OC	Iurida; Scorpionidae; Scorpionidae; Scorpioninae; Pandinus.			
OX	NCBI_TaxID=55084;			
NP	[1]			
NP	NUCLEOTIDE SEQUENCE [MRNA].			
RA	Rogowski R.S., Collins J.H., O'Neill T.J., Gustafson T.A.,			
RA	Werkman T.R., Rogowski M.A., Tenenholz T.C., Weber D.J.,			
RA	Blaustein M.P.;			
RU	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	PROTEIN SEQUENCE OF 13-47.			
RC	TISSUE=Venom;			
RC	MEDLINE=97070422; PubMed=8913348;			
RA	Rogowski R.S., Collins J.H., O'Neill T.J., Gustafson T.A.,			
RA	Werkman T.R., Rogowski M.A., Tenenholz T.C., Weber D.J.,			
RA	Blaustein M.P.;			
RT	"three new toxins from the scorpion Pandinus imperator selectively			
RT	block certain voltage-gated K+ channels."			
RL	Mol. Pharmacol. 50:1167-1177(1996).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 13-47, AND FUNCTION.			
RC	TISSUE=Venom;			
RC	MEDLINE=96304303; PubMed=8660410; DOI=10.1007/s002329900084;			
RX	Gomez-Lagunas F., Olamendi-Portugal T., Zamudio F.Z., Possenti L.D.,			
RA	"Two novel toxins from the venom of the scorpion Pandinus imperator			

RT show that the N-terminal amino acid sequence is important for their
 RT affinities towards Shaker B K⁺ channels.";
 RL J. Membr. Biol. 152:49-56(1996).
 [4]
 RN STRUCTURE BY NMR.
 RP MEDLINE=97215813; PubMed=9662103; DOI=10.1021/bi962842;
 RX Tenenholz T.C., Rogowski R.S., Collins J.H., Blaustein M.P.,
 RA Weber D.J.;
 RT "Solution structure for Pandinus toxin K-alpha (Pitx-K alpha), a
 RT selective blocker of A-type potassium channels.";
 RL Biochemistry 36:2763-2771(1997).
 CC -1- FUNCTION: Potent inhibitor of the A-type voltage-gated potassium
 CC channels. Most potent inhibitor of Kv1.2/KCNA2 channels.
 CC Reversibly block the Shaker B potassium-channels (Kv1.1 sub-
 CC family).
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
 CC channel inhibitor subfamily.
 CC -----
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 CC
 CC EMBL; U79579; AAB52576.1; -, mRNA.
 DR PIR; T10471; T10471.
 DR PDB; 2PTA; NMR; @=13-47.
 DR Linkhub; P55927; -
 DR InterPro; IPR001947; Scorpion_toxins.
 DR Pfam; PF00451; Toxin_2; 1.
 DR PRINTS; PR00286; CHARYBOTOXIN.
 DR ProDom; PD003586; Scorpion_toxins; 1.
 DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
 KW 3D-structure; Direct protein sequencing; Ionic channel inhibitor;
 KW Neurotoxin; Potassium channel inhibitor; Signal; Toxin.
 FT SIGNAL
 FT PEPIDE
 FT 13 47 Potassium channel-blocking toxin Pitx-K-
 FT alpha.
 FT /FTid=PRO_0000035328.
 FT
 FT DISULFID 16 37
 FT DISULFID 22 42
 FT DISULFID 26 44
 FT NON_TER 1 1
 FT STRAND 17 18
 FT HELIX 19 29
 FT TURN 30 30
 FT STRAND 31 31
 FT STRAND 35 38
 FT TURN 39 40
 FT STRAND 41 45
 SQ SEQUENCE 47 AA; 5434 MW; 2188BF110A37BD7C CRC64;
 Query March 100.0%; Score 47; DB 1; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 5 DYKDDDDK 12
 RESULT 2
 Q8NFN6 HUMAN PRELIMINARY; PRT; 319 AA.
 AC Q8NFN6;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE RGS3 isoform RGS3S.
 OS Homo sapiens (Human).
 GN Name=RGS3;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22032988; PubMed=12036301; DOI=10.1006/geno.2002.6773;
 RA Kell J.H., Srikumar D., Harrison K., Wilson G.L., Shi C.S.;
 RT "Additional 5' exons in the RGS3 locus generate multiple mRNA
 RT transcripts, one of which accounts for the origin of human PDZ-RGS3.";
 RL Genomics 79:860-868(2002).
 CC -1- SIMILARITY: Contains 1 RGS domain.
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 CC
 CC EMBL; AF490838; AAM33253.1; -, mRNA.
 DR HSSP; P49799; IAGR.
 DR EMBL; ENSG0000019835; Homo sapiens.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR InterPro; IPR000342; RGS.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; Reg1_Gproteins; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS0132; RGS; 1.
 SQ SEQUENCE 319 AA; 36094 MW; 998632C6E9B1F0F3 CRC64;
 Query March 100.0%; Score 47; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDDK 8
 Db 312 DYKDDDDK 319
 RESULT 3
 Q36Q46 MARRY PRELIMINARY; PRT; 246 AA.
 AC Q36Q46;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Uncharacterized conserved membrane or secreted protein precursor.
 GN ORFNames=MaquDRAPT_1112;
 OS Marinobacter aquaeolei VT8.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Marinobacter.
 OX NCBI_TaxID=351348;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VT8;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome of Marinobacter aquaeolei VT8.";
 RT Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RT -1- CAUTION: The sequence shown here is derived from an
 RT EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 RT preliminary data.
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 CC
 CC EMBL; AL061000011; EAO98985.1; -, Genomic DNA.
 CC Signal.
 FT SIGNAL 1 22 Potential.


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SQ  SEQUENCE      246 AA; 26731 MW; C1CCEB680E0E24EA CRC64;
Query Match      91.5%; Score 43; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 223 DYDDDDK 230

RESULT 4
Q4X9J6 PLACH PRELIMINARY; PRT; 154 AA.
ID Q4X9J6 PLACH PRELIMINARY; PRT; 154 AA.
AC Q4X9J6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypoetical protein (Fragment).
GN ORFNames=PC404555.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Stinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: CAJ01008539; CAH86427.1; -; Genomic_DNA.
DR InterPro: IPR006484; PYST-B; 1.
DR TrRPFMS; TIGR01597; PYST-B; 1.
KW Hypoetical protein.
FT NON TER 154
SQ SEQUENCE 154 AA; 18627 MW; 3CC4E0E30746F404 CRC64;

Query Match      89.4%; Score 42; DB 2; Length 154;
Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 76 DYDDDDK 83

RESULT 5
Q7Y283 PLACH PRELIMINARY; PRT; 284 AA.
ID Q7Y283 PLACH PRELIMINARY; PRT; 284 AA.
AC Q7Y283;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE PC10106C.
GN ORFNames=PC10106C;
OS Plasmodium chabaudi chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=31271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AS;
RX MEDLINE=22672904; PubMed=12787350;
RX DOI=10.1046/j.1365-2958.2003.03491.x;
RA Fischer K., Chavich M., Huestis R., Wilson D.W., Kemp D.J., Saul A.;
RT "Ten families of variant genes encoded in subtelomeric regions of
RT multiple chromosomes of Plasmodium chabaudi, a malaria species that
RT undergoes antigenic variation in the laboratory mouse.";
RL Mol. Microbiol. 48:1209-1223(2003).
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CC -----
DR EMBL: AY149028; AAC06133.1; -; Genomic_DNA.
DR InterPro: IPR006484; PYST-B.
DR TrRPFMS; TIGR01597; PYST-B; 1.
SQ SEQUENCE 284 AA; 34079 MW; 31E34DD0F6243FAC CRC64;

Query Match      89.4%; Score 42; DB 2; Length 284;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 72 DYDDDDK 79

RESULT 6
Q6FN57 CANGA PRELIMINARY; PRT; 586 AA.
ID Q6FN57 CANGA PRELIMINARY; PRT; 586 AA.
AC Q6FN57;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Similar to sp|P38748 Saccharomyces cerevisiae YHL010C.
GN OrderdeducNames=CAGC0K025639;
OS Candida glabrata (Yeast) (Totipotopsis glabrata); Saccharomycetes;
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Geoffard N., Frangeul L., Aigle M., Anboud V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Catolico L., Contandriou F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Ortiz S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.-F., Straub M.-L., Sureau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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CC -----
DR EMBL: CR380957; CAG61298.1; -; Genomic_DNA.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; F:protein ubiquitination; IEA.
DR InterPro: IPR011422; BRAP2.
DR InterPro: IPR001841; ZnF_RING.
DR InterPro: IPR001607; ZnF_UBP.
```


DR Pfam: PF07576; BRAP2.1.
 DR Pfam: PF00097; zF-C3HC4.1.
 DR Pfam: PF02148; zF-UBP.1.
 DR SMART: SM00184; RING.1.
 DR SMART: SM00290; ZNF-UBP.1.
 DR PROSITE: PS50089; zF_RING_2.1.
 DR Complete proteome; Metal-Binding; Zinc; Zinc-finger.
 SW SEQUENCE 586 AA; 68333 MW; 550DF456268A1321 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 586;
 Best Local Similarity 87.5%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8
 Db 401 NYKDDDDK 408

RESULT 7
 Q2PEW5_TRIPR PRELIMINARY; PRT; 603 AA.
 AC Q2PEW5
 DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DE Putative phosphoinositide specific phospholipase C.
 OS Trifolium pratense (Red clover).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eutroside 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 OC Trifolium.
 OC NCBI_TaxID=57577;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:13679984; DOI=10.1007/s00122-003-1412-z;
 RA Isobe S., Klimentko I., Iwashita S., Gau M., Kozlov N.N.;
 RT "First RFLP linkage map of red clover (Trifolium pratense L.) based on
 RT cDNA probes and its transferability to other red clover germplasm.",
 RL Theor. Appl. Genet. 108:105-112(2003).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sato S., Isobe S., Asamizu E., Nakamura Y., Ohmido N., Sakurai N.,
 RA Klimentko I., Sasamoto S., Wada T., Watanabe A., Tabata S.;
 RT "Comprehensive structural analysis of the genome of red clover
 RT (Trifolium pratense).";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AB336785; BAE71237.1; -, mRNA.
 SQ SEQUENCE 603 AA; 68714 MW; FA71D84631E30A31 CRC64;

Query Match 89.4%; Score 42; DB 2; Length 603;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
 Db 311 DYKDDDD 317

RESULT 8
 O6FK24_CANGA PRELIMINARY; PRT; 1365 AA.
 AC O6FK24
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Similar to sp|P35177|Saccharomyces cerevisiae YBR081c SP7
 DE Transcriptional activator.
 GN OrderedLocNames=CAGL0M01738g;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitospotic Saccharomycetales; Candida.
 OC NCBI_TaxID=5478;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RX PubMed:15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marc C., Neveglise C., Talla E.,
 RA Goffard N., Fangeul L., Aigle M., Anthonard V., Babor A., Barde V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Catolico L., Confantolero F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.,
 RL "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
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 DR EMBL: CR380959; CAG62396.1; -, Genomic DNA.
 DR InterPro: IPR001487; Bromodomain.
 DR Pfam: PF00439; Bromodomain.1.
 DR PRINTS: PR00503; BROMODOMAIN.
 DR SMART: SMO0297; BROMO.1.
 DR PROSITE: PS00633; BROMODOMAIN_1; 1.
 DR PROSITE: PS50014; BROMODOMAIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 1385 AA; 157899 MW; E722C657091CE53E CRC64;

Query Match 89.4%; Score 42; DB 2; Length 1385;
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8
 Db 546 DYKDDNDK 553

RESULT 9
 Q91BJ4_NPVST PRELIMINARY; PRT; 399 AA.
 AC Q91BJ4
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Hypothetical protein.
 OS Spodoptera litura multicausid nucleopolyhedrovirus (SplmNPV).
 OC Virusess; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OC NCBI_TaxID=46242;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=G2;
 RX MEDLINE=21425398; PubMed=11531416; DOI=10.1006/viro.2001.1056;
 RA Yang Y., Yu J., Wang L., Hu X., Bao W., Li G., Chen C., Han H., Hu S.,
 RA Yang H.;
 RT "Sequence analysis of the Spodoptera litura multicausid
 RT nucleopolyhedrovirus genome.";
 RL Virology 287:391-404(2001).
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 CC -----
 DR EMBL: AF25155; AA101710.1; -, Genomic DNA.
 KW Hypothetical protein.

SQ SEQUENCE 399 AA; 47305 MW; 877F2E6A5DE0E1E1 CRC64;
 Query Match 87.2%; Score 41; DB 2; Length 399;
 Best Local Similarity 87.5%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 360 DYADDDDK 367

RESULT 10
 SPR28 YEAST STANDARD; PRT; 423 AA.
 ID SPR28 YEAST STANDARD; PRT; 423 AA.
 AC 004921;
 DT 26-APR-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1996, sequence version 1.
 DT 07-MAR-2006, entry version 33.
 DE Sporulation-regulated protein 28.
 GN Name=SPR28; Ordered locus names=YDR218C; ORF names=YD9934.03C;
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313263; PubMed=9169867;
 RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballista J.P.G.,
 RA Barges M., Baron L., Becker A., Bileau N., Bloeker H., Blugeon C.,
 RA Boskovic J., Brandt P., Bruckner M., Buitrago M.J., Coester F.,
 RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,
 RA Goffeau A., Gomez-Perez A., Granotier C., Hanemann V., Hankeln T.,
 RA Hohelsel J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,
 RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
 RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Patricio N.,
 RA Paulin L., Perez J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
 RA Puydt H., Purnelle B., Raemussen S.W., Remacha M.A., Revuelta J.L.,
 RA Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer W.,
 RA Scharte M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
 RA Soter-Mita A., Urtastazu L.A., Verhasselt P., Vissers S., Voet M.,
 RA Volckaert G., Wagner G., Wandut R., Wedler E., Wieders H., Woelfl S.,
 RA Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K.,
 RA Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L.D.,
 RA Niblett D., Odell C., Oliver K., Rajadream M.A., Richards C.,
 RA Shore L., Walsh S.V., Barrell B.G., Dietrich F.S., Molligan J.T.,
 RA Allen E., Araujo R., Aviles E., Berro A., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Hunkle-Smith S., Hyman R.W.,
 RA Komp C., Lahekari D., Lew H., Lin D., Mosedale D., Nakahara K.,
 RA Namach A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S.,
 RA Schroeder M., Shogren T., Shroff N., Winant A., Yelton M.A.,
 RA Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R.,
 RA Cooper J., Ding H., Du Z., Favell A., Fulton L., Gattung S.,
 RA Greco T., Hallsworth K., Hawkins J., Haller L.W., Jier M.,
 RA Johnson D., Johnson L., Kirsten J., Kucaba T., Langston Y.,
 RA Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M.,
 RA Pauley A., Peluso D., Rifkin L., Riles L., Taich A., Trevaekis E.,
 RA Vignati D., Wilcox L., Woldman P., Vaudin M., Wilson R.,
 RA Waterston R., Albertmann K., Han J., Heumann K., Kleene K.,
 RA Mewes H.-W., Zollner A., Zaccaria P.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV.";
 RN Nature 387:75-78(1997).
 RP SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND INTERACTIONS WITH CDC11
 AND SPR3.
 RP MEDLINE=97039860; PubMed=8885406;
 RA de Virgili C., Demarini D.J., Pringle J.R.;
 RT "SPR28, a sixth member of the septin gene family in *Saccharomyces*
 RT *cerevisiae* that is expressed specifically in sporulating cells.";
 RL Microbiol 147:2897-2905(1996).
 CC -!- FUNCTION: Septins are GTPases involved in cytokinesis that
 CC assemble into filaments and form a ring at the cleavage site. May
 CC act by recruiting MYO1 and HOF1, a protein involved in septation.

CC to the site of cleavage. Septins are also involved in cell
 CC morphogenesis, bud site selection, chitin deposition, cell cycle
 CC regulation, cell compartmentalization and spore wall formation
 CC (By similarity).
 CC -!- SUBUNIT: Interacts with itself. Interacts with CDC11 and SPR3;
 CC probably to form a ring at the bud neck.
 CC -!- INTERACTION:
 CC P32458: CDC11; NbExp=2; InAct=EBI-38416, EBI-4178;
 CC -!- SUBCELLULAR LOCATION: Membrane-associated. Present at the bud neck
 CC during cell division. Probably interacts with phosphatidylinositol 5-
 CC phosphate (By similarity). Localizes to ring-like structures
 CC around each of the four nuclear lobes at the onset and during
 CC meiosis II. Concentrated initially at the leading edge of the
 CC developing prospore wall.
 CC -!- DEVELOPMENTAL STAGE: Expressed during meiosis and asexual
 CC formation. First expressed at the beginning of meiosis I, and is
 CC highly expressed prior meiosis II.
 CC -!- SIMILARITY: Belongs to the septin family.
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 CC -----
 CC EMBL; Z48612; CA88498.1; -; Genomic DNA.
 CC PIR; S59425; S59425.
 CC InAct; Q04921; -.
 CC DR Ensembl; YDR218C; *Saccharomyces cerevisiae*.
 CC DR SGD; S000002626; SPR28.
 CC DR BioCyc; SCER-S28-01:SCER-S28-01-001235-MONOMER; -.
 CC DR Linkhub; Q04921; -.
 CC DR GO; GO:0000144; C:septin ring (sensu *Saccharomyces*); TAS.
 CC DR GO; GO:0005515; F:structural binding; IPI.
 CC DR GO; GO:0007047; P:cell wall organization and biogenesis; TAS.
 CC DR GO; GO:0009092; P:cellular morphogenesis; TAS.
 CC DR InterPro; IPR000038; Cell Div GTP Bd.
 CC DR PANTHER; PTHR18884; GTP Cell Div; 2.
 CC DR Pfam; PF00735; GTP CDC; 1.
 CC DR Prodom; PD002565; GTP Cell Div; 1.
 CC DR Cell cycle; Cell division; Coiled coil; Complete proteome;
 CC GTP-binding; Membrane; Nucleotide-binding.
 CC KW GTP-binding; Nucleotide-binding.
 CC FT FT 38 45
 CC FT COMPBIAS 60 68
 CC FT FT 384 417
 CC FT FT 60 68
 CC FT FT 48193 MW; EB8D3C0F47CD41DB CRC64;
 SQ SEQUENCE 423 AA; 48193 MW; EB8D3C0F47CD41DB CRC64;
 Query Match 87.2%; Score 41; DB 1; Length 423;
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 62 DYDDDDDK 69

RESULT 11
 Q21W25 RHOPA PRELIMINARY; PRT; 452 AA.
 AC Q21W25;
 DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
 DT 07-MAR-2006, sequence version 1.
 DT 07-MAR-2006, entry version 1.
 DE Trigger factor.
 GN ORFNames=RPB_2562;
 OS *Rhodospseudomonas palustris* Hae2.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodospseudomonas.
 OX NCBI_TaxID=316058;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=HaA2;
 RA US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,
 RA Hamon N., Isaman S., Plitnick S., Chain P., Malacri S., Shin M.,
 RA Vergez L., Schmutz J., Larimer F., Land M., Hauser L., Pelletier D.A.,
 RA Kyriakides N., Anderson I., Oda Y., Harwood C.S., Richardson P.,
 RT "Complete sequence of Rhodospseudomonas palustris HaA2,"
 RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: CP000250; ABD07265.1; -; Genomic DNA.
 DR SEQUENCE 452 AA; 5011 MW; 4F805CD1AC1A2E5D CRC64;

Query Match 87.2%; Score 41; DB 2; Length 452;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
 DB 443 YKDDDDK 449

RESULT 12
 ID Q6VZM2 CNPV PRELIMINARY; PRT; 1767 AA.
 AC Q6VZM2-
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE CNP125 variola B22R-like protein.
 GN Name=CNP125;
 OS Canarypox virus (CNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=44088;
 RX NCBI [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC VR-111;
 RX PubMed14671117; DOI=10.1128/JVI.78.1.353-366.2004;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RT "The genome of canarypox virus."
 RL J. Virol. 78:353-366(2004).
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 CC -----
 DR EMBL: AY318871; AAR83471.1; -; Genomic DNA.
 DR InterPro: IPR007490; Poxvirus_B22R.
 DR Pfam: PF04395; Poxvirus_B22R; 1.
 SO SEQUENCE 1767 AA; 195286 MW; 1408E4F8C52547A5 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 1767;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 1680 DYKDDDDK 1687

RESULT 13
 ID Q8UKJ5 GVIRU PRELIMINARY; PRT; 322 AA.
 AC Q8UKJ5;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Orf18.
 GN Name=orf18;
 OS Helicobacter zea virus 1.
 OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA viruses.

OX NCBI_TaxID=29250;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22174892; PubMed=12186886;
 RX DOI=10.1128/JVI.76.18.9024-9034.2002;
 RA Cheng C.H., Liu S.M., Chow T.Y., Hsiao Y.Y., Wang D.P., Huang J.J.,
 RA Chen H.H.;
 RT "Analysis of the complete genome sequence of the Hs-1 virus suggests
 that it is related to members of the Baculoviridae,"
 RL J. Virol. 76:9024-9034(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheng C.H., Liu H.M., Hsiao Y.Y., Chow T.Y., Chen H.H.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Chao Y.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Chen H.H., Yeh W.B., Tso D.J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheng C.H., Hsiao Y.Y., Liu S.M., Chow T.Y., Chen H.H.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AF451898; AAN04411.1; -; Genomic DNA.
 SO SEQUENCE 322 AA; 36706 MW; 22B25C1209717A90 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 322;
 Best Local Similarity 75.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
 DB 271 DYKDDDDK 278

RESULT 14
 ID Q4N797 THEPA PRELIMINARY; PRT; 432 AA.
 AC Q4N797;
 DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 02-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE ATP-dependent helicase, putative.
 GN ORFNames=TP01_0923;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OC NCBI_TaxID=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RX PubMed=15994558; DOI=10.1126/science.1110439;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoabai A., Domingi A.R., Maaswo D.,
 RA Crabtree J., Wortman J.R., Haas B., Angluoni S.V., Creasy T.H., Lu C.,
 RA Sun B., Silva J.C., Utebäck T.R., Feldblyum T.V., Perera M.,
 RA Allen J., Nielsen W.C., Taracha E.L., Salzberg S.L., White O.R.,
 RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
 RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
 Lymphocytes,"
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;

RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Meidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoabi A., Wasaso D., Crabtree J., Wortman J.R.,
 RA Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Uteback T., Feldlyum T., Petrea M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC -----
 DR EMBL_AAGK01000001; EMBL34161.1; -; Genomic DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0001656; F:nucleotide binding; IEA.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 DR ATP-binding; Helicase; Hydrolase.
 KW SEQUENCE 432 AA; 49387 MW; 02F0BE597876EE1E CRC64;
 SQ

Query Match 83.0%; Score 39; DB 2; Length 432;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 Db 264 NYKDDDDR 271

RESULT 15
 ID Q7UQZ7 RHOB A PRELIMINARY; PRT; 506 AA.
 AC Q7UQZ7;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Probable acetylornithine aminotransferase (EC 2.6.1.11).
 GN OrderedLocustNames=RB5984;
 OS Rhodopirella baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OC NCBI_TaxID=117;
 RN [1]
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=1;
 RX MEDLINE=22735913; Pubmed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardoc T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
 RA Schlesner H., Mann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
 CC aminotransferase family.
 CC -----
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 CC -----
 DR EMBL_BX294143; CAD74545.1; -; Genomic DNA.
 DR GO: GO:0003992; F:acetylornithine transaminase activity; IEA.
 DR GO: GO:0030170; F:pyridoxal phosphate binding; IEA.

DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR005814; AminoTrans_3.
 DR PANTHER: PTHR11986; AminoTrans_3; 1.
 DR Pfam: PF00202; AminoTrans_3; 1.
 KW AminoTransferase; Complete proteome; Pyridoxal phosphate; Transferase.
 SQ SEQUENCE 506 AA; 54062 MW; 49F0AC9D3C4272C1 CRC64;
 QY 1 DYKDDDK 8
 Db 439 DYEDDDDE 446

Query Match 83.0%; Score 39; DB 2; Length 506;
 Best Local Similarity 75.0%; Pred. No. 5.5e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 Db 439 DYEDDDDE 446

RESULT 16
 ID CWC25_YARLI STANDARD; PRT; 561 AA.
 AC 06C1V6;
 DT 22-NOV-2005, integrated into UniProtKB/Swiss-Prot.
 DT 16-AUG-2004, sequence version 1.
 DT 07-MAR-2006, entry version 14.
 DE Pre-mRNA-splicing factor CWC25.
 GN Name=CWC25; OrderedLocustNames=YAL10F13057g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetaceae; Dipodascaceae; Yarrowia.
 OC NCBI_TaxID=4952;
 RN [1]
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=CLIB 122 / B 150;
 RX Pubmed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Antouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchet S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boissame A., Boyer J., Catolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,
 RA Hentraye F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicand J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellens S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 CC -1- FUNCTION: Involved in pre-mRNA splicing (By similarity).
 CC -1- SUBUNIT: Associated with the spliceosome (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nucleus (By similarity).
 CC -1- SIMILARITY: Belongs to the CWC25 family.
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 CC -----
 DR EMBL_CR382132; CAG78163.1; -; Genomic DNA.
 KW Coiled coil; Complete proteome; mRNA processing; mRNA splicing;
 KW Nuclein protein; Spliceosome.
 FT CHAIN 1 561
 FT FT
 FT COILED 22 64
 FT FT COILED 495 545
 FT FT COMPIAS 166 353
 FT FT SEQUENCE 561 AA; 66044 MW; 61374B600C4CB6B CRC64;
 SQ

Query Match 83.0%; Score 39; DB 1; Length 561;
 Best Local Similarity 75.0%; Pred. No. 6.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 Db 439 DYEDDDDE 446

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Db          419 EYKDEDDK 426

RESULT 17
OS4DNA_DICDI PRELIMINARY; PRT; 648 AA.
ID OS4DNA_DICDI
AC OS4DNA;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=DD80184366;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Korthornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Louised H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAF10100268; EAL61185.1; -; Genomic DNA.
DR GO; GO:0008324; F: cation transporter activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR006262; Lipase_AS.
DR InterPro; IPR006162; Pfamne_S.
DR Pfam; PF02386; TrkH; 1.
DR POSITIVE; PS00120; LIPASE_SER; UNKNOWN_1.
DR POSITIVE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR KW Hypothetical protein.
SQ SEQUENCE 648 AA; 73510 MW; 32A77CDEDE84E505 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 648;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
Db 107 DFKDDDD 114

RESULT 18
OS4MT9_CLOPE PRELIMINARY; PRT; 706 AA.
ID OS4MT9_CLOPE
AC OS4MT9;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.

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DT 07-FEB-2006, entry version 19.
DE Hypothetical protein CPE0599.
GN OrderedLocustNames=CPE0599;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1502;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
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CC -----
DR EMBL; BA000016; BAB80305.1; -; Genomic DNA.
DR Biocyc; CPE0599; CPE0599-MONOMER; -.
DR LinkHub; OS4MT9; -.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0004003; F: ATP-dependent DNA helicase activity; IEA.
DR GO; GO:0003677; F: DNA binding; IEA.
DR GO; GO:0006281; P: DNA repair; IEA.
DR InterPro; IPR00212; UVRD-helicase.
DR PANTHER; PTHR11070; UVRD-helicase; 1.
DR Pfam; PF00580; UVRD-helicase; 2.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 706 AA; 82992 MW; 85B3A4EBB35478A CRC64;

Query Match 83.0%; Score 39; DB 2; Length 706;
Best Local Similarity 75.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
Db 51 EYKDEDDK 58

RESULT 19
OS4UVO_DICDI PRELIMINARY; PRT; 1254 AA.
ID OS4UVO_DICDI
AC OS4UVO;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=DD80204740;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Korthornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louised H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,

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RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrel B., Kuapa A.;
 RT "The genome of the social amoeba *Dictyostelium discoideum*.";
 RL Nature 0:0-0(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC
 CC EMBL; AAF101000069; EAL67058.1; -; Genomic_DNA.
 DR Hypochemical protein.
 KM
 SQ SEQUENCE 1254 AA; 146907 MW; A53C93E69754EC61 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 1254;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
 ||:||||:
 Db 880 DYEDDDK 887

RESULT 20
 046YH5_RALEJ PRELIMINARY; PRT; 110 AA.
 ID 046YH5_RALEJ
 AC 046YH5;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Probable signal peptide protein.
 GN OrderedLocustNames-Reut A2446;
 OS Ralstonia eutropha (strain JMP134) (Alcaligenes eutrophus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Cupriavidus.
 NCBI_TaxID=264198;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Goltzman E., Martinez W.,
 RA Schmutz J., Latimer F., Land M., Lykidis A., Richardson P.;
 RT "Complete sequence of chromosome 1 of *Ralstonia eutropha* JMP134.";
 RL Submitted (MUG-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; CP000090; AA261808.1; -; Genomic_DNA.
 DR Complete proteome.
 KM
 SQ SEQUENCE 110 AA; 11880 MW; AC13E71F3914FF89 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 110;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
 ||:||||:
 Db 83 DYDDDDK 90

RESULT 21
 05COA2_CRYPV PRELIMINARY; PRT; 125 AA.
 ID 05COA2_CRYPV
 AC 05COA2;
 DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 12-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypochemical protein.
 GN ORFNames=cgd4_1500;
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.

OX NCBI_TaxID=5807;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Iowa type II;
 RX PubMed=15044751; DOI=10.1126/science.1094786;
 RA Abrahamson M.S., Templeton T.J., Enomoto S., Abraham J.E., Zhu G.,
 RA Lianco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
 RA Banker A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
 RA Anantharaman V., Aravind L., Kapur V.;
 RT "Complete genome sequence of the apicomplexan, *Cryptosporidium*
 RT parvum.";
 RL Science 304:441-445(2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC
 CC EMBL; AAE01000009; EAK87605.1; -; Genomic_DNA.
 DR Hypochemical protein.
 KM
 SQ SEQUENCE 125 AA; 14670 MW; 77D0BDCCFB44094A CRC64;

Query Match 80.9%; Score 38; DB 2; Length 125;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDD 7
 ||:||||:
 Db 60 DYKDDDD 66

RESULT 22
 09FM73_ARATH PRELIMINARY; PRT; 154 AA.
 ID 09FM73_ARATH
 AC 09FM73;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Arabidopsis thaliana genomic DNA, chromosome 5, p1 clone:MDF20.
 GN OrderedLocustNames=At5g55650;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98290546; PubMed=9628582; DOI=10.1093/dnares/5.1.41;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 CC -----
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 CC
 CC EMBL; AB009050; BAB09232.1; -; Genomic_DNA.
 DR TAIR; At5g55650; -;
 SQ SEQUENCE 154 AA; 17650 MW; 7A4C895328B7E2DC CRC64;

Query Match 80.9%; Score 38; DB 2; Length 154;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDD 7
 ||:||||:
 Db 84 DYEDDD 90

RESULT 23


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RESULT 26
O4X8B5_PLACH PRELIMINARY; PRT; 265 AA.
AC O4X8B5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypochemical protein (Fragment).
GN ORFNames=PC405060.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN 1)
RP NUCLEOTIDE SEQUENCE.
RP PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcho C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Stiden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAJ01008940; ECH86861.1; -; Genomic_DNA.
KM Hypochemical protein.
FT NON_TER 265
SQ SEQUENCE 265 AA; 239664 MW; BD11AB5B5085C4CF CRC64;

Query Match 80.9%; Score 38; DB 2; Length 265;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 103 DFKDDDD 109

RESULT 27
O9LJV8_ARATH PRELIMINARY; PRT; 294 AA.
AC O9LJV8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE GB|AA16629.1.
GN OrderedLocustNames=At3g29075;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 1)
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=2036309; PubMed=10907853; DOI=10.1093/dnares/7.3.217;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.,
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RT and BAC clones."
RL DNA Res. 7:217-221(2000).
RN 12)
RP NUCLEOTIDE SEQUENCE.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -----

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CC -----
DR EMBL; AP000388; BAB02950.1; -; Genomic_DNA.
DR EMBL; AB018121; BAB02950.1; JOINED; Genomic_DNA.
DR TAIR; At3g29075; -.
SQ SEQUENCE 294 AA; 34452 MW; 98164D6FAFD1533F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 294;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 211 DYVDDDEK 218

RESULT 28
O54YA8_DICDI PRELIMINARY; PRT; 301 AA.
AC O54YA8;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypochemical protein.
GN ORFNames=DOB0205379;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN 1)
RP NUCLEOTIDE SEQUENCE.
RP STRAIN=AX4;
RP PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafanski K., Xu O.,
RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivo F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaut P., Fey P.,
RA Pilcher G., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Korhonen A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Church C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Kuzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Salto T.,
RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
RA Knights A., Loussed H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaitsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 435:43-57(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAF101000052; EAL68337.1; -; Genomic_DNA.
KM Hypochemical protein.
SQ SEQUENCE 301 AA; 35014 MW; 15B6A20128BCF37 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 301;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 112 DYSDDDDE 119

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RESULT 29
VHCG_METVO STANDARD; PRT; 306 AA.
ID VHCG_METVO
AC Q00406;
DT 16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE F420-non-reducing hydrogenase vhc subunit G (EC 1.12.99.-).
GN Name=vhcg;
OS Methanococcus voltae.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2188;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RC STRAIN=DSM 1537 / PS;
RX MEDLINE=92293118; PubMed=1603063;
RA Halboch S., Klein A.;
RT "Methanococcus voltae harbors four gene clusters potentially encoding
RT two [NiFe] and two [NiFeSe] hydrogenases, each of the cofactor F420-
RT reducing or F420-non-reducing types.";
RL Mol. Genet. 233:217-224(1992).
RN [2]
RP TRANSCRIPTIONAL REGULATION.
RC STRAIN=DSM 1537 / PS;
RX PubMed=8121392; DOI=10.1007/BF00281785;
RA Berghoefer Y., Agha-Amiri K., Klein A.;
RT "Selenium is involved in the negative regulation of the expression of
RT selenium-free [NiFe] hydrogenases in Methanococcus voltae.";
RL Mol. Genet. 242:369-373(1994).
CC -1- SUBUNIT: The F420-non-reducing hydrogenase vhc is composed of
CC three subunits: vhca, vhcd and vhcg (By similarity).
CC -1- INDUCTION: By selenium deprivation.
CC -1- SIMILARITY: Belongs to the [NiFe]/[NiFeSe] hydrogenase small
CC subunit family.
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CC -----
DR EMBL, X61203; CAA43505.1; -; Genomic_DNA.
DR PIR, S32834; S32834.
DR InterPro: IPR006137; Oxidored_g6.
DR Pfam: PF01058; Oxidored_g6; 1.
KW Oxidoreductase.
FT CHAIN 1 306 F420-non-reducing hydrogenase vhc subunit
FT G.
FT SEQUENCE 306 AA; 33636 MW; 2A88AC3EAE194DB CRC64;
SQ
Query Match 80.9%; Score 38; DB 1; Length 306;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYKDDDD 8
DB 260 DYKDDDD 267

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
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CC -----
DR EMBL, AAC00100025; EAL01427.1; -; Genomic_DNA.
DR EMBL, AAC00100023; EAL01667.1; -; Genomic_DNA.
DR GO, GO:0005489; F:electron transporter activity; IEA.
DR GO, GO:0006118; P:electron transport; IEA.
DR InterPro: IPR012336; Thioridoxin-like_fold.
DR InterPro: IPR006662; Thioridoxin-like_fold.
DR InterPro: IPR006663; Thioridoxin_dom2.
DR InterPro: IPR012335; Thioridoxin_fold.
DR Pfam: PF00085; Thioridoxin_1.
DR PRINTS: PF00421; THIOREDOXIN.
KW Hypothetical protein; Redox-active center.
SQ SEQUENCE 332 AA; 39236 MW; 94A2A754F35DF5EB CRC64;
QY 1 DYKDDDD 7
DB 318 DYKDDDD 324

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RESULT 31
Q4XYM1_PLACH PRELIMINARY; PRT; 369 AA.
ID Q4XYM1_PLACH
AC Q4XYM1;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein (Fragment).
GN ORFNames=PC000687.02.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Karacos F.C., Janse C.O., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL, CAJ01002240; CAJ77989.1; -; Genomic_DNA.
DR InterPro: IPR000436; Suen1_SCR_CCP.
DR Pfam: PF00084; Suen1_1.
DR SMART, SM00032; CCP, 1.

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RN NUCLEOTIDE SEQUENCE.
RP PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Omond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnici D.J., Yates J.R. III,
RA Karafos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DDbj whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL: CAJ01003901; CAH80746.1; -; Genomic_DNA.
CC DR GO: 0005615; C:extracellular space; IEA.
CC DR GO: 0005125; F:cytokine activity; IEA.
CC DR InterPro: IPR012351; Cytokine_4_hlx.
CC KW Cytokine; Hypothetical protein.
SQ SEQUENCE 475 AA; 56352 MW; 1F1E3BBFA3CE8829 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 475;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDDK 8
Db 369 DYQDDDK 376

RESULT 36
MAOL YERPE STANDARD; PRT; 565 AA.
ID MAOL YERPE STANDARD; PRT; 565 AA.
AC Q8ZG09; Q7AVB1; Q7CHQ5;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 27.
DE NAD-dependent malic enzyme (EC 1.1.1.38) (NAD-ME).
GN Name=efcA; OrderedLocustNames=YPO1511.y2658.y11401;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=632;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagsis K., Kariyasev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527 (2001).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=KIM5 / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";

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RL J. Bacteriol. 184:4601-4611 (2002).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=91001 / Biovar Mediaevalis;
RC PubMed=15568893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin R., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197 (2004).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = pyruvate + CO(2) + NADH.
CC -1- COFACTOR: Divalent cations, magnesium or manganese (By
CC similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SIMILARITY: Belongs to the malic enzymes family.
CC -----
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CC -----
CC EMBL: AJ414148; CAC90334.1; -; Genomic_DNA.
CC DR EMBL: AE013868; AAM66211.1; -; Genomic_DNA.
CC DR EMBL: AE017132; AAS61642.1; -; Genomic_DNA.
CC DR PIR: AC0184; AC0184.
CC DR HSSP: P40927; 1GQ2.
CC DR GenomeReviews: AE009952.GR.y2658.
CC DR GenomeReviews: AE017042.GR.y11401.
CC DR GenomeReviews: AL590842.GR.YPO1511.
CC DR BiOCyc: YPES187410.y2658-MONOMER; -.
CC DR BiOCyc: YPES229193.YP1401-MONOMER; -.
CC DR BiOCyc: YPES632.YPO1511-MONOMER; -.
CC DR HAMAP: MF_01619; -; 1.
CC DR InterPro: IPR012301; Malic_N.
CC DR InterPro: IPR012302; Malic_NAD_bd.
CC DR InterPro: IPR001891; Malic_oxred.
CC DR PANTHER: PTHR10893; Malic_oxred; 1.
CC DR Pfam: PF00390; malic; 1.
CC DR PIRSF: PIRSF000106; ME; 1.
CC DR PRINTS: PR00072; MALOXRDYASE.
CC DR PROSITE: PS00331; MALIC ENZYMES; 1.
CC KW Complete proteome; Metal-binding; NAD; Oxidoreductase.
CC CHAIN 1 565
FT ACT SITE 104 104 /FTID=PRO_000016040.
FT ACT SITE 175 175 Proton donor (By similarity).
FT METAL 246 246 Proton acceptor (By similarity).
FT METAL 247 247 Divalent metal cation (By similarity).
FT METAL 247 247 Divalent metal cation (By similarity).
FT BINDING 157 157 Divalent metal cation (By similarity).
FT BINDING 270 270 NAD (By similarity).
FT BINDING 270 270 NAD (By similarity).
FT SITE 418 418 NAD (By similarity).
FT SITE 270 270 Important for activity (By similarity).
SQ SEQUENCE 565 AA; 62828 MW; F57C1183BEC4A3D CRC64;

Query Match 80.9%; Score 38; DB 1; Length 565;
Best Local Similarity 75.0%; Pred. No. 8.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDDK 8
Db 66 DFKDDDK 73

RESULT 37
MAOL YERPS STANDARD; PRT; 565 AA.
ID MAOL YERPS STANDARD; PRT; 565 AA.
AC Q6C6D0;
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 07-MAR-2006, entry version 12.
DE NAD-dependent malic enzyme (EC 1.1.1.38) (NAD-ME).

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GN Name=sfca: OrderedLocuNames=YPTB1526;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
ON NCBI_TaxID=633;
RX NCBIOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=IP32953 / Serotype I;
RC PubMed=1535858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerlin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.W., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Himebusch U., Marceau M., Medigue C.,
RA Smoot M., Chantal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Darbush A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pests through whole-genome
RT comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = pyruvate + CO(2) + NADH.
CC -1- COFACTOR: Divalent cations, magnesium or manganese (By
CC similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SIMILARITY: Belongs to the malic enzymes family.
CC
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC EMBL: BX36398; CAH20765.1; -; Genomic DNA.
CC GenomeReviews: BX36398_CR; YPTB1526.
CC HAMAP: MF_01619; -; 1.
CC InterPro: IPR012301; Malic_N.
CC InterPro: IPR012302; Malic_NAD_bd.
CC InterPro: IPR001891; Malic_oxred.
CC PANTHER: PTHR10893; Malic_oxred; 1.
CC Pfam: PF00390; malic; 1.
CC Pfam: PF03949; Malic_M; 1.
CC PRINTS: PR00072; MALOXRDPTASE.
CC DR PIRSF: PIRSF00106; ME; 1.
CC DR PIRSF: PR00072; MALOXRDPTASE.
CC DR PROSITE: PS00331; MALIC ENZYMES; 1.
CC KM Complete proteome; Metal-binding; NAD; Oxidoreductase.
CC FT CHAIN 1 565
CC /FTID=PRO_0000160241.
CC ACT SITE 104 104 Proton donor (By similarity).
CC ACT SITE 175 175 Proton acceptor (By similarity).
CC METAL 246 246 Divalent metal cation (By similarity).
CC METAL 247 247 Divalent metal cation (By similarity).
CC METAL 270 270 Divalent metal cation (By similarity).
CC BINDING 157 157 NAD (By similarity).
CC BINDING 270 270 NAD (By similarity).
CC BINDING 418 418 NAD (By similarity).
CC SITE 270 270 Important for activity (By similarity).
CC SEQUENCE 565 AA; 62828 MW; F57C1183ECC4AAAD3 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 565;
Best Local Similarity 75.0%; Pred. NO. 8.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OX NCBI_TaxID=28985;
ON NCBIOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RC PubMed=1529592; DOI=10.1038/nature02579;
RX Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugebauer C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchon S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bistrane A., Boyer J., Cattolico L., Confenietti F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Karst A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Oztas S., Ozer-Kalogropoulos O.,
RA Pellanz S., Potier S., Richard G.-F., Strub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenon-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Buchner C., Caudron B., Scarpelli C., Galliardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in Yeasts."
RL Nature 430:35-44(2004).
CC -1- FUNCTION: Required for the first step of diaphamide biosynthesis,
CC the transfer of 3-amino-3-carboxypropyl from S-adenosyl-L-
CC methionine to a histidine residue. Diaphamide is a post-
CC translational modification of histidine which occurs in elongation
CC factor 2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -1- SIMILARITY: Belongs to the DPH2 family.
CC
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CC
CC EMBL: CR382124; CAH00295.1; -; Genomic DNA.
CC InterPro: IPR002728; diaphamide_syn.
CC InterPro: IPR010014; DPH2.
CC PANTHER: PTHR10762; diaphamide_syn; 2.
CC Pfam: PF01866; Diaphamide_syn; 1.
CC DR TIGRFAMs: TIGR00272; DPH2; 1.
CC KM Complete proteome.
CC FT CHAIN 1 587
CC /FTID=PRO_0000083390.
CC SEQUENCE 587 AA; 66189 MW; 4F51D875B767EC1A CRC64;

Query Match 80.9%; Score 38; DB 1; Length 587;
Best Local Similarity 85.7%; Pred. NO. 9.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DYKDDDDK 8
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ID DPH2_KLULA STANDARD; PRT; 587 AA.
AC QGCS50;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE diaphamide biosynthesis protein 2.
GN Name=DPH2; OrderedLocuNames=KLUA0D02948g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

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RESULT 39
DPH2_KLULA
ID Q55CB4_DICDI PRELIMINARY; PRT; 588 AA.
AC Q55CB4;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=DDB0190829;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliales; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandran M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu O.,
RA Tunggal B., Kummerfeld S., Madera M., Kontorov B.A., Rivero F.,
RA Bankler A.T., Lehmann R., Hamlin N., Davis R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

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RA Kethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Fadrocher P., Desany B., Just E., Morio T., Roet R., Chuchet C.M.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
 RA Buchrieser C., Madroper A., Felder M., Thangavelu M., Johnson D.,
 RA Knights A., Louieged H., Mungall K.L., Oliver K., Plice C.,
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
 RA Sanders M., Ma J., Kohata Y., Sharp S., Simmonds M.N., Spiegler S.,
 RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winkler T.,
 RA Tanaka Y., Shulsky G., Schleicher M., Weinstein G.M., Rosenthal A.,
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Bartell B.G.,
 RA Kuspa A.,
 RA "The genome of the social amoeba *Dictyostelium discoideum*,"
 RL Nature 435:43-57(2005).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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EMBL: AAF10100011; EAL72415.1; -; Genomic_DNA.
 DR InterPro: IPR006575; RMD.
 DR InterPro: IPR002867; znf_C6HC.
 DR Pfam: PF01485; IIR; 1.
 DR Pfam: PF05773; RMD; 1.
 DR SMART: SM00647; IIR; 1.
 DR SMART: SM00591; RMD; 1.
 DR PROSITE: PS50908; RMD; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 588 AA; 67624 MW; 8AD824B3DD6F07A CRC64;

Query Match 80.9%; Score 38; DB 2; Length 588;
 Best Local Similarity 85.7%; Pred. No. 9.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
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 Db 101 DYEDDD 107

RESULT 40
 Q6BYD0 DEBHA PRELIMINARY; PRT; 590 AA.
 ID Q6BYD0 DEBHA
 AC Q6BYD0
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Debaryomyces hansenii chromosome A of strain CBS767 of Debaryomyces
 DE hansenii.
 GN OrderedLocustNames=DRHA0A10868g;
 OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxID=4959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
 RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
 RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boissière A., Boyer J., Cattolico L., Confiantieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantuya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicand J.-M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pelenz S., Potier S., Richard G.-F., Strand M.-L., Suleau A.,
 RA Svenen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Boločin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Winkler P., Souclet J.-L.,
 RT "Genome evolution in yeasts,"
 RL Nature 430:35-44(2004).
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EMBL: CR392133; CAG84758.1; -; Genomic_DNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004377; F:glycolipid 2-alpha-mannosyltransferase acti. .; IEA.
 DR GO: GO:0006486; P:protein amino acid glycosylation; IEA.
 DR InterPro: IPR002685; Glyco trans 15.
 DR Pfam: PF01793; Glyco_transf_15; 1.
 KM Complete proteome.
 SQ SEQUENCE 590 AA; 69412 MW; A3762251468590F1 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 590;
 Best Local Similarity 75.0%; Pred. No. 9.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
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 Db 27 DYSDDD 34

RESULT 41
 Q2UGP9 ASPOR PRELIMINARY; PRT; 629 AA.
 ID Q2UGP9 ASPOR
 AC Q2UGP9
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Predicted protein.
 GN ORFNames=A09002300761;
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RIB 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arita T., Akita O., Kashiwagi Y., Aoe K., Gomi K.,
 RA Horituchi H., Kitamoto K., Kodayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nieman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhattacharya D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
 RA Hoshiyama A., Ichinomiya M., Igatahshi R., Washita K., Juvadi P.R.,
 RA Kato M., Kato Y., Kiri T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama Y., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Kuroki T., Koyama Y., Minetoki T., Suhrman S., Tanaka A., Isono K.,
 RA Kubura S., Ogatawara N., Kikuchi H.,
 RT "Genome sequencing and analysis of *Aspergillus oryzae*,"
 RL Nature 438:1157-1161(2005).
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 CC -----

EMBL: AP007157; BA859266.1; -; Genomic_DNA.
 SQ SEQUENCE 629 AA; 68502 MW; 5821BD2EBB21145F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 629;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
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 Db 182 DYEDDD 188

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RESULT 42
O2UF79 ASPOR PRELIMINARY; PRT; 782 AA.
AC O2UF79;
DT 24-JUN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JUN-2006, sequence version 1.
DE Phosphatidylinositol 4-kinase.
GN ORFNames=A0090026000314;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eucristales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RI8 40;
RX PubMed=16372010; DOI=10.1038/nature04300;
RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
RA Kusumoto K., Atima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
RA Horuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
RA Bahatnagar D., Cleveland T.E., Fedorova N.D., Gotch O., Horikawa H.,
RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Urvadi P.R.,
RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
RA Mortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
RA Kihara S., Ogasawara N., Kikuchi H.;
RT "Genome sequencing and analysis of Aspergillus oryzae.";
RL Nature 438:1157-1161(2005).
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CC -----
EMBL: AP007159; BAE59786.1; -; Genomic DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
KW Kinase.
SQ SEQUENCE 782 AA; 89076 MW; B35FPBD2EA712335 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 782;
Best Local Similarity 75.0%; Pred. NO. 1.3e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 27 DYSDDDQ 34

RESULT 43
O3QT20 GRHOB PRELIMINARY; PRT; 804 AA.
AC O3QT20;
DT 23-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Hypochemical protein precursor.
GN ORFNames=RosedRAFT_1857;
OS Silicibacter sp. TM1040.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxID=292414;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Silicibacter sp.
RT TM1040.";
RU Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Silicibacter sp. TM1040.";
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TM1040;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
EMBL: AAFG02000004; EAM57069.1; -; Genomic DNA.
DR EMBL: AAFG02000004; EAM57069.1; -; Genomic DNA.
KW Hypochemical protein; Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 804 AA; 87577 MW; 7132035950682D7C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 804;
Best Local Similarity 87.5%; Pred. NO. 1.3e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 207 DYKDDDK 214

RESULT 44
O96505 DROME PRELIMINARY; PRT; 823 AA.
AC O96505;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DE 07-FEB-2006, entry version 21.
DE SIR2.
GN Name=SIR2; ORFNames=CG5216;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22549451; PubMed=12663533;
RA Astrom S.U., Cline T.W., Rine J.;
RT "The Drosophila melanogaster sir2(+) Gene Is Nonessential and Has Only
RT Minor Effects on Position-Effect Variegation.";
RL Genetics 163:931-937(2003).
CC -----
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CC -----
EMBL: AF068758; AAC79684.1; -; mRNA.
DR HSSP; P5386; 101A.
DR FLYBase; FBgn0024291; Sir2.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0005634; C:nucleus; IDA.
DR GO: GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.
DR INTERPRO: IPR003000; SIR2.
DR PANTHER: PTHR11085; SIR2; 1.
DR Pfam; PF02146; SIR2; 1.
DR PROSITE; PSS0305; SIR2; 1.
SQ SEQUENCE 823 AA; 92024 MW; 5EF09F1A46235E7F CRC64;

Query Match 80.9%; Score 38; DB 2; Length 823;
Best Local Similarity 75.0%; Pred. NO. 1.3e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DYKDDDDX 8
 DB 698 DYSDDDE 705

RESULT 45
 Q9VK34 DROME PRELIMINARY; PRT; 823 AA.
 ID Q9VK34 DROME
 AC Q9VK34
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE CG5216-PA.
 GN Name=Sir2; ORFNames=Dmel CG5216;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
 RA Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
 RA Jaiswal M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodali C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
 RA George R.A., Hoekins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svrtk R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J.W., Svrtk R.,
 RA Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective."
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Huang Y., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bertencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Ruess S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise B., George R.,
 RA Hoekins R., Stapleton M., Pacle J., Park S., Svrtk R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase;
 RL Submitted (JUN-2006) to the EMBL/GenBank/DBJ databases.
 CC CC
 CC -i- INTERACTION:
 CC Q9V860:CG6459; NBExp=1; Inact=EBI-83837, EBI-151216;
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 CC EMBL; AE003639; AAF53248.1; -; Genom1C_DNA.
 CC HSSP; P53686; 1Q1A.
 CC Inact; Q9VK34; -;
 CC Flybase; FBGN004291; Sir2.
 CC GO; GO:0005737; C:cytoplasm; IDA.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC GO; GO:0017136; F:NAD-dependent histone deacetylase activity; IDA.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC InterPro; IPR003000; SIR2.
 CC PANTHER; PTHR11085; SIR2; 1.
 CC Pfam; PF02146; SIR2; 1.
 CC PROSITE; PS50303; SIRTUIN; 1.
 CC SEQUENCE 823 AA; 91837 MW; 3DD1EBA975A263D3 CRC64;
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Query Match 80.9%; Score 38; DB 2; Length 823;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
 DB 698 DYSDDDE 705

RESULT 46
 Q4Y026 PLACH PRELIMINARY; PRT; 862 AA.
 ID Q4Y026 PLACH
 AC Q4Y026
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Anaplastin-rich antigen Pfafs-14, putative (Fragment).
 GN ORFNames=PC000038.02.0;
 OS Plasmodium chabaudi.


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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=5825;
[1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janssen C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC distributed under the Creative Commons Attribution-NonDerivs license
CC
CC
DR EMBL, CAJ01001857, CAH77164.1, -, Genomic_DNA.
CC
FT NON_TER 1
SQ SEQUENCE 862 AA; 101452 MW; 32BC06EFA06BAFF4 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 862;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 378 DFNDDDDK 385

RESULT 47
Q6CG65_YARLI PRELIMINARY; PRT; 926 AA.
ID Q6CG65_YARLI
AC Q6CG65;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 21-FEB-2006, entry version 19.
DE Yarrowia lipolytica chromosome B of strain CLIB122 of Yarrowia
DE lipolytica.
GN OrderedLocNames=YALI10B005289;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxId=4952;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Dujuns P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne B., Bleykasten C.,
RA Boismarie A., Boyer J., Cartolico L., Confanioli F., de Darvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Giropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire N., Lesur I., Ma L., Muller H.,
RA Niclaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Porter S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekla F., Wesolowski-Louvel M., Weshof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolocin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -----
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CC distributed under the Creative Commons Attribution-NonDerivs license
CC
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CC -----
CC EMBL, CR382128, CAG82561.1, -, Genomic_DNA.
DR GO: 0005488; F-binding; IEA.
DR InterPro, IPR011990; TPR-like_helical.
DR InterPro, IPR001440; TPR_1.
DR InterPro, IPR013105; TPR_2.
DR InterPro, IPR013026; TPR_region.
DR Pfam, PF00515; TPR 1; 4.
DR SMART, SM00028; TPR; 3.
DR PROSITE, PSS0005; TPR; 7.
DR PROSITE, PSS0293; TPR_REGION; 3.
DR Complete proteome; Repeat; TPR repeat.
SQ SEQUENCE 926 AA; 105464 MW; 0894AED20AD98CD3 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 926;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 12 DYEDDD 18

RESULT 48
Q416J9_GIBZE PRELIMINARY; PRT; 1018 AA.
ID Q416J9_GIBZE
AC Q416J9;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypoetical protein.
DE ORFNames=FG07159.1;
GN Glibberella zeae (Fusarium graminearum).
OS Glibberella zeae (Fusarium graminearum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Glibberella.
OX NCBI_TaxId=5518;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=PH-1 / NRRL 31084;
RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata U., Chang J.,
RA Choepel Y., Collimore A., Cook A., Cooke P., Corum B., Deatellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D.,
RA Galagan J.E., Gardyna S., Gnerre S., Graham L., Grand-Pierre N.,
RA Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
RA Iliev I., Jaffe D., Johnson R., Jones C., Kamai M., Kanat A.,
RA Karatas A., Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
RA Lui A., Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J.,
RA Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J.,
RA Menes L., Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C.,
RA Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
RA O'Neil D., Oliver J., Peterson K., Phunkhang P., Piere N.,
RA Percell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
RA Rogov P., Roman J., Schauer S., Schuback R., Seaman S., Severy P.,
RA Shtinov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,
RA Stubbs M., Talmas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zairoun U., Zembek L., Zimmer A., Zody M.,
RA Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC
DR EMBL, AACM01000301, EAA76618.1, -, Genomic_DNA.
DR Complete proteome; Hypoetical protein.
SQ SEQUENCE 1018 AA; 114167 MW; 07DFCD7B0F0A11F4 CRC64;
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Query Match 80.9%; Score 38; DB 2; Length 1018;
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 DB 545 DYEDDDD 551

RESULT 49
 IFH1_YEAST STANDARD; PRT; 1085 AA.
 AC P39520;
 DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1995, sequence version 1.
 DT 07-MAR-2006, entry version 38.
 DE Protein IFH1 (Protein RRP3).
 GN Name=IFH1; Synonyms=RRP3; OrderedLocNames=YLR223C; ORFNames=L8083.9;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=ATCC 28383 / FL100;
 RX MEDLINE=95304839; PubMed=7785326;
 RA Chereil I., Thuriaux P.,
 RT "The IFH1 gene product interacts with a fork head protein in
 RT Saccharomyces cerevisiae.";
 RL Yeast 11:261-270(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288c / AB972;
 RX MEDLINE=9733267; PubMed=9169871.
 RA Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,
 RA Ansorge W., Benes V., Bruckner M., Delius H., Dubois E.,
 RA Duescherhoef A., Entian K.-D., Floeth M., Goffeau A., Hebling U.,
 RA Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K.,
 RA Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,
 RA Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E.,
 RA Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M.,
 RA Rinke M., Rose M., Scharfe M., Scherenz B., Scholler P., Schwager C.,
 RA Schwarz S., Underwood A.P., Urrutazu L.A., Vandenbol M.,
 RA Vershaestel P., Vierendeels F., Voet M., Voickert G., Voss H.,
 RA Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
 RA Hani U., Hohlbein J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 RN [3]
 RP LEVEL OF PROTEIN EXPRESSION.
 RX MEDLINE=22933965; PubMed=14562106; DOI=10.1038/nature02046;
 RA Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A.,
 RA Dephoure N., O'Shea E.K., Weissman J.S.;
 RT "Global analysis of protein expression in yeast.";
 RL Nature 425:737-741(2003).
 CC -1- FUNCTION: Controls the pre-rRNA processing machinery in
 CC conjunction with PHL1. Could convert PHL1 from a repressor to an
 CC activator.
 CC -1- INTERACTION: NDEXP=1; INACT=EBI-9054, EBI-38337;
 CC Q08673:SR1; NDEXP=1; INACT=EBI-9054, EBI-38337;
 CC -1- SUBCELLULAR LOCATION: Nucleus (Probable).
 CC -1- MISCELLANEOUS: Present with 1430 molecules/cell.
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 CC EMBL: Z29488; CAAG3624.1; -; Genomic DNA.
 CC EMBL: U19027; AAB67412.1; -; Genomic DNA.
 CC PIR: S55352; S55352.
 CC INACT: P39520; -;
 CC Germonline: 142285; -;
 CC Ensembl: YLR223C; Saccharomyces cerevisiae.

DR GenomeReviews: Y13138 GR; YLR223C.
 DR SGD: S000004213; IFH1.
 DR BiOCCy: SCER-S28-01:SCER-S28-01-004107-MONOMER; -.
 DR Linkhub: P39520; -.
 DR GO: GO:0005730; C:nucleolus; IDA.
 DR GO: GO:0005515; F:protein binding; IPI.
 DR GO: GO:0003700; F:transcription factor activity; IGI.
 DR GO: GO:0006348; P:chromatin silencing at telomere; IMP.
 DR GO: GO:0006363; P:rRNA processing; IGI.
 DR GO: GO:0006383; P:transcription from RNA polymerase III promoter; IGI.
 KW Complete proteome; Nuclear protein; Transcription;
 KW Transcription regulation.
 FT CHAIN 1 1085 Protein IFH1.
 FT FTID=PRO_0000084164.
 FT FTID=PRO_0000084164.
 FT SEQUENCE 1085 AA; 122492 MW; BEIC7DEF06213F80 CRC64;
 Query Match 80.9%; Score 38; DB 1; Length 1085;
 Best Local Similarity 85.7%; Pred. No. 1.8e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 DB 612 DYEDDDD 618

RESULT 50
 Q4P6M8_USTMA PRELIMINARY; PRT; 1212 AA.
 ID Q4P6M8;
 AC Q4P6M8;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein.
 GN ORFNames=UM04235.1;
 OS Ustilago maydis 521.
 CC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 CC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 CX NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=521;
 RA Birren B.W., Nisbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Alt-Zehra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Bilenstein B., Bloom T., Bye J., Boguslavsky L.,
 RA Bowesky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S.E., Camarata J., Campo K., Chang J., Cheahatsang Y.,
 RA Clitmore M., Collamore A., Considine T., Cook A., Cooke P., Corum B.,
 RA Chomo C., David R., Dawoe T., Degray S., Dodge S., Dooley K.,
 RA Dorje P., Dorjee K., Dorris U., Dufley N., Dupes A., Elkins T.,
 RA Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J.E., Geartn G., Gnerre S.,
 RA Glikre A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hognopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Uffe D., Jones C., Kamal M., Kamat A., Kamyvessels M., Karlsson B.,
 RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
 RA Lui A., Ma L.-J., Mabbitt R., Macdonald J., Maclean C., Mayor J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mancini E.,
 RA McCarthy M., McDonough S., McGehe T., Melatim J., Menes L.,
 RA Mesitov J., Mihalav A., Mihova T., Mikelsen T., Mlenka V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C.B., Nizazi M., Norbu C.,
 RA Norbu N., O'Donnell P., Okoawo O., O'Leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Recta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settippalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Souguez C.,
 RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,

RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tsafaye S., Theodore J., Thoutantsev Y., Topham K.,
RA Towey S., Tsamir T., Tsono N., Vallee D., Vassiliev H.,
RA Venkatachalam V.S., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangli T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.S.;
RT "The genome sequence of *Ustilago maydis*.";
RT Submitted (PEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL: AACPO1000150; EAK85284.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro: IPR001138; Fungi_Trcscp_N.
DR Pfam: PF04082; Fungal_trans; 1.
DR Pfam: PF00172; Zn_club; 1.
DR SMART: SM00066; GAL4; 1.
DR PROSITE: PS00463; ZN2_CY6_FUNGAL_1; UNKNOWN_1.
DR PROSITE: PS50048; ZN2_CY6_FUNGAL_2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Transcription; Transcription regulation; Zinc.
SQ SEQUENCE 1212 AA; 131152 MW; 7182BA4E422BF507 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1212;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 851 DYEDDD 857

RESULT 51
Q7MKW4_PORGI PRELIMINARY; PRT; 1228 AA.
AC Q7MKW4;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 21-FEB-2006, entry version 22.
DE DNA polymerase III, alpha subunit.
GN Name:dnaiB; Ordered locus names:PG0035; ORFNames=PG_0035;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroidales (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
[1]
RA NCBILOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=W83.
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eissen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
CC -!- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) =
CC diphosphate + DNA(n+1).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -----
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CC -----
CC EMBL: AE015924; AAQ65289.1; -; Genomic_DNA.
DR TIGR: PG0035; -;
DR BioCyc: PGIN242619; PG0035-MONOMER; -;
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:000408; F:3'-5' exonuclease activity; IEA.
DR GO; GO:0003889; F:alpha DNA polymerase activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006260; F:DNA replication; IEA.
DR InterPro: IPR011708; DNA_pol3_alpha.
DR InterPro: IPR004365; OB_RNA_NA_bd.
DR InterPro: IPR003141; Pesterase_PHP_N.
DR InterPro: IPR004013; PHP_C.
DR InterPro: IPR004805; PolC_alpha.
DR Pfam: PF07733; DNA_pol3_alpha; 1.
DR Pfam: PF02811; PHP; 1.
DR Pfam: PF01336; RNA_anti; 1.
DR SMART: SM00481; POLIITAC; 1.
DR TIGRPFAMs: TIGR00594; polc; 1.
KW Complete proteome; DNA replication; DNA-directed DNA polymerase;
KW Nucleotidyltransferase; Transferase.
SQ SEQUENCE 1228 AA; 139197 MW; 39B848DEFC7783 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1228;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 357 EYKDDDD 363

RESULT 52
Q81LD1_PLAF7 PRELIMINARY; PRT; 1267 AA.
AC Q81LD1;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Hypothetical protein.
GN ORFNames=PL14_0313;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
[1]
RA NCBILOTIDE SEQUENCE.
RP STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eissen J.A., Rutherford K., Salzberg S.L., Craig S.,
RA Chan M.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiuoli S.,
RA Pereira M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA Venter J.C., Carnucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
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CC -----
CC EMBL: AE014821; AAN36926.1; -; Genomic_DNA.
DR InterPro: IPR002048; EF_hand_Ca_bd.
DR PROSITE: PS00018; EF_HAND_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1267 AA; 152262 MW; 239F91EBBD942C80 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1267;

Beet Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 855 NYKDDDEK 862

RESULT 53
PDS5_YEAST STANDARD; PRT: 1277 AA.

AC 004264; Q04780; Integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 1.
DT 07-MAR-2006, entry version 35.
DE Sister chromatid cohesion protein PDS5 (Precocious dissociation of
DE sisters protein 5).
GN Name=PDS5; OrderedLocustNames=YMR076C; ORFNames=YM9582.01C, YM916.15C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;

[1]
NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RA MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagsi K., Lyne G., Mould S., Odeh C., Pearson D., Rajandream M.A.,
RA Rice F., Skelton J., Walsh S.V., Whitehead S., Barrall B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XII.";
RL Nature 387:90-93(1997).
RN [2]
RP FUNCTION AND SUBCELLULAR LOCATION.
RX MEDLINE=20517447; PubMed=11062262; DOI=10.1083/jcb.151.3.613;
RA Hartman T., Stead K., Koshland D., Guacci V.;
RT "Pds5p is an essential chromosomal protein required for both sister
RT chromatid cohesion and condensation in Saccharomyces cerevisiae.";
RL J. Cell Biol. 151:613-626(2000).
RN [3]
RP FUNCTION.
RX MEDLINE=21065936; PubMed=11137006; DOI=10.1016/S0960-9822(00)00854-X;
RA Panizza S., Tanaka T., Hochwagen A., Eisenhaber F., Nasmyth K.;
RT "Pds5 cooperates with cohesin in maintaining sister chromatid
RT cohesion.";
RL Curr. Biol. 10:1557-1564(2000).
RN [4]
RP ACETYLATION.
RX PubMed=11864574; DOI=10.1016/S0960-9822(02)00681-4;
RA Ivanov D., Schleiffer A., Eisenhaber F., Mechtler K., Haering C.H.,
RA Nasmyth K.;
RT "Pds5 is a novel acetyltransferase that can acetylate proteins
RT involved in cohesion.";
RL Curr. Biol. 12:323-328(2002).
RN [5]
RP LEVEL OF PROTEIN EXPRESSION.
RX MEDLINE=22923965; PubMed=14562106; DOI=10.1038/nature02046;
RA Gaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A.,
RA Dephoure N., O'Shea E.K., Weissman J.S.;
RT "Global analysis of protein expression in yeast.";
RL Nature 425:337-341(2003).
CC -!- FUNCTION: Essential for the establishment and maintenance of
CC sister chromatid cohesion at centromere proximal and distal
CC regions during S phase. Also required for chromosomal
CC condensation.
CC -!- INTERACTION:
CC Self; NDCxp-1; InAct=EBI-13077, EBI-13077;
CC -!- PTM: Acetylated by ECO1.
CC -!- MISCELLANEOUS: Present with 7720 molecules/cell.
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CC -----
DR EMBL: Z49259; CAA89322.1; -; Genomic DNA.
DR EMBL: Z49952; CAA88801.1; -; Genomic DNA.
DR PIR: S54451, S54451.
DR InAct: Q04264; -;
DR GeneOnline: 142743; -;
DR Ensemble: YMR076C; Saccharomyces cerevisiae.
DR GenomeReviews: Z71257 GR; YMR076C.
DR SGD: S000004681; PDS5_
DR BioCyc: SCER-828-01; SCER-828-01-004587-MONOMER; -;
DR LinkHub: Q04264; -;
DR GO: GO:0000794; C:condensed nuclear chromosome, IDA.
DR GO: GO:0042802; F:protein self binding, IPI.
DR GO: GO:0007076; P:mitotic chromosome condensation, IMP.
DR GO: GO:0007064; P:mitotic sister chromatid cohesion, IMP.
DR GO: GO:0006473; P:protein amino acid acetylation, IDA.
DR InterPro: IPR011989; ARM-1like.
DR InterPro: IPR000357; HEAT, 1.
DR Pfam: PF02985; HEAT, 1.
DR Acetylation: Cell cycle; Cell division; Complete proteome; Mitosis;
KW Nuclear protein.
FT CHAIN 1 1277 Sister chromatid cohesion protein PDS5.
FT /FTID=PRO_000056280.
SQ SEQUENCE 1277 AA; 147041 MW; 9DF40A5274FD9623 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 1277;
Beet Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 1265 DYKDDDD 1271

RESULT 54
Q6FN28 CANGA
ID Q6FN28 CANGA PRELIMINARY; PRT: 1305 AA.
AC Q6FN28;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 20.
DE Similar to sp|P12753 Saccharomyces cerevisiae YNL250w RAD50 DNA repair
DE protein.
GN OrderedLocustNames=CAGLOJ077889;
OS Candida glabrata (yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bostrame A., Boyer J., Carlotto L., Confanioli F., de Darvar A.,
RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerret A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Ocas S., Olier-Kalogeropoulos O.,
RA Pellens S., Portier S., Richard G.-F., Strub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissenbach J.,
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
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CC
CC EMBL: CR380956; CAG60997.1; -; Genomic DNA.

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DR GO; GO:0005694; C:cytosome; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030870; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0004518; F:nuclease activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0051276; P:chromosome organization and biogenesis; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR004584; Rad50.
DR InterPro; IPR007517; Rad50_Zn_hook.
DR InterPro; IPR003395; SMC_N.
DR InterPro; IPR013134; Zn_hook_Rad50.
DR Pfam; PF04423; Rad50_zn_hook; 1.
DR Pfam; PF02463; SMC_N; 1.
DR TIGRPFAM; TIGR00606; rad50; 1.
DR Complete proteome.
SQ SEQUENCE 1305 AA; 150668 MW; 7489860D317CFE80 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1305;
Best Local Similarity 87.5%; Pred. No. 2.2e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 1095 DYKDDDD 1102

RESULT 55
Q81B1 PLAF7 PRELIMINARY; PRT; 1523 AA.
AC Q81B1.
DT 01-MAR-2003; integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003; sequence version 1.
DT 07-FEB-2006; entry version 16.
DE Hypothetical protein PF10185w.
GN Name=PF10185w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagers K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorlov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders S., Stevens K.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Simmonds M.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulistio J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531(2002).
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CC -----
DR EMBL; AL929355; CAD51723.1; -; Genomic_DNA.
DR InterPro; IPR013320; ConA_like_subgrp.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF03815; LCCL; 1.
DR PROSITE; PSS0820; LCCL; 1.
DR PROSITE; PSS0231; RICIN_B_LLECTIN; 1.

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KM Hypothetical protein; Repeat.
SQ SEQUENCE 1523 AA; 178335 MW; DAAD8056B3C97C7D CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1523;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
DB 809 DYKDDDD 816

RESULT 56
Q81B8 PLAF7 PRELIMINARY; PRT; 1687 AA.
AC Q81B8.
DT 01-MAR-2003; integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003; sequence version 1.
DT 21-FEB-2006; entry version 13.
DE Hypothetical protein MAL8P1.18.
GN Name=MAL8P1.18;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Berriman M., Churcher C.M., Harris B., Harris D.,
RA Mungall K.L., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagers K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorlov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders S., Stevens K.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Simmonds M.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulistio J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531(2002).
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CC -----
DR EMBL; AL944507; CAD51099.1; -; Genomic_DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR00804; Clat_adaptor_s.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR003029; S1_RNA_bd.
DR SMART; SM00316; S1; 2.
DR PROSITE; PSS0989; CLAT_ADAPTOR_S; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 1687 AA; 203792 MW; C850B170184C0467 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 1687;
Best Local Similarity 85.7%; Pred. No. 2.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 315 DYKDDDD 321

RESULT 57
Q4XUN1 PLAF7 PRELIMINARY; PRT; 1818 AA.
AC Q4XUN1.
DT 05-JUL-2005; integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005; sequence version 1.
DT 07-FEB-2006; entry version 4.
DE Hypothetical protein (fragment).
GN ORFNames=PC000259.03.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
RX MEDLINE=15637271; DOI=10.1126/science.1103717;
RA Hall N., Kariis M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza U.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III;

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RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
 RA Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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 CC
 DR EMBL, CAJ01003023; CAJ79380.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1818 1818
 SQ SEQUENCE 1818 AA; 212574 MW; 66385CDD5FBE512C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1818;
 Best Local Similarity 75.0%; Pred. No. 3.1e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
 |||:||||
 Db 1693 DYSDDEBK 1700

RESULT 58

O4UBC4 THEAN

ID O4UBC4 THEAN PRELIMINARY; PRT; 1921 AA.

AC O4UBC4; 05-JUL-2005, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Hypothetical protein.

GN ORFNames=TA18820;

OS Theileria annulata.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

NCBI_TaxID=5874;

OX [1]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=Ankara isolate clone C9;

RX PubMed=1594597; DOI=10.1258/jrm.98.7.320;

RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,

RA Kerhoun A., Aslett M., Bishop R., Bouchier C., Cochet M.,

RA Coulson R.M.R., Cronin A., de Villiers E.P., Frazer A., Foster N.,

RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,

RA Larke N., Lord A., Maier P., McKellar S., Mooney P., Morton F.,

RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitch E.,

RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,

RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,

RA Langley G., Rajandream M.A., McKeever D., Shiels B., Tait A.,

RA Barrell B., Hall N.;

RT "Genome of the host-cell transforming parasite *Theileria annulata*RT compared with *T. parva*.";

RL Science 309:131-133(2005).

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CC EMBL, CR940352; CAI75877.1; -; Genomic_DNA.

DR EMBL, CR940352; CAI75877.1; -; Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 1921 AA; 225331 MW; C15605816DA5711C CRC64;

Query Match 80.9%; Score 38; DB 2; Length 1921;

Best Local Similarity 85.7%; Pred. No. 3.3e+03;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
 |||:||||
 Db 155 DYSDDD 161

RESULT 59

O5ASE7 EMENI

ID O5ASE7 EMENI PRELIMINARY; PRT; 2051 AA.

AC O5ASE7; 26-APR-2005, integrated into UniProtKB/TrEMBL.

DT 26-APR-2005, sequence version 1.

DT 07-MAR-2006, entry version 10.

DE B1MB EMENI CELL DIVISION-ASSOCIATED PROTEIN B1MB.

GN ORFNames=AN8783.2;

OS *Aspergillus nidulans* F5SC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emericella.

NCBI_TaxID=227321;

OX [1]

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=F5SC 4; DOI=10.1038/nature04341;

RX PubMed=16372000; DOI=10.1038/nature04341;

RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-U., Wortman J.R.,

RA Batzoglou S., Lee S.-I., Bastenkmann M., Spevak C.C., Clutterbuck J.,

RA Kapitonov V., Jurka J., Scanzocchio C., Farman M., Butler J.,

RA Purcell S., Harris S., Braus G.H., Drant O., Busch S., D'Entfert C.,

RA Boucher C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,

RA Doonan J.H., Yu J., Vlenken K., Pain A., Freitag M., Selker E.U.,

RA Archer D.B., Penhaly M.A., Oakley B.R., Momany M., Tanaka T.,

RA Kumagai T., Asai K., Machida M., Nieman W.C., Dunning D.W.,

RA Caddick M., Hynes M., Paolletti M., Fischer R., Miller B.L., Dyer P.S.,

RA Sachs M.S., Osmant S.A., Birren B.W.;

RT "Sequencing of *Aspergillus nidulans* and comparative analysis with A.RT *fumigatus* and A. *oryzae*.";

RL Nature 438:1105-1115(2005).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

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CC EMBL, AACD01000161; EAA60576.1; -; Genomic_DNA.

DR EMBL, AACD01000161; EAA60576.1; -; Genomic_DNA.

DR GO: GO:0005634; C:nucleus; IEA.

DR GO: GO:0005488; F:binding; IEA.

DR GO: GO:0008233; F:peptidase activity; IEA.

DR GO: GO:0051301; P:cell division; IEA.

DR GO: GO:0006508; P:proteolysis; IEA.

DR InterPro: IPR005314; Peptidase C50.

DR PANTHER: PTHR12792; Peptidase_C50; 1.

DR Pfam: PF03568; Peptidase_C50; 1.

KW Cell division; Hydrolase.

SQ SEQUENCE 2051 AA; 225809 MW; 97E9C0EC70590464 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2051;

Best Local Similarity 85.7%; Pred. No. 3.5e+03;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
 |||:||||
 Db 883 DYQDDDD 889

RESULT 60

B1MB EMENI

ID B1MB EMENI STANDARD; PRT; 2067 AA.

AC P33144; 01-OCT-1993, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-1993, sequence version 1.

DT 07-FEB-2006, entry version 30.

DE Separin (EC 3.4.22.49) (Separase) (Cell division-associated protein

DE b1mb).

GN Name=b1mb;

OS *Emmericella nidulans* (*Aspergillus nidulans*).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emericella.

NCBI_TaxID=162425;

```

RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP STRAIN=4773; PubMed=1639810;
RX MEDLINE=92348436; Pubmed=1639810;
RA May G.S., McGoldrick C.A., Holt C.L., Denison S.H.;
RT "The blm3 mutation of Aspergillus nidulans uncouples DNA replication
  from the completion of mitosis.";
RL J. Biol. Chem. 267:15737-15743(1992).
CC -1- FUNCTION: Required for nuclear division. Could function in the
  mitotic spindle.
CC -1- CATALYTIC ACTIVITY: All bonds known to be hydrolyzed by this
  endopeptidase have arginine in P1 and an acidic residue in P4. P6
  is often occupied by an acidic residue or by an hydroxy-amino-acid
  residue, the phosphorylation of which enhances cleavage.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- SIMILARITY: Belongs to the peptidase C50 family.
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DR EMBL: M83232; AAA33297.1; ALT_TERM; Genomic_DNA.
DR PIR: A42854; A42854.
DR MEROPS: C50.001; -.
DR InterPro: IPR005314; Peptidase_C50.
DR InterPro: IPR011990; TPR-like helical.
DR PANTHER: PTHR12792; Peptidase_C50; 1.
DR Pfam: PF03568; Peptidase_C50_1.
KW Cell cycle; Cell division; Chromosome partition; Hydrolyase; Mitosis;
  Nuclear protein; Protease; Thiol protease.
FT CHAIN 1 2067
FT FTID=PRO.0000205902.
FT ACT SITE 1964 1964 By similarity.
SQ SEQUENCE 2067 AA; 227926 MW; E0655D939EC148DB CRC64;

Query Match 80.9%; Score 38; DB 1; Length 2067;
Best Local Similarity 85.7%; Pred. No. 3.5e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 899 DYQDDDD 905

RESULT 61
ID 097225_PLA7 PRELIMINARY; PRT; 2226 AA.
AC 097225;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 3.
DT 07-FEB-2006, entry version 21.
DE Hypothetical protein MAL3P2.2.
GN Name=MAL3P2.2; Synonyms=PPC0165w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=99376085; Pubmed=10448855; DOI=10.1038/22964;
RX Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
  Churcher C.M., Craig A., Davies R.M., Devlin K., Feltham T.,
  Gantler S., Gwilliam R., Hamlin N., Harris B., Holroyd S., Hornsby T.,
  Horrocks P., Jorgels K., Jassal B., Kyes S., McLean J., Moulé S.,
  Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
  Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
  Whitehead S., Woodward J.R., Newbold C., Barrall B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
  falciparum";
RL Nature 400:532-538(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=2255708; Pubmed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Beriman M., Churcher C.M., Harris B., Harris D.,
  Mungall K.L., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
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RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
  Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
  Cronin A., Davies R.M., Davis P., Dear P., Dearden F., Doggett J.,
  Feltham T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
  Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
  Humphray S., Jorgels K., James K.D., Johnson D., Kenyon A.,
  Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
  Line A., Maddison M., McLean J., Mooney P., Moulé S., Murphy L.,
  Oliver K., Ormond D., Price C., Quail M.A., Rabinovitch E.,
  Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
  Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
  Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
  Sulston J.E., Craig A., Newbold C., Barrall B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
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DR EMBL: AL034558; CAB38989.3; -; Genomic DNA.
DR GO: GO:0005815; C:microtubule organizing center; IEA.
DR GO: GO:000922; C:spindle pole; IEA.
DR GO: GO:000226; P:microtubule cytoskeleton organization and b. .; IEA.
DR InterPro: IPR007259; SPC97_SPC98.
DR PANTHER: PTHR19302; SPC97_SPC98; 1.
DR Pfam: PF04130; SPC97_SPC98; 1.
KW Hypothetical protein.
SQ SEQUENCE 2226 AA; 267976 MW; 8690501ED4994768 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2226;
Best Local Similarity 85.7%; Pred. No. 3.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 218 DYQDDDD 224

RESULT 62
ID 05KID7_CRYNE PRELIMINARY; PRT; 2384 AA.
AC 05KID7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE 1-phosphatidylinositol-3-phosphate 5-kinase, putative.
GN OrderdocusNames=CND03330;
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
  Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=5207;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=JEC21;
RX Pubmed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amodeo P., Bruno D.,
  Vamathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
  Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
  D'Souza C.A., Fox D.S., Grinberg V., Fu U., Fukushima M., Haas B.J.,
  Huang J.C., Jambon G., Jones S.J.W., Koo H.L., Krzyzanski M.I.,
  Kwon-Chung K.J., Lengeler K.B., Maiti R., Maira M.A., Maira R.E.,
  Matheson C.A., Mitchell T.G., Petrea M., Riggs F.R., Salzberg S.L.,
  Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
  Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
  Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
  Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
  Cryptococcus neoformans";
RL Science 307:1321-1324(2005).
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```

DR EMBL: AE017344; AAW43260.1; -; Genomic DNA.
 DR GO: GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016301; F:kinase activity; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0044267; F:cellular protein metabolism; IEA.
 DR InterPro: IPR002423; Cpn60/TCP-1.
 DR InterPro: IPR002498; PIP5K.
 DR InterPro: IPR00306; Znf FYVE.
 DR Pfam: PF00118; Cpn60_TCP1; 1.
 DR Pfam: PF01363; FYVE; 1.
 DR Pfam: PF01504; PIP5K; 1.
 DR SMART: SM00064; FYVE; 1.
 DR PROSITE: PS0178; ZF_FYVE; 1.
 KW Complete proteome; Kinase.
 SO SEQUENCE 2384 AA; 26368 MW; AD29D2B0BF2F793 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2384;
 Best Local Similarity 85.7%; Pred. No. 4.1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7
 Db 429 EYKDDDD 435

RESULT 63

OS05U02_CRYNE PRELIMINARY; PRT; 2432 AA.
 AC 055U02;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=CNB03020;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 CC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 CX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 Wicks B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

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 CC -----
 DR EMBL: AAEY0100020; EAL21247.1; -; Genomic DNA.
 DR GO: GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR002498; PIP5K.
 DR InterPro: IPR00306; Znf FYVE.
 DR Pfam: PF00118; Cpn60_TCP1; 1.
 DR Pfam: PF01363; FYVE; 1.
 DR Pfam: PF01504; PIP5K; 1.
 DR SMART: SM00064; FYVE; 1.
 DR PROSITE: PS0178; ZF_FYVE; 1.
 KW Hypothetical protein.
 SO SEQUENCE 2432 AA; 268925 MW; A5A9E486EDC898EE CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2432;
 Best Local Similarity 85.7%; Pred. No. 4.2e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7
 Db 429 EYKDDDD 435

RESULT 64

OS081AM1_PLAF7 PRELIMINARY; PRT; 2577 AA.
 AC 081AM1;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Hypothetical protein MAL8P1.153.
 GN Name=MAL8P1.153;
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CX NCBI_TaxID=36329;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
 Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AL844507; CAD51342.1; -; Genomic DNA.
 DR GO: GO:0046872; F:metal ion binding; IEA.
 DR GO: GO:0044222; F:metallopeptidase activity; IEA.
 DR GO: GO:0009405; P:pachogonensis; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR011591; Botulinum.
 DR ProDom: PD001963; Botulinum; 1.
 KW Hypothetical protein.
 SO SEQUENCE 2577 AA; 299293 MW; 025BBC240587F4D7 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 2577;
 Best Local Similarity 85.7%; Pred. No. 4.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYKDDDD 7
 Db 1103 EYKDDDD 1109

RESULT 65

OS08T86_PLAFA PRELIMINARY; PRT; 119 AA.
 AC 08T86;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Erythrocyte membrane protein 1 (Fragment).
 GN Name=var;
 OS Plasmodium falciparum.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CX NCBI_TaxID=3633;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2183615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
 RA Fowler B.V., Peters J.M., Gatton M.L., Chen N., Cheng O.;
 RT "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
 genes among Asia-Pacific isolates."
 RL Mol. Biochem. Parasitol. 120:117-126(2002).

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 CC -----

Query Match 80.9%; Score 38; DB 2; Length 2577;
 Best Local Similarity 85.7%; Pred. No. 4.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;


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DR EMBL: AY054812; AAL11176.1; -; Genomic DNA.
DR EMBL: AY054843; AAL11207.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 14141 MW; B4CSEA748DDABBE5 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 119;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 45 YKDEDDK 51

RESULT 66
ID 06S859_PLAFA PRELIMINARY; PRT; 132 AA.
AC 06S859;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Erythrocyte membrane protein 1 (Fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15122533; DOI=10.1086/383250;
RA Kaestli M., Cortes A., Lagog M., Ott M., Beck H.-P.;
RT "Longitudinal Assessment of Plasmodium falciparum var Gene
RT Transcription in Naturally Infected Asymptomatic Children in Papua New
RT Guinea.";
RL Infect. Dis. 189:1942-1951 (2004).
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CC -----
DR EMBL: AY462771; MAR32011.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 15767 MW; E1320176782A6AF CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 132;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 50 YKDEDDK 56

RESULT 67
ID 07RB94_PLAYO PRELIMINARY; PRT; 136 AA.
AC 07RB94;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=PY06254;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=17XN1;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

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RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jane C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL: AABL01002092; EAA18432.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 136 AA; 16664 MW; BDF23EE968AD6A27 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 136;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 107 EYDDDDK 114

RESULT 68
ID 04Y0T6_PLACH PRELIMINARY; PRT; 142 AA.
AC 04Y0T6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=PC103434.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berrihan M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza U.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL: CAJ01001887; CAH77226.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 142 AA; 16322 MW; SCC0816338829E34 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 142;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 110 DYDDDDK 117

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RESULT 69
OSTKFL1 ORYSA PRELIMINARY; PRT; 164 AA.
ID 05TKFL1
AC 05TKFL1
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein OSJNB0030114.15 (Hypothetical protein
OSJNB0086G17.6).
GN Name=OSJNB0030114.15; Synonyms=OSJNB0086G17.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=33947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee H.-F.,
RA Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Lu P.-C.,
RA Wei F.-J., Wu C.-C., Wu S.-W., Yang K.-C., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNB0086G17 genomic sequence.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee H.-F.,
RA Lee M.-C., Leu H.-L., Li Y.-F., Lin S.-J., Lin Y.-C., Lu P.-C.,
RA Wei F.-J., Wu C.-C., Wu S.-W., Yang K.-C., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNB0086G17 genomic sequence.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AC144455; AAV57795.1; -; Genomic_DNA.
DR EMBL; AC136217; AAV59389.1; -; Genomic_DNA.
DR Gramene; OSTKFL1; -;
KM Hypothetical protein.
SQ SEQUENCE 164 AA; 19188 MW; DE35652258B747CB CRC64;

Query Match 78.7%; Score 37; DB 2; Length 164;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 147 DYSDDD 153

RESULT 70
O4Y3M3 PLACH PRELIMINARY; PRT; 168 AA.
ID O4Y3M3
AC O4Y3M3
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PC000369.01.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

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RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.C., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
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CC preliminary data.
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CC -----
DR EMBL; AALX0100008; EAP4635.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 179 AA; 20526 MW; BB41828BC1F0657 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 179;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 67 DYKDDDK 8
DB 67 DYKDDDK 74

RESULT 71
O2ZA91 9GAMM PRELIMINARY; PRT; 179 AA.
ID O2ZA91
AC O2ZA91
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
GN ORFNames=Shewm4DRAPT_1640;
OS Shewanella sp. MR-4;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=60480;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=MR-4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella sp. MR-4.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=MR-4;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome of Shewanella sp. MR-4.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AALX0100008; EAP4635.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 179 AA; 20526 MW; BB41828BC1F0657 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 179;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

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Db 155 DYSDDDD 161

RESULT 72

Q35Y65_9GAMM PRELIMINARY; PRT; 179 AA.

AC Q35Y65; 06-DEC-2005, integrated into UniProtKB/TrEMBL.

DT 06-DEC-2005, sequence version 1.

DE Hypothetical protein.

GN ORFNames=Shewm7DRAFT_1872;

OS Shewanella sp. MR-7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

NCBI_TaxID=60481;

NP NUCLEOTIDE SEQUENCE.

RP STRAIN=MR-7;

RG US DOE Joint Genome Institute (JGI-ORNL);

RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,

RT Hammon N., Istrail S., Pitluck S., Richardson P.,

RL "Sequencing of the draft genome and assembly of Shewanella sp. MR-7.";

CC Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.

CC [2]

CC NUCLEOTIDE SEQUENCE.

RP STRAIN=MR-7;

RG US DOE Joint Genome Institute (JGI-ORNL);

RA Larimer F., Land M.;

RT "Annotation of the draft genome of Shewanella sp. MR-7.";

CC Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: ALA01000019; EAP23723.1; -; Genomic_DNA.

CC Hypothetical protein.

CC SEQUENCE 179 AA; 20504 MW; BB4A13DC035F0657 CRC64;

SO

Query Match 78.7%; Score 37; DB 2; Length 179;

Best Local Similarity 85.7%; Pred. No. 3.8e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 155 DYSDDDD 161

RESULT 73

Q366F4_9GAMM PRELIMINARY; PRT; 179 AA.

AC Q366F4; 06-DEC-2005, integrated into UniProtKB/TrEMBL.

DT 06-DEC-2005, sequence version 1.

DE Hypothetical protein.

GN ORFNames=Shewana3DRAFT_0257;

OS Shewanella sp. ANA-3.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

NCBI_TaxID=94122;

NP NUCLEOTIDE SEQUENCE.

RP STRAIN=ANA-3;

RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Deter J.C., Glavina T.,

RT Hammon N., Istrail S., Pitluck S., Richardson P.,

RL "Sequencing of the draft genome and assembly of Shewanella sp. ANA-

3.";

RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.

CC [2]

CC NUCLEOTIDE SEQUENCE.

RP STRAIN=ANA-3;

RG US DOE Joint Genome Institute (JGI-ORNL);

RA Larimer F., Land M.;

RT "Annotation of the draft genome of Shewanella sp. ANA-3.";

CC Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

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preliminary data.

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CC -----

CC EMBL: ALA01000054; EAP17904.1; -; Genomic_DNA.

CC Hypothetical protein.

CC SEQUENCE 179 AA; 20504 MW; BB4A13DC035F0657 CRC64;

SO

Query Match 78.7%; Score 37; DB 2; Length 179;

Best Local Similarity 85.7%; Pred. No. 3.8e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 155 DYSDDDD 161

RESULT 74

Q8EFW6_SHEON PRELIMINARY; PRT; 179 AA.

AC Q8EFW6; 01-MAR-2003, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.

DE Hypothetical protein.

GN ORFNames=SO_1849;

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

NCBI_TaxID=70863;

NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RP STRAIN=MR-1;

RG MEDLINE=22297686; PubMed=12368913; DOI=10.1038/nbt749;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Sehadri R., Ward N.L., Methe B.A.,

RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.D.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,

RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,

RA Lee K., Berry K.J., Lee C., Mueller J., Kouri H.M., Gill J.,

RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,

RA Venter J.C., Neilson K.H., Fraser C.M.;

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

Shewanella oneidensis.";

RL Nat. Biotechnol. 20:1118-1123(2002).

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CC -----

CC EMBL: AE014299; AAN54901.1; -; Genomic_DNA.

DR BioCyc: SONE211586; SO1849-MONOMER; -; _

KM Complete proteome; Hypothetical protein.

SO SEQUENCE 179 AA; 20517 MW; F68878E2D4AAB653 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 179;

Best Local Similarity 85.7%; Pred. No. 3.8e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 155 DYSDDDD 161

RESULT 75
ID Q2M3Y9_PHYIN PRELIMINARY; PRT; 197 AA.
AC Q2M3Y9; 21-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DE 21-FEB-2006, entry version 1.
DE 205 proteasome subunit.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Phytophthora.
NCBI_TaxID=4787;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DDR7602;
RA Kamoun S., Kannekanti T.-D., Win J.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY961472; AA143418.1; -, mRNA.
KW Proteasome.
SQ SEQUENCE 197 AA; 22308 MW; C067102DCFB81314 CRC64;
Query Match 78.7%; Score 37; DB 2; Length 197;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 YKDDDD 8
Db 28 YKDDDD 34
RESULT 76
ID Q42415_PLABE PRELIMINARY; PRT; 225 AA.
AC Q42415;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DE Hypothetical protein (Fragment).
GN ORFNames=PB000975.00.0;
OS Plasmodium berthei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berziman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Church C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
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DR EMBL; CA101000723; CAH94968.1; -, Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 225 AA; 27208 MW; 0BEFF4DB8264244 CRC64;
Query Match 78.7%; Score 37; DB 2; Length 225;

Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYKDDDD 8
Db 123 DYKDDDD 130
RESULT 77
ID Q5CPE3_CRYPV PRELIMINARY; PRT; 259 AA.
AC Q5CPE3;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=cgds_4610;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimeriida;
OC Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RX PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abraham J.E., Zhu G.,
RA Lacroix C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Kontorov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum."
RL Science 304:441-445(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
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DR EMBL; AB0100017; EAK87298.1; -, Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 259 AA; 29923 MW; E37F2455F468C3B CRC64;
Query Match 78.7%; Score 37; DB 2; Length 259;
Best Local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYKDDDD 7
Db 175 DYKDDDD 181
RESULT 78
ID Q74H22_LACJO PRELIMINARY; PRT; 268 AA.
AC Q74H22;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE Hypothetical protein.
GN OrderedLocuNames=LJ0673; ORFNames=LJ_0673;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
NCBI_TaxID=33959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RX PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pitet A.-C., Zwalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium

RT Lactobacillus johnsonii NCC 533. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
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 CC -----
 CC EMBL: AE017198; AAS09548.1; -; Genomic_DNA.
 CC GenomeReviews; AE017198 GR; LJ0673.
 CC BioCyc: LJ08257314:LJ0673-MONOMER; -;
 CC DR GO: GO:0003824; F: catalytic activity; IEA.
 CC DR InterPro: IPR013094; AB_Hydrolase_3.
 CC DR InterPro: IPR000379; Ser_estrs.
 CC DR Pfam: PF07859; Abhydrolase_3; 1.
 CC KM Complete proteome: Hypothetical protein.
 CC SEQUENCE 268 AA; 30797 MW; 5319ABE0CEB19A9F CRC64;
 QY
 Db 1 DYKDDDD 8
 94 DYTDDDQ 101
 Query Match 78.7%; Score 37; DB 2; Length 268;
 Best Local Similarity 75.0%; Pred. No. 5.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 79
 054U43 D1CD1
 ID 054U43 D1CD1 PRELIMINARY; PRT; 299 AA.
 AC 054U43;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=DD80204132;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OC NCBI_TaxId=44689;
 [1]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RX PubMed=15875012; DOI=10.1038/nature03481;
 RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.A.,
 RA Sungang R., Berriman M., Song J., Olsen R., Safranek J., Xu Q.,
 RA Tuncgil B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Banker A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Fairbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K.D., Quiles M., Madan Babu M., Salto T.,
 RA Buchrieser C., Wardrop A., Felder M., Thangavelu M., Johnson D.,
 RA Knights A., Louised H., Mungall K.L., Oliver K., Price C.,
 RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
 RA Sanders M., Ma J., Kohara Y., Sharp S., Simmons M.N., Spiegler S.,
 RA Tivey A., Sganou S., White B., Walker D., Woodward J.R., Winckler T.,
 RA Tanaka Y., Shaulsky G., Gishler M., Weinstock G.M., Rosenthal A.,
 RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzner M.,
 RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
 RA Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 435:43-57(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
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 CC preliminary data.
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 CC -----
 CC EMBL: AAF101000072; EAL6940.1; -; Genomic_DNA.
 CC DR Hypothetical protein.
 KM SEQUENCE 299 AA; 34386 MW; BEAD000562DC563B CRC64;
 SQ

Query Match 78.7%; Score 37; DB 2; Length 299;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DYKDDDD 7
 Db 252 DYKDDDD 258
 RESULT 80
 038DT4 9TRYP
 ID 038DT4 9TRYP PRELIMINARY; PRT; 335 AA.
 AC 038DT4;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=TB09.211.2220;
 OS Trypanosoma brucei.
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OC NCBI_TaxId=5691;
 [1]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=927/4 GUTa10.1;
 RX PubMed=16020724; DOI=10.1126/science.1112812;
 RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
 RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
 RA Chedin E., Peacock C., Bartholomew D.C., Haas B.J., Tran A.-N.,
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
 RA Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
 RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Petersen J.,
 RA Salzberg S.L., Shallow J., Silva J.C., Sundaram J., Westerberger S.,
 RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
 RA Hall N.;
 RT "Comparative genomics of trypanosomatid parasitic protozoa";
 RL Science 309:404-409(2005).
 [2]
 NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=927/4 GUTa10.1;
 RX PubMed=16020726; DOI=10.1126/science.1112842;
 RA Berriman M., Ghedin E., Hertz-Fowler C., Blandin G., Renauld H.,
 RA Bartholomew D.C., Lennard N.J., Caler E., Hamlin N.B., Haas B.,
 RA Bohme U., Hamrick L., Aslett M.A., Shallow J., Marcello L., Hou L.,
 RA Wickstead F., Alsmark U.C.M., Arrowsmith C., Atkin R.J., Barron A.J.,
 RA Bringaud F., Brooks K., Carrington M., Cherevach I.,
 RA Chillingworth T.-J., Churcher C., Clark L.N., Corton C.H., Cronin A.,
 RA Davies R.M., Doggett J., Djikeng A., Feldlyum T., Field M.C.,
 RA Fraser A., Goodhead I., Hance Z., Harper D., Harris B.R., Hauser H.,
 RA Hostetler J., Ivens A., Jagers K., Johnson D., Johnson J., Jones K.,
 RA Kerhornou A.X., Koo H., Larke N., Landfear S., Larkin C., Leech V.,
 RA Lane A., Lord A., Macleod A., Mooney P.J., Moule S., Martin D.M.A.,
 RA Morgan G.W., Mungall K., Norbertczak H., Ormond D., Pai G.,
 RA Peacock C.S., Peterson J., Quail M.A., Rabinowitsch E.,
 RA Rajandream M.-A., Reiter C., Salzberg S.L., Sanders M., Schobel S.,
 RA Sharp S., Simmons M., Simpson A.J., Tallon L., Turner C.M.R.,
 RA Tait A., Tivey A.R., Van Aken S., Walker D., Wanless D., Wang S.,
 RA White B., White O., Whithead S., Woodward J., Wortman J., Adams M.D.,
 RA Embley T.M., Gull K., Ullu E., Barry J.D., Fairlamb A.H.,
 RA Opperdoes F., Barrell B.G., Donelson J.E., Hall N., Frazer C.M.,
 RA Melville S.E., El-Sayed N.M.;
 RT "The genome of the African trypanosome Trypanosoma brucei";
 RL Science 309:416-422(2005).
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 CC -----
 CC EMBL: CM000207; EANT7036.1; -; Genomic_DNA.
 CC DR Hypothetical protein.
 KM SEQUENCE 335 AA; 38122 MW; AB5C219A51BA4B0 CRC64;
 Query Match 78.7%; Score 37; DB 2; Length 335;
 Best Local Similarity 85.7%; Pred. No. 7.4e+02;
 SQ

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 |||||
 Db 13 DYKDND 19

RESULT 81
 Q6C9S5_YARLI PRELIMINARY; PRT; 341 AA.
 ID Q6C9S5_YARLI
 AC Q6C9S5
 DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE Yarrowia lipolytica chromosome D of strain CLIB122 of Yarrowia
 DE lipolytica.
 GN OrderedLocustNames=YALIID08734g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]

NCBIOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CLIB 122 / E 150;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Babé V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boistrame A., Boyer J., Cattoi L., Confiantoleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.-M., Nikoleki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in Yeasts."
 RL Nature 430:35-44(2004).
 CC -----
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 CC -----
 DR EMBL: CR382130; CAG80775.1; -; Genomic_DNA.
 DR InterPro: IPR013256; Chromatin_SPT2.
 DR Complete proteome.
 SQ SEQUENCE 341 AA; 38489 MW; C7ACBF8FBFC3AD0 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 341;
 Best Local Similarity 85.7%; Pred. No. 7.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 |||||
 Db 291 DYSDDD 297

RESULT 82
 BROM1_ANACO STANDARD; PRT; 351 AA.
 ID BROM1_ANACO
 AC 023791
 DT 24-JAN-2006, integrated into UniProtKB/Swiss-Prot.
 DT 01-JAN-1998, sequence version 1.
 DT 07-MAR-2006, entry version 30.
 DE Ananas comosus (Pineapple).
 OS Ananas comosus (Pineapple).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
 OC Ananas.
 OX NCBI_TaxID=4615;
 RN [1]

RP NCBIOTIDE SEQUENCE [mRNA].
 RC STRAIN=cv. N67-10; TISSUE=fruit;
 RA Mura E., Aramaki H., Takata Y., Kono A., Okamoto Y., Ota S.;
 RT "Cloning and sequencing of fruit bromelain."
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Broad specificity for cleavage of proteins,
 CC but strong preference for Z-Arg-Arg-|-NHMe among small molecule
 CC substrates.
 CC -----
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the peptidase C1 family.
 CC -----
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 CC -----
 DR EMBL: D14059; BAA21849.1; -; mRNA.
 DR PIR: T10503; T10503.
 DR HSSP: P07711; ICYL.
 DR MEROPS: C01.028; -.
 DR InterPro: IPR001699; Pept. cys AS.
 DR InterPro: IPR013128; Peptidase_C1A.
 DR InterPro: IPR000668; Peptidase_C1A.
 DR InterPro: IPR013201; Propeptide_129.
 DR PANTHER: PTHR12411; Peptidase_C1; 1.
 DR Pfam: PF08246; Inhibitor_129; 1.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPAIN.
 DR PRODOM: PD000158; Peptidase_C1; 1.
 DR SMART: SM00645; Pept_C1; 1.
 DR PROSITE: PS00640; THIOL_PROTEASE ASN; 1.
 DR PROSITE: PS00139; THIOL_PROTEASE CYS; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE HIS; 1.
 KW Allergen; Hydrolase; Protease; Signal; Thiol protease; Zymogen.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 121 /Ftrid=PRO_0000045809.
 FT CHAIN 122 351 Bromelain.
 FT FT Ftrid=PRO_0000045810.
 FT ACT_SITE 147 147 By similarity.
 FT ACT_SITE 279 279 By similarity.
 FT DISULFID 144 184 By similarity.
 FT DISULFID 178 217 By similarity.
 FT DISULFID 273 325 By similarity.
 SQ SEQUENCE 351 AA; 39055 MW; 33781C55144242B0 CRC64;

Query Match 78.7%; Score 37; DB 1; Length 351;
 Best Local Similarity 85.7%; Pred. No. 7.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8
 |||||
 Db 48 YKDDDK 54

RESULT 83
 BANT_ANTMA STANDARD; PRT; 364 AA.
 ID BANT_ANTMA
 AC Q9FYZ9;
 DT 16-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Benzoyl carboxyl methyltransferase (EC 2.1.1.-) (S-adenosyl-L-
 DE methionine:benzoic acid carboxyl methyltransferase).
 GN Name=BANT;
 OS Antirrhinum majus (Garden snapdragon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Plantaginaceae; Antirrhineae;
 OC Antirrhinum.
 OX NCBI_TaxID=4151;
 RN [1]

NCBIOTIDE SEQUENCE [mRNA], PARTIAL PROTEIN SEQUENCE, DEVELOPMENTAL
 RP STAGE, AND TISSUE SPECIFICITY.
 RX MEDLINE=20312758; PubMed=10852939; DOI=10.1105/epc.12.6.949;

RA Dudareva N., Murfitt L.M., Mann C.J., Gorenstein N., Kolosova N.,
 RA Kish C.M., Bonham C., Wood K.;
 RT "Developmental regulation of methyl benzoate biosynthesis and emission
 in snapdragon flowers.";
 RL Plant Cell 12:949-961(2000).
 CC -1- FUNCTION: Converts benzoic acid into the volatile ester methyl
 benzoates. This scent, mostly produced in a rhythical, diurnal
 manner, attracts the pollinators.
 CC -1- TISSUE SPECIFICITY: Expressed only in the upper and lower petal
 lobes. Not found in the corolla tubes, anthers, pistils, sepals
 and ovaries.
 CC -1- DEVELOPMENTAL STAGE: Expressed in mature flowers with a peak 6 to
 7 days postanthesis.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily.
 CC -----
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 CC -----
 DR EMBL: AF196492; AAF98284.1; -; mRNA.
 DR HSSP: Q9SPV4; 1M6E.
 DR InterPro: IPR005299; Methyltransf_6.
 DR Pfam: PF03492; Methyltransf_7; 1.
 DR KW Direct protein sequencing; Methyltransferase; Transferase.
 FT CHAIN 1 364
 FT /FTid=PRO_0000204466.
 FT COMPRTAS 292 295
 FT SEQUENCE 364 AA; 41011 MW; C10C8E864A581419 CRC64;
 SQ
 Query Match 78.7%; Score 37; DB 1; Length 364;
 Best Local Similarity 75.0%; Pred. No. 8.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 DB 289 DYTDDDDQ 296
 RESULT 84
 ID 053LKL_ORYSA PRELIMINARY; PRT; 451 AA.
 AC 053LKL;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE P-box domain, putative.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
 OC Eubacteriodes; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maici R., Lin H.,
 RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblum T., Tsilirin T.,
 RA Bera J., Kim M., Jin S., Padrosch D., Vuong H., Overton II L.,
 RA Reardon M., Weaver B., Johri S., Lewis M., Uteback T., Van Aken S.,
 RA Norton J., Haas B., Koo H., Ziemann V., Hsiao J., Jobst S.,
 RA de Vazelles A., White O., Salzberg S., Frazer C.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL: AC145321; AA95043.1; -; Genomic_DNA.
 DR InterPro: IPR001810; F-box.
 DR Pfam: PF00646; F-box; 1.
 DR SMART: SM00256; FBOX; 1.
 DR PROSITE: PSS0181; FBOX; 1.

SQ SEQUENCE 451 AA; 51414 MW; 53E24E4CE7C6771E CRC64;
 Query Match 78.7%; Score 37; DB 2; Length 451;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YKDDDK 8
 DB 414 YEDDDDK 420
 RESULT 85
 ID TIG_RHOPA STANDARD; PRT; 452 AA.
 AC 06N5L2;
 DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-MAR-2006, entry version 10.
 DE Trigger factor (TF).
 GN Name=tig; OrderedLocNames=RPA2962;
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodospirillum.
 OX NCBI_TaxID=1076;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larter F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 photosynthetic bacterium Rhodospirillum rubrum.";
 RL Nat. Biotechnol. 22:55-61(2004).
 CC -1- FUNCTION: Involved in protein export. Acts as a chaperone by
 maintaining the newly synthesized protein in an open conformation
 (By similarity).
 CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family. Tig subfamily.
 CC -1- SIMILARITY: Contains 1 PPIase FKBP-type domain.
 CC -----
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 CC -----
 DR EMBL: BX572602; CAE28403.1; -; Genomic_DNA.
 DR GenomeReviews: BX571963 GR; RPA2962.
 DR BioCyc: RPA258594.RPA2962-MONOMER; -.
 DR HAMAP: MF_00303; -; 1.
 DR InterPro: IPR001179; FKBP_PPIase.
 DR InterPro: IPR005215; Trig_fac.
 DR InterPro: IPR008880; Trigger_C.
 DR InterPro: IPR008881; Trigger_N.
 DR Pfam: PF00254; FKBP_C; 1.
 DR Pfam: PF05698; Trigger_C; 1.
 DR Pfam: PF05697; Trigger_N; 1.
 DR PIRSF: PIRSF003095; Trigger_factor; 1.
 DR TRIGFAMS: TRIGR00115; tig; 1.
 DR PROSITE: PSS0059; FKBP_PPIase; 1.
 KW Cell cycle; Cell division; Chaperone; Complete proteome; Isomerase;
 KW Rotamase.
 FT CHAIN 1 452
 FT /FTid=PRO_0000179415.
 FT DOMAIN 171 256
 FT SEQUENCE 452 AA; 50097 MW; 9DCE13323A8B5800 CRC64;
 SQ
 Query Match 78.7%; Score 37; DB 1; Length 452;
 Best Local Similarity 85.7%; Pred. No. 1e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YKDDDK 8
 DB 443 YKDDDK 449

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RESULT 86
Q2R949_ORYSA PRELIMINARY; PRT; 485 AA.
ID Q2R949_ORYSA
AC Q2R949_
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE F-box domain, putative.
GN ORFNames=LOC_0811903970;
OS Oryza sativa (Japanese cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wang R.A., McCombie W.A., Ouyang S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL, DP000010; ABA91967.1; -; Genomic DNA.
SQ SEQUENCE 485 AA; 55570 MW; F65EC789BB4635F4 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 485;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
Db 448 YEDDDK 454

RESULT 87
Q6BV75_DEBHA PRELIMINARY; PRT; 487 AA.
ID Q6BV75_DEBHA
AC Q6BV75_
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Similarities with CA06121|IPF17545 Candida albicans.
GN OrderedLocustNames=DEHA0C054789;
OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 36239 / CBS 767;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Caaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boissière A., Boyer J., Cartolico C., Confantieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead L., Ferry-Dumazet H., Gropi A.,
RA Hantreaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicoud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Porter S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekla F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souleir J.-L.;
RT Genome evolution in yeasts.
RL Nature 430:35-44(2004).
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DR EMBL, CR382135; CAG85944.1; -; Genomic DNA.

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KW Complete proteome.
SQ SEQUENCE 487 AA; 55772 MW; 1DBDC3E39E4959E3 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 487;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 404 DYSDDDD 410

RESULT 88
Q56XW8_ARATH PRELIMINARY; PRT; 487 AA.
ID Q56XW8_ARATH
AC Q56XW8_
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE Hypothetical protein At1g48400.
GN Name=At1g48400;
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusawa M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL, AK21555; BAD94953.1; -; mRNA.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR006566; FBD.
DR InterPro: IPR013101; LTR_2.
DR InterPro: IPR010916; TONB_Box_N.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00579; FBD; 1.
DR SMART: SM00256; FBOX; 1.
DR PROSITE: PS00181; FBOX; 1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 487 AA; 55627 MW; 910FAB97D525B818 CRC64;

Query Match
Best Local Similarity 78.7%; Score 37; DB 2; Length 487;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 282 DYSDDDD 288

RESULT 89
VE2_HP20 STANDARD; PRT; 497 AA.
ID VE2_HP20
AC PS0766;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Regulatory protein E2.
GN Name=E2;
OS Human papillomavirus type 20.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Betapapillomavirus.

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OX NCB1_TaxId=31547;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Delius H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U31778; AA79390.1; -; Genomic_DNA.
DR HSSP; P03122; 2BP.
DR InterPro; IPR012677; a_b_pla1c_nuc_bd.
DR InterPro; IPR00427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; PPV_E2_Cf_1.
DR Pfam; PP00508; PPV_E2_N; 1.
DR ProDom; PD000672; E2_Cf_1.
DR ProDom; PD000678; E2_N; 1.
FT CHAIN
FT 1
FT 497
FT /FtrId=PRO_0000133199.
SQ SEQUENCE 497 AA; 56120 MW; 497CA28B5337CE5 CRC64;

Query Match      78.7%; Score 37; DB 1; Length 497;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8
DB 139 YQDDDK 145

RESULT 90
Q9SX72_ARATH PRELIMINARY; PRT; 513 AA.
ID Q9SX72_ARATH
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE F1AL7.5 protein.
GN Name=F1AL7.5; OrderedLocNames=Atlg48400;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCB1_TaxId=3702;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Vysotskii V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Li J., Gonzale A., Liu A., Vaysberg M.,
RA Sakano H., Chin C., Choi E., Chlou J., Altafi H., Araujo R.,
RA Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Homng B., Huizer L., Khan S., Kim C., Palm C., Rowley D.,
RA Shin P., Walke M., Davis R.W., Ecker J.R., Federspiel N.A.,
RA Theologis A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AC007932; AAD49757.1; -; Genomic_DNA.
DR PIR; B96524; B96524.
DR TAIR; Atlg48400; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR InterPro; IPR013101; LTR_Box_N.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00646; F-box_1.
DR Pfam; SM00579; FBD; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00181; FBOX; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
SQ SEQUENCE 513 AA; 58618 MW; 81A562DBB3DDA0F8 CRC64;

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Query Match      78.7%; Score 37; DB 2; Length 513;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 282 DYSDDD 288

RESULT 91
Q59MN9_CANAL PRELIMINARY; PRT; 524 AA.
ID Q59MN9_CANAL
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Hypothetical protein SRB8 (Fragment).
DE Name=SRB8; ORFNames=CA019.736, CA019.0355;
GN Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCB1_TaxId=237561;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AAC001000222; EAK91730.1; -; Genomic_DNA.
DR EMBL; AAC001000221; EAK91744.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER
FT 524
FT 524
FT SQ SEQUENCE 524 AA; 60272 MW; 2B051E0F462E7283 CRC64;

Query Match      78.7%; Score 37; DB 2; Length 524;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 392 DYNDDD 398

RESULT 92
Q8IEG8_PLAF7 PRELIMINARY; PRT; 554 AA.
ID Q8IEG8_PLAF7
AC Q8IEG8;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein MAL13P1.75.
GN Name=MAL13P1.75;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCB1_TaxId=36329;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=3D7;
RA Harris B., Lennard N., Clark L., Line A., Barron A., Corton C.,
RA Barriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
RA Ormond D., Sanders M., Hayes M., Hall S., Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -----

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 CC -----
 DR EMBL: AL844509; CAD52291.1; -, Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 554 AA; 65670 MW; 332A13B5174CDA85 CRC64;
 Query Match 78.7%; Score 37; DB 2; Length 554;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 DB 344 DYKDDDK 351
 RESULT 93
 ID Q5JL08 ORYSA PRELIMINARY; PRT; 567 AA.
 AC Q5JL08;
 DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DE HSV-1 stimulating-related protein-like (HSV-1 stimulation-related 1-like).
 GN Name=P0459B04.31; Synonym=P0020E09.1;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
 OC Eriatodae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 Hijienita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
 Katsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 Maehata K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 Shimokawa T., Shomura A., Song J., Takazaki Y., Terada K., Tsuji K.,
 Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 Zhang H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
 Yano M., Jiang J., Gojobori T.;
 RA "The genome sequence and structure of rice chromosome 1.";
 RT Nature 420:312-316(2002).
 RL -----
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 CC -----
 DR EMBL: AP003627; BAD87849.1; -, Genomic_DNA.
 DR EMBL: AP003228; BAD87032.1; -, Genomic_DNA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR000005; HTHARAC.
 DR InterPro: IPR004353; Yeast73DUF.
 DR PANTHER: PTHR13027; Yeast73DUF; 1.
 DR Pfam: PF03164; DUF254; 1.
 DR PRINTS: PR01546; YEAST73DUF.
 DR PROSITE: PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
 SQ SEQUENCE 567 AA; 63751 MW; 1AB0B30FE1BE148B CRC64;
 Query Match 78.7%; Score 37; DB 2; Length 567;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 DB 44 DYDDDD 51

RESULT 94
 ID Q610D3 CAEBR PRELIMINARY; PRT; 664 AA.
 AC Q610D3;
 DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
 DT 23-NOV-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Hypothetical protein CBG07065 (Fragment).
 GN Name=CBG07065;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AF16;
 RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
 RA Stein L.D., Bao Z., Blasler D., Blumenthal T., Brent M.R., Chen N.,
 Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
 D'Enochio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,
 Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
 Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Mink P.,
 Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Schumann M.,
 Speth J., Stajich J.E., Wei C., Wiley D., Wilson R.K., Durbin R.,
 Waterston R.H.;
 RA "The genome sequence of *Caenorhabditis briggsae*: a platform for
 RT comparative genomics.";
 RT PLoS Biol. 1:166-192(2003).
 RL PLoS Biol. 1:166-192(2003).
 CC CAUTION: The sequence shown here is derived from an
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 CC -----
 DR EMBL: CA00100031; CAB2879.1; -, Genomic_DNA.
 DR InterPro: IPR001678; Fmu_NOL1/Nop2p.
 DR InterPro: IPR011023; Nop2p.
 DR InterPro: IPR006174; rRNAsub_mtfase.
 DR Pfam: PF01189; NOL1_Nop2_Fmu; 1.
 DR ProDom: PD005242; NusB_region; 1.
 DR TIGRFAMs: TIGR00446; nop2p; 1.
 DR PROSITE: PS01153; NOL1_Nop2_SUN; 1.
 KW Complete proteome; Hypothetical protein.
 FT NON TER 664
 SQ SEQUENCE 664 AA; 73746 MW; 67D8CA766879BD3 CRC64;
 Query Match 78.7%; Score 37; DB 2; Length 664;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DYKDDDD 7
 DB 94 DYSDDD 100
 RESULT 95
 ID Q5AAB5 CANAL PRELIMINARY; PRT; 690 AA.
 AC Q5AAB5;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein.
 GN ORENAME=Ca019.9993;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC5314;

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RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S., Thorstenson Y.R., Agabian N., Magee P.T.,
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
CC -!- CAUTION: The sequence shown here is derived from an
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CC -----
DR EMBL; AACQ01000040; EAK99642.1; -; Genomic_DNA.
DR InterPro; IPR013154; ADH_N.
KM Hypothetical protein.
SQ SEQUENCE 690 AA; 79582 MW; 6B4989CDDCB7FA0C CRC64;

Query Match 78.7%; Score 37; DB 2; Length 690;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 615 DYKDND 621

RESULT 96
Q6VZ25 CNPV PRELIMINARY; PRT; 690 AA.
AC Q6VZ25;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 10.
DE CNPV322 ankryrin repeat protein.
GN Name=CNPV322;
OS Canariyox virus (CNPV).
OC Viruses; dsDNA viruses, no RNA stage; Foxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OC NCBI_TaxID=44088;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC VR-111;
RX PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
RA Tullman E.R., Alonso C.L., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of canariyox virus."
RL J. Virol. 78:353-366(2004).
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CC -----
DR EMBL; AY318871; AAR83668.1; -; Genomic_DNA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK_6.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK_5.
DR PROSITE; PSS00297; ANK_REPEAT_REGION; 2.
DR PROSITE; PSS0088; ANK_REPEAT; 3.
KM ANK repeat; Repeat.
SQ SEQUENCE 690 AA; 79416 MW; F279541301AA6310 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 690;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 533 DYSDDD 539

RESULT 97
Q5AA27 CANAL PRELIMINARY; PRT; 691 AA.
ID Q5AA27 CANAL

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AC Q5AA27;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN ORFNames=Ca019.2457;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S., Thorstenson Y.R., Agabian N., Magee P.T.,
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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CC -----
DR EMBL; AACQ01000041; EAK99554.1; -; Genomic_DNA.
DR InterPro; IPR013154; ADH_N.
KM Hypothetical protein.
SQ SEQUENCE 691 AA; 79808 MW; 312D03A62F0EF773 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 691;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 616 DYKDND 622

RESULT 98
Q54D84_DICD1
ID Q54D84_DICD1 PRELIMINARY; PRT; 697 AA.
AC Q54D84;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=DD0184391;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OC NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RX PubMed=15875012; DOI=10.1038/nature03481;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Nadera M., Konfortov B.A., Riveo F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Wuzny D.M., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
RA Buchrieser C., Wardrop A., Feider M., Thangavelu M., Johnson D.,
RA Knights A., Louised H., Mungall K.L., Oliver K., Price C.,
RA Quail M.A., Urushihara H., Hernandez J., Rabinowitsch E., Steffen D.,
RA Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
RA Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
RA Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
RA Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,

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RA Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
RA Kuapa A.;
RL "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 435:43-57(2005).
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CC -----
DR EMBL; AAF101000268; EAL61197.1; -; Genomic_DNA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR00210; BTB.
DR Pfam; PF00651; BTB; 1.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
KM Hypothetical protein.
SQ SEQUENCE 697 AA; 79148 MW; FC49F887CE23AC6C CRC64;

Query Match 78.7%; Score 37; DB 2; Length 697;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 437 DFTDDDDK 444

RESULT 99
Q5A932 CANAL PRELIMINARY; PRT; 700 AA.
ID Q5A932 CANAL PRELIMINARY; PRT; 700 AA.
AC Q5A932
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORENAMES=CaO19.10812, CaO19.3302;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federopiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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CC -----
DR EMBL; AAC001000045; EAK99193.1; -; Genomic_DNA.
DR EMBL; AAC001000042; EAK99468.1; -; Genomic_DNA.
DR InterPro; IPR005036; CBM_21.
DR Pfam; PF03370; CBM_21; 1.
KM Hypothetical protein.
SQ SEQUENCE 700 AA; 78182 MW; E2A5C0C72D41E9P2 CRC64;

Query Match 78.7%; Score 37; DB 2; Length 700;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 168 DYSDDD 174

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RESULT 100
Q4N9L1 THEBA PRELIMINARY; PRT; 702 AA.
ID Q4N9L1 THEBA PRELIMINARY; PRT; 702 AA.
AC Q4N9L1
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE RNA helicase, putative.
GN ORENAMES=TP01_0103;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RX PubMed=15994558; DOI=10.1126/science.1110439;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabi A., Domingo A.R., Wasawo D.,
RA Crabtree J., Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C.,
RA Suh B., Silva J.C., Utecherback T.R., Feldblyum T.V., Perteau M.,
RA Allen J., Nieman W.C., Taracha E.L., Salzberg S.L., White O.R.,
RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
RT "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
RT Lymphocytes."
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utecherback T., Feldblyum T., Perteau M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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DR GO; GO:0005524; F:ATP binding; IEA.
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KM Helicase.
SQ SEQUENCE 702 AA; 81499 MW; 2924092F65B679AE CRC64;

Query Match 78.7%; Score 37; DB 2; Length 702;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDDK 8
DB 527 YKDDDDK 533

Search completed: June 29, 2006, 11:40:41
Job time : 319 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:40:57 ; Search time 49 Seconds
(without alignments)
14.291 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYXDDDK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

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SUMMARIES

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250	47	100.0	8	2	US-09-080-140-30	Sequence 30, Appl	323	47	100.0	10	5	PCT-US93-04717-26	Sequence 26, Appl
251	47	100.0	8	2	US-09-298-404-19	Sequence 19, Appl	324	47	100.0	10	5	PCT-US95-12960-1	Sequence 1, Appl
252	47	100.0	8	2	US-09-667-947A-40	Sequence 40, Appl	325	47	100.0	11	2	US-09-026-776-23	Sequence 23, Appl
253	47	100.0	8	2	US-09-728-911-11	Sequence 11, Appl	326	47	100.0	11	2	US-08-720-565-16	Sequence 16, Appl
254	47	100.0	8	2	US-10-158-825-147	Sequence 147, App	327	47	100.0	11	2	US-09-374-664-1	Sequence 1, Appl
255	47	100.0	8	2	US-10-002-392A-10	Sequence 10, Appl	328	47	100.0	11	2	US-09-964-201A-23	Sequence 23, Appl
256	47	100.0	8	2	US-09-688-286D-6	Sequence 6, Appl	329	47	100.0	11	2	US-08-375-199B-16	Sequence 16, Appl
257	47	100.0	8	2	US-10-350-104B-3	Sequence 3, Appl	330	47	100.0	11	2	US-09-848-616-147	Sequence 147, App
258	47	100.0	8	2	US-09-997-623-47	Sequence 47, Appl	331	47	100.0	12	1	US-10-283-028-16	Sequence 16, Appl
259	47	100.0	8	2	US-10-245-227D-9	Sequence 9, Appl	332	47	100.0	12	1	US-08-963-856-16	Sequence 16, Appl
260	47	100.0	8	2	US-10-284-083-12	Sequence 12, Appl	333	47	100.0	12	1	US-08-350-884-53	Sequence 53, Appl
261	47	100.0	8	2	US-09-092-397A-21	Sequence 21, Appl	334	47	100.0	12	1	US-08-709-173-53	Sequence 53, Appl
262	47	100.0	8	2	US-10-183-770A-16	Sequence 16, Appl	335	47	100.0	12	1	US-08-701-124-23	Sequence 23, Appl
263	47	100.0	8	2	US-10-372-874-21	Sequence 21, Appl	336	47	100.0	12	1	US-08-709-177-53	Sequence 53, Appl
264	47	100.0	8	2	US-10-668-453-1	Sequence 1, Appl	337	47	100.0	12	2	US-08-792-832A-9	Sequence 9, Appl
265	47	100.0	8	2	US-10-308-373-5	Sequence 5, Appl	338	47	100.0	12	2	US-09-130-825-23	Sequence 23, Appl
266	47	100.0	8	2	US-10-195-707B-40	Sequence 40, Appl	339	47	100.0	12	2	US-09-455-061-23	Sequence 23, Appl
267	47	100.0	8	2	US-09-875-338-94	Sequence 94, Appl	340	47	100.0	12	2	US-09-622-839-14	Sequence 14, Appl
268	47	100.0	8	2	US-10-632-694A-9	Sequence 9, Appl	341	47	100.0	12	2	US-09-969-192-23	Sequence 23, Appl
269	47	100.0	8	2	US-08-743-86B-3	Sequence 3, Appl	342	47	100.0	13	1	US-10-318-142-14	Sequence 14, Appl
270	47	100.0	8	3	US-10-157-447-5	Sequence 5, Appl	343	47	100.0	13	1	US-08-222-616-41	Sequence 41, Appl
271	47	100.0	8	3	US-09-844-508-14	Sequence 14, Appl	344	47	100.0	13	1	US-08-446-908-7	Sequence 7, Appl
272	47	100.0	8	3	US-10-019-735-17	Sequence 17, Appl	345	47	100.0	13	1	US-08-690-011A-48	Sequence 48, Appl
273	47	100.0	8	3	US-10-143-618-29	Sequence 29, Appl	346	47	100.0	13	1	US-08-871-161-7	Sequence 7, Appl
274	47	100.0	8	3	US-10-835-096-16	Sequence 16, Appl	347	47	100.0	13	1	US-08-871-161-7	Sequence 7, Appl
275	47	100.0	8	3	US-10-241-476-26	Sequence 26, Appl	348	47	100.0	13	2	US-09-299-495E-48	Sequence 48, Appl
276	47	100.0	8	3	US-10-006-069A-225	Sequence 225, App	349	47	100.0	13	2	US-09-982-610-41	Sequence 41, Appl
277	47	100.0	8	3	US-09-876-790-11	Sequence 11, Appl	350	47	100.0	13	2	US-10-009-332-33	Sequence 33, Appl
278	47	100.0	8	3	US-09-837-992-45	Sequence 45, Appl	351	47	100.0	13	5	PCT-US95-04228-41	Sequence 41, Appl
279	47	100.0	8	3	US-10-133-797A-28	Sequence 28, Appl	352	47	100.0	13	7	5395760-16	Patent No. 5395760
280	47	100.0	8	5	PCT-US93-10034-1	Sequence 1, Appl	353	47	100.0	13	7	US-08-411-795B-403	Sequence 403, App
281	47	100.0	8	5	PCT-US94-08119-15	Sequence 15, Appl	354	47	100.0	14	1	US-08-446-908-9	Sequence 9, Appl
282	47	100.0	8	5	PCT-US94-12913A-15	Sequence 15, Appl	355	47	100.0	14	1	US-08-231-205A-9	Sequence 9, Appl
283	47	100.0	8	5	PCT-US95-00362-3	Sequence 3, Appl	356	47	100.0	14	1	US-08-469-319A-403	Sequence 403, App
284	47	100.0	8	5	PCT-US95-06530-7	Sequence 7, Appl	357	47	100.0	14	1	US-08-871-161-9	Sequence 9, Appl
285	47	100.0	8	5	PCT-US95-08534-3	Sequence 3, Appl	358	47	100.0	14	1	US-08-871-161-9	Sequence 9, Appl
286	47	100.0	8	5	PCT-US95-12960-2	Sequence 2, Appl	359	47	100.0	14	2	US-08-764-114-403	Sequence 403, App
287	47	100.0	8	5	PCT-US95-15781-6	Sequence 6, Appl	360	47	100.0	14	2	US-08-469-419-403	Sequence 403, App
288	47	100.0	8	5	PCT-US96-10895-7	Sequence 7, Appl	361	47	100.0	14	2	US-09-181-244B-5	Sequence 5, Appl
289	47	100.0	8	7	5194375-7	Patent No. 5194375	362	47	100.0	14	2	US-09-937-126-4	Sequence 4, Appl
290	47	100.0	8	7	5198342-3	Patent No. 5198342	363	47	100.0	15	2	US-09-896-915-2	Sequence 2, Appl
291	47	100.0	8	7	5395760-6	Patent No. 5395760	364	47	100.0	15	2	US-08-817-145-19	Sequence 19, Appl
292	47	100.0	9	1	US-08-605-002A-17	Sequence 17, Appl	365	47	100.0	16	2	US-09-252-656B-57	Sequence 57, Appl
293	47	100.0	9	1	US-08-950-449A-19	Sequence 19, Appl	366	47	100.0	16	2	US-09-285-912A-15	Sequence 15, App
294	47	100.0	9	2	US-08-968-747-4	Sequence 4, Appl	367	47	100.0	17	1	US-08-651-818A-22	Sequence 22, Appl
295	47	100.0	9	2	US-07-602-848B-9	Sequence 9, Appl	368	47	100.0	17	2	US-09-184-826-22	Sequence 22, Appl
296	47	100.0	9	2	US-09-645-456A-28	Sequence 28, Appl	369	47	100.0	17	2	US-09-832-464-22	Sequence 22, Appl
297	47	100.0	9	2	US-09-425-324A-28	Sequence 28, Appl	370	47	100.0	18	1	US-08-670-175-8	Sequence 8, Appl
298	47	100.0	9	2	US-09-645-791-28	Sequence 28, Appl	371	47	100.0	21	2	US-09-266-462-1	Sequence 1, Appl
299	47	100.0	9	2	US-09-700-820C-10	Sequence 10, Appl	372	47	100.0	21	2	US-09-266-462-1	Sequence 1, Appl
300	47	100.0	9	2	US-09-872-136B-11	Sequence 11, Appl	373	47	100.0	21	2	US-09-297-269-21	Sequence 21, Appl
301	47	100.0	9	2	US-10-039-659A-19	Sequence 19, Appl	374	47	100.0	21	2	US-09-809-517A-30	Sequence 30, Appl
302	47	100.0	9	2	US-09-826-312A-17	Sequence 17, Appl	375	47	100.0	22	1	US-08-701-124-29	Sequence 29, Appl
303	47	100.0	9	2	US-09-352-171-1	Sequence 1, Appl	376	47	100.0	22	2	US-09-130-225-29	Sequence 29, Appl
304	47	100.0	9	2	US-09-786-442B-13	Sequence 13, Appl	377	47	100.0	22	2	US-09-455-061-29	Sequence 29, Appl
305	47	100.0	9	2	US-09-896-915-6	Sequence 6, Appl	378	47	100.0	22	2	US-09-969-192-29	Sequence 29, Appl
306	47	100.0	9	2	US-09-896-915-39	Sequence 39, Appl	379	47	100.0	22	2	US-09-270-767-35444	Sequence 35444, A
307	47	100.0	9	2	US-09-622-500B-8	Sequence 8, Appl	380	47	100.0	22	2	US-09-270-767-50661	Sequence 50661, A
308	47	100.0	9	2	US-09-919-408A-11	Sequence 11, Appl	381	47	100.0	22	2	US-09-809-517A-33	Sequence 33, Appl
309	47	100.0	9	3	US-10-835-096-17	Sequence 17, Appl	382	47	100.0	22	2	US-09-667-365-1948	Sequence 1948, Ap
310	47	100.0	10	1	US-08-835-501-26	Sequence 26, Appl	383	47	100.0	23	2	US-09-370-767-34566	Sequence 34566, A
311	47	100.0	10	1	US-08-435-501-26	Sequence 26, Appl	384	47	100.0	23	2	US-09-270-767-49783	Sequence 49783, A
312	47	100.0	10	1	US-08-568-072-1	Sequence 1, Appl	385	47	100.0	24	2	US-09-266-462-4	Sequence 4, Appl
313	47	100.0	10	1	US-08-713-928B-14	Sequence 14, Appl	386	47	100.0	24	2	US-08-634-060-26	Sequence 26, Appl
314	47	100.0	10	2	US-08-559-397A-35	Sequence 35, Appl	387	47	100.0	25	1	US-08-700-846-9	Sequence 9, Appl
315	47	100.0	10	2	US-09-046-785-1	Sequence 1, Appl	388	47	100.0	29	5	PCT-US94-05150-37	Sequence 37, Appl
316	47	100.0	10	2	US-08-961-309-68	Sequence 68, Appl	389	47	100.0	30	1	US-08-634-060-39	Sequence 39, Appl
317	47	100.0	10	2	US-09-620-956-10	Sequence 10, Appl	390	47	100.0	34	2	US-09-896-915-8	Sequence 8, Appl
318	47	100.0	10	2	US-09-611-152-10	Sequence 10, Appl	391	47	100.0	35	2	US-09-460-145-9	Sequence 9, Appl

392	47	100.0	35	2	US-09-800-170-26	Sequence 26, Appl
393	47	100.0	35	2	US-09-895-547-9	Sequence 9, Appl
394	47	100.0	35	2	US-09-285-912A-66	Sequence 66, Appl
395	47	100.0	35	2	US-10-266-388-9	Sequence 9, Appl
396	47	100.0	40	2	US-09-669-516C-15	Sequence 15, Appl
397	47	100.0	42	2	US-09-053-866-5	Sequence 5, Appl
398	47	100.0	42	2	US-09-479-130-5	Sequence 5, Appl
399	47	100.0	42	2	US-09-472-130A-5	Sequence 5, Appl
400	47	100.0	43	2	US-09-962-756-1289	Sequence 1289, Ap
401	47	100.0	46	2	US-09-962-756-2191	Sequence 2191, Ap
402	47	100.0	48	2	US-09-962-756-2195	Sequence 2195, Ap
403	47	100.0	49	2	US-10-084-298-10	Sequence 10, Appl
404	47	100.0	53	1	US-08-651-818A-19	Sequence 19, Appl
405	47	100.0	53	2	US-09-184-826-19	Sequence 19, Appl
406	47	100.0	53	2	US-09-832-464-19	Sequence 19, Appl
407	47	100.0	54	1	US-08-651-818A-23	Sequence 23, Appl
408	47	100.0	54	2	US-09-184-826-23	Sequence 23, Appl
409	47	100.0	54	2	US-09-832-464-23	Sequence 23, Appl
410	47	100.0	57	2	US-09-962-756-2147	Sequence 2147, Ap
411	47	100.0	57	2	US-09-962-756-2179	Sequence 2179, Ap
412	47	100.0	61	2	US-09-962-756-2176	Sequence 2176, Ap
413	47	100.0	64	2	US-09-962-756-2148	Sequence 2148, Ap
414	47	100.0	64	2	US-09-962-756-2160	Sequence 2160, Ap
415	47	100.0	64	2	US-09-962-756-2180	Sequence 2180, Ap
416	47	100.0	65	2	US-09-962-756-2170	Sequence 2170, Ap
417	47	100.0	68	1	US-08-330-638D-2	Sequence 2, Appl
418	47	100.0	68	1	US-08-906-746A-2	Sequence 2, Appl
419	47	100.0	70	2	US-09-962-756-2112	Sequence 2112, Ap
420	47	100.0	70	2	US-09-962-756-2193	Sequence 2193, Ap
421	47	100.0	72	2	US-09-962-756-2114	Sequence 2114, Ap
422	47	100.0	72	2	US-09-962-756-2116	Sequence 2116, Ap
423	47	100.0	72	2	US-09-962-756-2192	Sequence 2192, Ap
424	47	100.0	72	2	US-09-962-756-2196	Sequence 2196, Ap
425	47	100.0	72	2	US-09-962-756-2197	Sequence 2197, Ap
426	47	100.0	74	2	US-09-962-756-2134	Sequence 2134, Ap
427	47	100.0	74	2	US-09-962-756-2189	Sequence 2189, Ap
428	47	100.0	76	2	US-09-962-756-2113	Sequence 2113, Ap
429	47	100.0	76	2	US-09-962-756-2182	Sequence 2182, Ap
430	47	100.0	76	2	US-09-962-756-2194	Sequence 2194, Ap
431	47	100.0	78	2	US-09-962-756-2115	Sequence 2115, Ap
432	47	100.0	78	2	US-09-962-756-2198	Sequence 2198, Ap
433	47	100.0	79	2	US-09-962-756-2201	Sequence 2201, Ap
434	47	100.0	80	2	US-09-962-756-2190	Sequence 2190, Ap
435	47	100.0	81	2	US-09-962-756-2200	Sequence 2200, Ap
436	47	100.0	84	2	US-09-299-495F-11	Sequence 11, Appl
437	47	100.0	84	2	US-09-826-312A-14	Sequence 14, Appl
438	47	100.0	84	2	US-10-108-767-14	Sequence 14, Appl
439	47	100.0	84	2	US-10-152-156-14	Sequence 14, Appl
440	47	100.0	84	3	US-10-835-096-14	Sequence 14, Appl
441	47	100.0	85	2	US-09-826-312A-15	Sequence 15, Appl
442	47	100.0	85	2	US-10-108-767-15	Sequence 15, Appl
443	47	100.0	85	2	US-10-152-156-15	Sequence 15, Appl
444	47	100.0	86	3	US-10-835-096-15	Sequence 15, Appl
445	47	100.0	86	3	US-09-826-312A-18	Sequence 18, Appl
446	47	100.0	86	3	US-09-962-756-2177	Sequence 2177, Ap
447	47	100.0	86	3	US-10-835-096-18	Sequence 18, Appl
448	47	100.0	88	1	US-08-690-011A-11	Sequence 11, Appl
449	47	100.0	90	2	US-09-962-756-2161	Sequence 2161, Ap
450	47	100.0	90	2	US-09-299-495F-9	Sequence 9, Appl
451	47	100.0	92	2	US-09-962-756-2171	Sequence 2171, Ap
452	47	100.0	92	2	US-09-962-756-2178	Sequence 2178, Ap
453	47	100.0	95	2	US-09-763-509-6	Sequence 6, Appl
454	47	100.0	96	2	US-09-962-756-2162	Sequence 2162, Ap
455	47	100.0	97	2	US-09-299-495F-19	Sequence 19, Appl
456	47	100.0	98	1	US-08-690-011A-19	Sequence 19, Appl
457	47	100.0	98	1	US-09-962-756-2172	Sequence 2172, Ap
458	47	100.0	105	1	US-08-383-348A-19	Sequence 19, Appl
459	47	100.0	105	1	US-08-383-804B-19	Sequence 19, Appl
460	47	100.0	105	1	US-08-383-748A-19	Sequence 19, Appl
461	47	100.0	105	1	US-08-814-309A-19	Sequence 19, Appl
462	47	100.0	105	1	US-08-690-011A-15	Sequence 15, Appl
463	47	100.0	105	2	US-09-299-495F-15	Sequence 15, Appl
464	47	100.0	108	2	US-09-473-551-15	Sequence 15, Appl

RESULT 1
US-08-089-458B-7
; Sequence 7, Application US/08089458B
; Patent No. 5359039
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig
; APPLICANT: Goodwin, Raymond
; TITLE OF INVENTION: Isolated Poxvirus A53R-Equivalent Tumor
; TITLE OF INVENTION: Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia Anne Perkins, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,458B
; FILING DATE: 07/09/93
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-089-4588-7

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 2
US-08-323-474-4
Sequence 4, Application US/08323474
Patent No. 5447860
GENERAL INFORMATION:
APPLICANT: Ziegler, Steven F.
TITLE OF INVENTION: NOVEL TYROSINE KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,474
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
FILING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-474-4

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 3

US-08-225-989-15
Sequence 15, Application US/08225989
Patent No. 5480981
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armitage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-225-989-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 4
US-08-086-335C-12
Sequence 12, Application US/08086335C

Patent No. 553863
GENERAL INFORMATION:
APPLICANT: Price, Virginia L.
TITLE OF INVENTION: Expression System Comprising Mutant Yeast Strain and Expressi
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,335C
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 1002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-086-335C-12

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 5
US-08-265-086-5
Sequence 5, Application US/08265086
Patent No. 5576191
GENERAL INFORMATION:
APPLICANT: Gayle, Margit
APPLICANT: Slack, Jennifer
APPLICANT: Gruss, Hans-Jueergen
APPLICANT: Sims, John E.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: No. 5576191el Cytokine That Binds ST2
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Macintosh

OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,086
FILING DATE: June 17, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2825
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-265-086-5

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 6
US-08-236-918A-16
Sequence 16, Application US/08236918A
Patent No. 5674704
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Alderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Power Macintosh
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644

;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE:
;; CLONE: FLAG peptide
US-08-236-918A-16

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 7
US-08-570-923-15
; Sequence 15, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armbrage, Richard J.
; APPLICANT: Grubbs, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430e1 Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

;; TELEFAX: (206)233-0644
;; TELE: 756822
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: FLAG peptide
US-08-570-923-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 8
US-08-446-908-6
; Sequence 6, Application US/08446908
; Patent No. 5705149
; GENERAL INFORMATION:
; APPLICANT: Namen, Anthony E.
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Lupton, Stephen D.
; APPLICANT: Mochizuki, Diane Y.
; TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,908
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,205
; FILING DATE: 21-APR-1994
; APPLICATION NUMBER: US 07/957,649
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,438
; FILING DATE: 13-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/255,209
; FILING DATE: 07-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/113,566
; FILING DATE: 26-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2104-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-446-908-6

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|||||
Db 1 DYKDDDK 8

RESULT 9
US-08-634-060-25
Sequence 25, Application US/08634060
Patent No. 5712136
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelink, Petrus W.
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5700
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-634-060-25

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|||||

Db 1 DYKDDDK 8

RESULT 10
US-08-231-205A-6
Sequence 6, Application US/08231205A
Patent No. 5714585
GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Lapton, Stephen D.
APPLICANT: Mochizuki, Diane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,205A
FILING DATE: 21-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113,566
FILING DATE: 26-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-231-205A-6

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|||||
Db 1 DYKDDDK 8

RESULT 11

US-08-446-922-1
; Sequence 1, Application US/08446922
; Patent No. 5716805
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; APPLICANT: Srinivasan, Subhashini
; TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,922
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/107,353
; FILING DATE: 08-13-93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 1003-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-446-922-1
Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8
RESULT 12
US-08-430-633-3
; Sequence 3, Application US/08430633
; Patent No. 5726286
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET

CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,633
; FILING DATE: 28-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG_peptide
US-08-430-633-3

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 13
US-08-580-014-15
; Sequence 15, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Juergen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-Dec-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 April, 1994
; APPLICATION NUMBER: US 07/966,775

FILING DATE: 27-OCT-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-580-014-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 14
US-08-670-354-7
Sequence 7, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368

FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-670-354-7

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 15
US-08-442-043A-15
Sequence 15, Application US/08442043A
Patent No. 5767064
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,043A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 05-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,415
FILING DATE: 16-MAY-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/091,519
FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,211
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2003-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG(r) peptide
US-08-442-043A-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 16
US-08-604-333-5
Sequence 5, Application US/08604333
GENERAL INFORMATION:
APPLICANT: Parneet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO

IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-604-333-5

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 17
US-08-308-881-7
Sequence 7, Application US/08308881
GENERAL INFORMATION:
PATENT NO. 5783672
APPLICANT: Mosley, Bruce
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-308-881-7

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 18
US-08-660-626-1

```
; Sequence 1, Application US/08660626
; Patent No. 5789655
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPIOTOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Asciti
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,626
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Valeta Gregg
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 07532/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-626-1

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 19
US-08-526-014-1
; Sequence 1, Application US/08526014
; Patent No. 5801227
; GENERAL INFORMATION:
; APPLICANT: Fanslow, William C. III
; APPLICANT: Zappone, Jodee
; APPLICANT: Alderson, Mark
; APPLICANT: Armitage, Richard J.
; TITLE OF INVENTION: ANTIBODIES TO CD40
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,014
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/130,541
; FILING DATE: October 1, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2816
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-526-014-1

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 20
US-08-684-687-6
; Sequence 6, Application US/08684687
; Patent No. 5830451
; GENERAL INFORMATION:
; APPLICANT: KIEFF, ELLIOTT D.
; APPLICANT: DEVERGNE, ODILE
; TITLE OF INVENTION: A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,687
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,092
; FILING DATE: 11-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-2441
; TELEFAX: 617-720-3500
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
```


LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
OTHER INFORMATION: /label= FLAG_EPTIPE
US-08-684-687-6

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 21
US-08-701-124-2
Sequence 2, Application US/08701124
Patent No. 5846782
GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.
APPLICANT: Roelivink, Petrus W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-701-124-2

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 22
US-08-649-341A-9
Sequence 9, Application US/08649341A
Patent No. 5847099
GENERAL INFORMATION:
APPLICANT: Lin, Lih-Ling

APPLICANT: Chen, Jennifer H.
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,341A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A,
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15232-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-341A-9

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 23
US-08-494-440B-13
Sequence 13, Application US/08494440B
Patent No. 5849501
GENERAL INFORMATION:

APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,440B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A,

REGISTRATION NUMBER: 32, 724
REFERENCE/DOCKET NUMBER: G15232A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-494-440B-13

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 24
US-08-729-345-4
Sequence 4, Application US/08729345
Patent No. 5849999
GENERAL INFORMATION:
APPLICANT: Neve, Rachael L.
APPLICANT: Berger-Sweeney, Joanne
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL
TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,345
FILING DATE: 16-OCT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04843/027001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-729-345-4

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8

DB 1 DYKDDDDK 8

RESULT 25
US-08-533-901B-15
Sequence 15, Application US/08533901B
Patent No. 5852173
GENERAL INFORMATION:
APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
TITLE OF INVENTION: PROTEINS AND INHIBITORS OF LIGAND BINDING
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,901B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-533-901B-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 26
US-08-670-175-1
Sequence 1, Application US/08670175
Patent No. 5854081
GENERAL INFORMATION:
APPLICANT: LINDEN, JOEL
APPLICANT: TAYLOR, HEIDI
APPLICANT: ROBEVA, ANNA
APPLICANT: WOODARD, ROBIN
APPLICANT: JIN, XIADWEI
TITLE OF INVENTION: STABLE EXPRESSION OF HUMAN ADENOSINE
TITLE OF INVENTION: RECEPTORS, AND ASSAYS EMPLOYING THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIYAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,175
FILING DATE: 20-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 494-176-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-670-175-1

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 27
US-08-777-405A-15
Sequence 15, Application US/08777405A
Patent No. 5858753
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-777-405A-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 28
US-08-620-694A-3
Sequence 3, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spitzers, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-08-620-694A-3

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 29

US-08-720-258-7
; Sequence 7, Application US/08720258
; Patent No. 5871740
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; TITLE OF INVENTION: Chemokine Inhibitor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple System 7.5.3
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,258
; FILING DATE: 26-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/575,715
; FILING DATE: 20-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,324
; FILING DATE: 29-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2620-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
; US-08-720-258-7

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 30
US-08-977-871A-15
; Sequence 15, Application US/08977871A
; Patent No. 5882910
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Meri F.
; APPLICANT: Holtzman, Douglas A

; TITLE OF INVENTION: No. 5882910e1 Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-977-871A-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 31

US-08-839-032A-19
; Sequence 19, Application US/08839032A
; Patent No. 5891675
; GENERAL INFORMATION:
; APPLICANT: Lin, Lin-Ling
; APPLICANT: Chen, Jennifer H.
; APPLICANT: Schievella, Andrea
; APPLICANT: Graham, James
; TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND PROTEINS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,032A
; FILING DATE:

```

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15232DDIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-839-032A-19

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 32
US-09-058-263-7
; Sequence 7, Application US/09058263
; Patent No. 5891997
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,263
; FILING DATE:
; PRIORITY INFORMATION:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
```

```

; CLONE: FLAG peptide
; US-09-058-263-7

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 33
US-08-870-518-27
; Sequence 27, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Galcheva-Gargova, Zoya
; TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FaacSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,518
; FILING DATE: 06-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,219
; FILING DATE: 06-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faase, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-870-518-27

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 34
US-08-936-854-3
; Sequence 3, Application US/08936854
; Patent No. 5925734
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
```

```
APPLICANT: COMEAU, MICHAEL
APPLICANT: FARAH, THERESA
APPLICANT: SPRIGGS, MELANIE
TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
TITLE OF INVENTION: That Bind MHC Class II Beta Chains
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,633
FILING DATE: 28-APR-1995
APPLICATION NUMBER: 08/235,397
FILING DATE: 04/26/94
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_ peptide
US-08-936-854-3

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 35
US-09-059-099-7
; Sequence 7, Application US/09059099
; Patent No. 5925740
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
```

```
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-09-059-099-7

Query Match      100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 36
US-08-713-928B-10
; Sequence 10, Application US/08713928B
; Patent No. 5929304
; GENERAL INFORMATION:
; APPLICANT: RADIN, DAVID N.
; APPLICANT: CRAMER, CAROLE L.
; APPLICANT: WEISSENBERG, DEBORAH L.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,928B
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,737
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7956-0011-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-713-928B-10

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 37
US-08-595-043A-1
Sequence 1, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-595-043A-1

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 38
US-08-690-011A-50
Sequence 50, Application US/08690011A
Patent No. 5942433
GENERAL INFORMATION:
APPLICANT: VINSON, Charles R.
APPLICANT: KRYLOV, Dmitry
TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
CELLULAR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,011A
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,654
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,496
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4190US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-011A-50

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 39
US-08-839-031A-15
Sequence 15, Application US/08839031A
Patent No. 5948638
GENERAL INFORMATION:
APPLICANT: Lin, Lih-Ling
APPLICANT: Chen, Jennifer H.
APPLICANT: Schievella, Andrea
APPLICANT: Graham, James
TITLE OF INVENTION: NOVEL TNF RECEPTOR DEATH DOMAIN LIGAND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge

STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/839,031A
APPLICATION NUMBER: US/08/839,031A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.,
REGISTRATION NUMBER: 41,323
REFERENCE/DOCKET NUMBER: GI5232BDIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-839-031A-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 40
US-08-762-106-3
Sequence 3, Application US/08762106
Patent No. 5948677
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPIOTOPE
TITLE OF INVENTION: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/762,106
APPLICATION NUMBER: US/08/762,106
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

US-08-762-106-3

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 41
US-09-016-366A-30
Sequence 30, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/016,366A
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-016-366A-30

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 42
US-08-700-846-8
Sequence 8, Application US/08700846
Patent No. 5962311
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: ROELVINK, PETRUS W.

APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
STATE: IL
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 74294
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-700-846-8

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 43
US-08-871-161-6
Sequence 6, Application US/08871161
Patent No. 5965122
GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Luppon, Stephen D.
APPLICANT: Mochizuki, Diane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,161
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,908
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/231,205
FILING DATE: 21-APR-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113,566
FILING DATE: 26-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Seease, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-871-161-6

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 44
US-08-832-935-1
Sequence 1, Application US/08832935
Patent No. 5965375
GENERAL INFORMATION:
APPLICANT: Valkirs, Gunars
TITLE OF INVENTION: Diagnostic Tests and Kits for
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,935
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367

REFERENCE/DOCKET NUMBER: 014907-001200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-935-1

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 45
US-08-482-728A-2
Sequence 2, Application US/08482728A
Patent No. 5968802
GENERAL INFORMATION:
APPLICANT: Wang, Bruce
APPLICANT: Fisher, Joseph
APPLICANT: Payan, Donald
TITLE OF INVENTION: No. 5968802el Nuclear Cyclophilin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobach, Test, Albritton
ADDRESSEE: & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,728A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61230/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-482-728A-2

RESULT 46
US-08-876-882-5
Sequence 5, Application US/08876882
Patent No. 5981201
GENERAL INFORMATION:
APPLICANT: Avraham, Hava
APPLICANT: Groopman, Jerome E.
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT
OF BREAST CANCER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,882
FILING DATE: 16-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/035,228
FILING DATE: 08-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Doreen, Hogle M.
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: NEBH97-01pA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-876-882-5

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 47
US-09-225-951-15
Sequence 15, Application US/09225951
Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NO. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-225-951-15

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 48
US-09-058-264-7
Sequence 7, Application US/09058264
Patent No. 6010886
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-09-058-264-7

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 49
US-08-991-426-8
Sequence 8, Application US/08991426
Patent No. 6013257
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NEUROTACTIN AND USES THEREFOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,426
FILING DATE: 16-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/851,160
FILING DATE: 05-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,798
FILING DATE: 07-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melkilejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-991-426-8

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 50

US-08-996-139-7
Sequence 7, Application US/08996139

Patent No. 6017729

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

APPLICANT: Galibert, Laurent

APPLICANT: Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

FILING DATE: 22 DECEMBER 1997

APPLICATION NUMBER: US/08/996,139

PRIORITY DATE: 14 OCTOBER 1997

APPLICATION NUMBER: USSN 60/064,671

PRIORITY DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/813,509

PRIORITY DATE: 23 DECEMBER 1996

APPLICATION NUMBER: USSN 08/772,330

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: FLAG_ peptide

US-08-996-139-7

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. Se+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 51

US-08-792-832A-7

Sequence 7, Application US/08792832A

Patent No. 6017734

GENERAL INFORMATION:

APPLICANT: Summers Dr., Max D.

APPLICANT: Braunsel Dr., Sharon C.

APPLICANT: Hong Dr., Tao

TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID

TITLE OF INVENTION: SEQUENCE AND USES THEREOF

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 30-JAN-1997

APPLICATION NUMBER: US/08/792,832A

CLASSIFICATION: 435

PRIORITY DATE: 07-JUL-1995

APPLICATION NUMBER: US 60/000,955

PRIORITY DATE: 03-JUL-1996

APPLICATION NUMBER: US 08/678,435

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TANK:190

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-792-832A-7

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. Se+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

RESULT 52

US-09-130-663-6

Sequence 6, Application US/09130663A

Patent No. 6020163

GENERAL INFORMATION:

APPLICANT: Conklin, Darrell C.

TITLE OF INVENTION: LIPOCALIN HOMOLOG

FILE REFERENCE: 97-24

CURRENT APPLICATION NUMBER: US/09/130,663A

CURRENT FILING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/054,867

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Flag affinity peptide

US-09-130-663-6

Query Match 100.0%; Score 47; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. Se+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
| | | | |
Db 1 DYKDDDK 8

RESULT 53
US-09-081-180-16
; Sequence 16, Application US/09081180
; Patent No. 6022847
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-180-16

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
| | | | |
Db 1 DYKDDDK 8

RESULT 54
US-09-040-786-16
; Sequence 16, Application US/09040786
; Patent No. 6025197
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave. E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,786
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-040-786-16

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
| | | | |
Db 1 DYKDDDK 8

RESULT 55
US-08-817-145-17
; Sequence 17, Application US/08817145
; Patent No. 6025329
; GENERAL INFORMATION:
; APPLICANT: UTSUMI, Jun
; APPLICANT: SUDO, Tetsuo
; APPLICANT: TANAKA, Yasuhiko
; APPLICANT: MATSUI, Mizuo
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC
; TITLE OF INVENTION: DISEASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP.
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,145
; FILING DATE: 02-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-230P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-145-17

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 56
US-08-307-896-9
Sequence 9, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
FILE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide sequence
US-08-307-896-9

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 57
US-08-785-247-9
Sequence 9, Application US/08785247
Patent No. 6040149
GENERAL INFORMATION:
APPLICANT: Kolesnick, Richard N.
APPLICANT: Liu, Jun
APPLICANT: Zhang, Yuhua
TITLE OF INVENTION: ASSAY FOR IDENTIFYING AGENTS WHICH ACT ON THE
TITLE OF INVENTION: CERAMIDE-ACTIVATED PROTEIN KINASE, KINASE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,247
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48582-A/JFW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-381-0526
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-785-247-9

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 58
US-08-938-830-8
Sequence 8, Application US/08938830
Patent No. 6040437
GENERAL INFORMATION:
APPLICANT: Lasby, Laurence A.
APPLICANT: Dowbenko, Donald J.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
TITLE OF INVENTION: Furox-Associated Proteins (PSTPIPs)
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-938-830-8

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 59
US-08-828-741B-9
Sequence 9, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-828-741B-9

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 60
US-08-819-177-14
Sequence 14, Application US/08819177
Patent No. 6043083

GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Dickens, Martin
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,177
FILING DATE: 28-Apr-11 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
OTHER INFORMATION: Flag epitope
US-08-819-177-14

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 61
US-09-143-470-14
Sequence 14, Application US/09143470
Patent No. 6043086
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NEURORACTIN AND USES THEREFOR
FILE REFERENCE: 09404/049001
CURRENT APPLICATION NUMBER: US/09/143,470
CURRENT FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-143-470-14

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDK 8

```
RESULT 62
US-08-950-720A-8
; Sequence 8, Application US/08950720A
; Patent No. 6046028
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Lok, Si
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: INSULIN HOMOLOG
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,720A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-950-720A-8

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8
```

```
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-225-2

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8
```

```
RESULT 64
US-09-022-255-3
; Sequence 3, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
```


TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-09-022-255-3

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 65
US-09-022-696-3
Sequence 3, Application US/09022696
Patent No. 6072037
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022, 696
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620, 694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410, 535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-09-022-696-3

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 66
US-08-883-036A-5
Sequence 5, Application US/08883036A
Patent No. 6072047
GENERAL INFORMATION:
APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle,
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883, 036A
FILING DATE: 26-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --to be assigned--
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829, 536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/815, 255
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/799, 861
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2625-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-08-883-036A-5

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

Db 1 DYKDDDK 8

RESULT 67
US-09-030-613-35
; Sequence 35, Application US/09030613
; Patent No. 6083706
; GENERAL INFORMATION:
; APPLICANT: Florjkiwicz, Robert Z.
; APPLICANT: Baird, J. Andrew
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tensburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-030-613-35

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 68
US-09-073-569-5
; Sequence 5, Application US/090735569
; Patent No. 6084088
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-073-569-5

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 69
US-08-566-190-20
; Sequence 20, Application US/08566190
; Patent No. 6090784
; GENERAL INFORMATION:
; APPLICANT: Warren, Stephen L.
; TITLE OF INVENTION: RNA Polymerase II Peptides and Methods of Use
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/566,190
; FILING DATE: 1-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-566-190-20

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 |||||
 Db 1 DYKDDDK 8

RESULT 70

US-09-110-618-5
 ; Sequence 5, Application US/09110618
 ; Patent No. 6090918
 ; GENERAL INFORMATION:
 ; APPLICANT: Parnet, Patricia et al.
 ; TITLE OF INVENTION: Receptor Designated 2P1
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/110,618
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/604,333
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Anderson, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2619
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; IMMEDIATE SOURCE:
 ; CLONE: FLAG peptide
 ; US-09-110-618-5

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 |||||
 Db 1 DYKDDDK 8

RESULT 71

US-09-022-253-3
 ; Sequence 3, Application US/09022253
 ; Patent No. 6096305
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William
 ; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/022,253
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/620,694
 ; FILING DATE: 21-MARCH-1996
 ; APPLICATION NUMBER: USSN 08/538,765
 ; FILING DATE: 7 AUGUST 1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/410,535
 ; FILING DATE: 23 MARCH 1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: No. 6096305 Relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; CLONE: FLAG_peptide
 ; US-09-022-253-3

Query Match 100.0%; Score 47; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
 |||||
 Db 1 DYKDDDK 8

RESULT 72

US-09-022-260-3
 ; Sequence 3, Application US/09022260
 ; Patent No. 6100235
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Fanslow, William
 ; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-09-022-260-3

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
| | | | |
Db 1 DYKDDDDK 8

RESULT 73
US-09-020-222-8
Sequence 8, Application US/09020222
Patent No. 611073
GENERAL INFORMATION:
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,222
FILING DATE: 06-Feb-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 02/07/1997
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-020-222-8

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
| | | | |
Db 1 DYKDDDDK 8

RESULT 74
US-09-053-866-6
Sequence 6, Application US/09053866
Patent No. 611075
GENERAL INFORMATION:
APPLICANT: Xu, Wenfeng
APPLICANT: Presnell, Scott R.
APPLICANT: Yee, David P.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR
TITLE OF INVENTION: PAR4 (ZCHEMR2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 611075e
US-09-053-866-6

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 75

US-08-816-346-50
; Sequence 50, Application US/08816346
; Patent No. 6127525
; GENERAL INFORMATION:
; APPLICANT: Crystal, Ronald G.
; APPLICANT: Falck-Pedersen, Erik
; APPLICANT: Gail, Jason
; APPLICANT: Kovsed, Inre
; APPLICANT: Wickham, Thomas J.
; TITLE OF INVENTION: CHIMERIC ADENOVIIRAL COAT PROTEIN AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA - 4900
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,346
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 67167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/616-5600
; TELEFAX: 312/616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-816-346-50

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 76
US-09-071-710-40
; Sequence 40, Application US/09071710
; Patent No. 6130043
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COHEN, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA

APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6130043e
US-09-071-710-40

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||
Db 1 DYKDDDDK 8

RESULT 77
US-08-888-429A-16
; Sequence 16, Application US/0888429A
; Patent No. 6136596
; GENERAL INFORMATION:
; APPLICANT: Davys, Roger J.
; APPLICANT: Whitmarsh, Alan
; APPLICANT: Tournier, Cathy
; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
; TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-888-429A-16

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 78
US-09-432-335-6
Sequence 6, Application US/09432335
Patent No. 6143720
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Flag affinity peptide
US-09-432-335-6

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 79
US-09-079-785-15
Sequence 15, Application US/09079785
Patent No. 6143869
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.

APPLICANT: Armistage, Richard J.
APPLICANT: Grusec, Hans-Jürgen
TITLE OF INVENTION: No. 6143869e1 Cytokine That Binds CD30
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,785
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-09-079-785-15

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 80
US-09-031-168-1
Sequence 1, Application US/09031168
Patent No. 6150583
GENERAL INFORMATION:
APPLICANT: Stanley B. Prusiner
APPLICANT: Glenn C. Telling

APPLICANT: Fred E. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPITOPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
City: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Asciit
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,168
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,626
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-031-168-1

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 56+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 1 DYKDDDDX 8

RESULT 81
US-09-335-411-50
Sequence 50, Application US/09335411
Patent No. 6153435
GENERAL INFORMATION:
APPLICANT: Crystal, Ronald G.
APPLICANT: Falck-Pedersen, Erik
APPLICANT: Gall, Jason
APPLICANT: Kovacs, Imre
APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA - 4900
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,411
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,346
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/616-5600
TELEFAX: 312/616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-335-411-50

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 56+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDX 8
Db 1 DYKDDDDX 8

RESULT 82
US-08-883-086-5
Sequence 5, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
City: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e

US-08-883-086-5

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
| | | | |
Db 1 DYKDDDDK 8

RESULT 83

US-08-912-276-24

; Sequence 24, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Scroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-912-276-24

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
| | | | |
Db 1 DYKDDDDK 8

RESULT 84
US-09-046-158A-20

; Sequence 20, Application US/09046158A
; Patent No. 6187552
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Kayes, Paul S.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING INHIBITORS OF
; TITLE OF INVENTION: JAK2/CYTOKINE RECEPTOR BINDING
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn Co., Intellectual Property
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,158A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Darnley Jr., James D.
; REGISTRATION NUMBER: 33,673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-2210
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-046-158A-20

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
| | | | |
Db 1 DYKDDDDK 8

RESULT 85

US-09-022-259-3

; Sequence 3, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


```
;
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG_peptide
;
US-09-022-259-3
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 86
US-09-022-257-3
; Sequence 3, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Farnlow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG_peptide
;
US-09-022-257-3
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 87
US-09-153-804-16
; Sequence 16, Application US/09153804
; Patent No. 6207380
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Paula N. Friedman
; APPLICANT: Julian Gordon
; APPLICANT: Steven C. Hodges
; APPLICANT: Michael R. Klass
; APPLICANT: Jon D. Kratochvil
; APPLICANT: Eric Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urinar
; FILE REFERENCE: 6180.US.01
; CURRENT APPLICATION NUMBER: US/09/153,804
; CURRENT FILING DATE: 1998-09-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
;
US-09-153-804-16
```

```
Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 88
US-09-105-343A-5
; Sequence 5, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
```

APPLICANT: WILEY, S.R.
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02859
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6207642e
US-09-105-343A-5

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 89
US-08-693-211-1
; Sequence 1, Application US/08693211
; Patent No. 6218516
; GENERAL INFORMATION:
; APPLICANT: Wilks, Andrew
; APPLICANT: Stacker, Steven
; APPLICANT: Oelrichs, Robert
; TITLE OF INVENTION: Antibodies Specific For the Extracellular Domain of NYK/PLK-1
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: LUD 5347
; CURRENT APPLICATION NUMBER: US/08/693,211
; CURRENT FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: PCT/US95/01727
; PRIOR FILING DATE: 1995-02-09
; PRIOR APPLICATION NUMBER: PM3793
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-693-211-1

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 90
US-08-944-483-75
; Sequence 75, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAUS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-944-483-75

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 91
US-09-227-717-5
; Sequence 5, Application US/09227717

Patent No. 6239268
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy W.
APPLICANT: Olierdorf, Tilman
APPLICANT: Liaw, Chen W.
APPLICANT: Cleveenger, William R.
TITLE OF INVENTION: INTERLEUKIN-1 TYPE 3 RECEPTORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,717
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/526,704
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: McMaster, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 690068.402C1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-227-717-5

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 92
US-08-995-659-7
Sequence 7, Application US/08995659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Marasovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US95 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US95 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US95 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG_peptide
US-08-995-659-7

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 93
US-09-525-397-40
Sequence 40, Application US/09525397
Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6252047e
US-09-525-397-40

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 94
US-09-320-774-3
Sequence 3, Application US/09320774
Patent No. 6265545
GENERAL INFORMATION:
APPLICANT: Jarvik, Jonathan W.
TITLE OF INVENTION: READING FRAME INDEPENDENT EPTOPE
FILING DATE: TAGGING
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESS: Harris Brotman
STREET: 202 Coast Blvd., Suite 111
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/320,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,106
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 654-2428
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-320-774-3

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 95
US-09-215-649A-7
Sequence 7, Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Marakovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-215-649A-7

Query Match          100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8
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RESULT 96
US-09-053-941-1
; Sequence 1, Application US/09053941
; Patent No. 6271354
; GENERAL INFORMATION:
; APPLICANT: SRINIVASAN, ALGARSAMY
; APPLICANT: KOPROWSKI, HILARY
; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
; FILE REFERENCE: CHIMERIC VIRAL Proteins
; CURRENT APPLICATION NUMBER: US/09/053,941
; CURRENT FILING DATE: 1998-04-02
; EARLIER APPLICATION NUMBER: 60/043,380
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-053-941-1

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 97
US-09-320-424-7
; Sequence 7, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN R.
; APPLICANT: GOODWIN, RAYMOND G.
; TITLE OF INVENTION: CYTOKINE THAT INDUCES APOPTOSIS
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic
US-09-320-424-7

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 98

US-09-214-278-25
; Sequence 25, Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic amino acid
US-09-214-278-25

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 99
US-09-140-084-9
; Sequence 9, Application US/09140084A
; Patent No. 630065
; GENERAL INFORMATION:
; APPLICANT: KIEKE, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: D6061CIP2
; CURRENT APPLICATION NUMBER: US/09/140,084A
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Epitope Tag
US-09-140-084-9

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 100
US-09-382-950-6
; Sequence 6, Application US/09382950
; Patent No. 630337
; GENERAL INFORMATION:
; APPLICANT: ROCHSCHILD, KENNETH
; APPLICANT: GITE, SADANAND
; APPLICANT: OLEJNIK, JERZY
; TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
; FILE REFERENCE: AMBER-03879
; CURRENT APPLICATION NUMBER: US/09/382,950
; CURRENT FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial/unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..T)
; OTHER INFORMATION: Synthetic
US-09-382-950-6

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Query Match      100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 DYKDDDDK 8
        |||||
Db      1 DYKDDDDK 8

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Search completed: June 29, 2006, 11:42:03
 Job time : 56 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:52:37 ; Search time 184 Seconds
(without alignments)
20.140 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47

Sequence: 1 DYKDDDK 8

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	47	100.0	8	3	US-09-728-401A-14
4	47	100.0	8	3	US-09-042-643-3
5	47	100.0	8	3	US-09-754-105-3
6	47	100.0	8	3	US-09-050-516-48
7	47	100.0	8	3	US-09-276-600-10
8	47	100.0	8	3	US-09-771-956-12
9	47	100.0	8	3	US-09-065-383-32
10	47	100.0	8	3	US-09-785-934-3
11	47	100.0	8	3	US-09-835-147-10
12	47	100.0	8	3	US-09-760-008A-14
13	47	100.0	8	3	US-09-728-911-11
14	47	100.0	8	3	US-09-193-329-65
15	47	100.0	8	3	US-09-013-329-65
16	47	100.0	8	3	US-09-790-823-26
17	47	100.0	8	3	US-09-809-517A-8
18	47	100.0	8	3	US-09-234-717-24
19	47	100.0	8	3	US-09-850-178-18
20	47	100.0	8	3	US-09-193-538-22
21	47	100.0	8	3	US-09-250-883-22
22	47	100.0	8	3	US-09-735-368-4
23	47	100.0	8	3	US-09-096-259-32
24	47	100.0	8	3	US-09-215-652-47
25	47	100.0	8	3	US-09-870-308-1
26	47	100.0	8	3	US-09-309-668A-1
27	47	100.0	8	3	US-09-855-722-25

28	47	100.0	8	3	US-09-817-413-1	Sequence 1, Appl1
29	47	100.0	8	3	US-09-193-663-9	Sequence 9, Appl1
30	47	100.0	8	3	US-09-887-855-7	Sequence 7, Appl1
31	47	100.0	8	3	US-09-904-245-3	Sequence 3, Appl1
32	47	100.0	8	3	US-09-245-603A-15	Sequence 15, Appl1
33	47	100.0	8	3	US-09-837-992-45	Sequence 45, Appl1
34	47	100.0	8	3	US-09-923-995-6	Sequence 6, Appl1
35	47	100.0	8	3	US-09-871-856-7	Sequence 7, Appl1
36	47	100.0	8	3	US-09-841-994-0	Sequence 40, Appl1
37	47	100.0	8	3	US-09-991-681-32	Sequence 32, Appl1
38	47	100.0	8	3	US-09-065-902-15	Sequence 15, Appl1
39	47	100.0	8	3	US-09-865-363-7	Sequence 7, Appl1
40	47	100.0	8	3	US-09-871-291-7	Sequence 7, Appl1
41	47	100.0	8	3	US-09-193-881-28	Sequence 28, Appl1
42	47	100.0	8	3	US-09-875-338-4	Sequence 94, Appl1
43	47	100.0	8	3	US-09-903-248-7	Sequence 7, Appl1
44	47	100.0	8	3	US-09-798-584-17	Sequence 17, Appl1
45	47	100.0	8	3	US-09-978-339-3	Sequence 3, Appl1
46	47	100.0	8	3	US-09-859-604-7	Sequence 7, Appl1
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48	47	100.0	8	3	US-09-844-508-14	Sequence 7, Appl1
49	47	100.0	8	3	US-09-888-358-17	Sequence 14, Appl1
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51	47	100.0	8	3	US-09-903-199-7	Sequence 7, Appl1
52	47	100.0	8	3	US-09-745-605-43	Sequence 43, Appl1
53	47	100.0	8	3	US-09-780-933-20	Sequence 20, Appl1
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55	47	100.0	8	3	US-09-995-193A-13	Sequence 13, Appl1
56	47	100.0	8	3	US-09-900-530A-13	Sequence 13, Appl1
57	47	100.0	8	3	US-09-923-246-37	Sequence 37, Appl1
58	47	100.0	8	3	US-09-973-145-6	Sequence 6, Appl1
59	47	100.0	8	3	US-09-825-651A-23	Sequence 23, Appl1
60	47	100.0	8	3	US-09-049-695A-21	Sequence 21, Appl1
61	47	100.0	8	3	US-09-092-297-21	Sequence 21, Appl1
62	47	100.0	8	3	US-09-903-023-7	Sequence 7, Appl1
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64	47	100.0	8	3	US-09-931-087A-19	Sequence 19, Appl1
65	47	100.0	8	3	US-09-263-959-985	Sequence 985, Appl1
66	47	100.0	8	3	US-09-969-192-2	Sequence 2, Appl1
67	47	100.0	8	3	US-09-840-243B-20	Sequence 20, Appl1
68	47	100.0	8	3	US-09-766-700A-8	Sequence 8, Appl1
69	47	100.0	8	3	US-09-843-245-12	Sequence 12, Appl1
70	47	100.0	8	3	US-09-989-350-19	Sequence 19, Appl1
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72	47	100.0	8	3	US-09-877-650-7	Sequence 7, Appl1
73	47	100.0	8	3	US-09-861-636-1	Sequence 1, Appl1
74	47	100.0	8	3	US-09-092-296-19	Sequence 19, Appl1
75	47	100.0	8	3	US-09-104-408-36	Sequence 36, Appl1
76	47	100.0	8	3	US-09-861-097-15	Sequence 15, Appl1
77	47	100.0	8	3	US-09-814-604-5	Sequence 5, Appl1
78	47	100.0	8	3	US-09-908-943A-186	Sequence 186, Appl1
79	47	100.0	8	3	US-09-997-623-47	Sequence 47, Appl1
80	47	100.0	8	3	US-09-995-898A-12	Sequence 12, Appl1
81	47	100.0	8	3	US-09-978-917A-47	Sequence 47, Appl1
82	47	100.0	8	3	US-09-436-184-7	Sequence 7, Appl1
83	47	100.0	8	3	US-09-950-634-23	Sequence 23, Appl1
84	47	100.0	8	3	US-09-846-033B-225	Sequence 225, Appl1
85	47	100.0	8	3	US-09-861-098-15	Sequence 15, Appl1
86	47	100.0	8	3	US-09-989-981A-12	Sequence 12, Appl1
87	47	100.0	8	3	US-09-993-180-33	Sequence 33, Appl1
88	47	100.0	8	3	US-09-759-595-7	Sequence 7, Appl1
89	47	100.0	8	3	US-09-999-220B-9	Sequence 9, Appl1
90	47	100.0	8	3	US-09-880-748-3238	Sequence 3238, Appl1
91	47	100.0	8	3	US-09-904-196B-14	Sequence 14, Appl1
92	47	100.0	8	3	US-09-972-473-19	Sequence 19, Appl1
93	47	100.0	8	3	US-09-922-226-39	Sequence 39, Appl1
94	47	100.0	8	3	US-09-774-381-21	Sequence 21, Appl1
95	47	100.0	8	3	US-09-876-790-11	Sequence 11, Appl1
96	47	100.0	8	3	US-09-932-613-183	Sequence 183, Appl1
97	47	100.0	8	3	US-09-782-587B-18	Sequence 18, Appl1
98	47	100.0	8	3	US-09-892-949-35	Sequence 35, Appl1
99	47	100.0	8	3	US-09-994-487-2	Sequence 2, Appl1
100	47	100.0	8	3	US-09-803-472-5	Sequence 5, Appl1

101	47	100.0	8	3	US-09-935-061-1	Sequence 1, Appl1	174	47	100.0	8	4	US-10-120-604-22	Sequence 22, Appl1
102	47	100.0	8	3	US-09-834-597-33	Sequence 33, Appl1	175	47	100.0	8	4	US-10-104-919-11	Sequence 11, Appl1
103	47	100.0	8	3	US-09-991-225-28	Sequence 28, Appl1	176	47	100.0	8	4	US-10-002-292A-10	Sequence 10, Appl1
104	47	100.0	8	3	US-09-925-055D-5	Sequence 5, Appl1	177	47	100.0	8	4	US-10-156-733-12	Sequence 12, Appl1
105	47	100.0	8	3	US-09-870-353A-31	Sequence 31, Appl1	178	47	100.0	8	4	US-10-263-677-21	Sequence 21, Appl1
106	47	100.0	8	3	US-09-870-932-7	Sequence 7, Appl1	179	47	100.0	8	4	US-10-067-649-28	Sequence 28, Appl1
107	47	100.0	8	3	US-09-746-375-15	Sequence 15, Appl1	180	47	100.0	8	4	US-10-127-816-42	Sequence 42, Appl1
108	47	100.0	8	3	US-09-861-012-15	Sequence 15, Appl1	181	47	100.0	8	4	US-10-269-353-68	Sequence 68, Appl1
109	47	100.0	8	3	US-09-932-322-183	Sequence 183, App	182	47	100.0	8	4	US-10-211-088-288	Sequence 288, App
110	47	100.0	8	3	US-09-962-736-1547	Sequence 1547, Ap	183	47	100.0	8	4	US-10-299-327-3	Sequence 3, Appl1
111	47	100.0	8	3	US-09-962-756-1779	Sequence 1779, Ap	184	47	100.0	8	4	US-10-128-559-74	Sequence 74, Appl1
112	47	100.0	8	3	US-09-080-140-30	Sequence 30, Appl1	185	47	100.0	8	4	US-10-313-135-7	Sequence 7, Appl1
113	47	100.0	8	3	US-09-897-787-8	Sequence 8, Appl1	186	47	100.0	8	4	US-10-133-797-28	Sequence 28, Appl1
114	47	100.0	8	3	US-09-972-473-19	Sequence 19, Appl1	187	47	100.0	8	4	US-10-005-956-553	Sequence 553, App
115	47	100.0	8	3	US-09-789-210-75	Sequence 75, Appl1	188	47	100.0	8	4	US-10-071-458-15	Sequence 15, Appl1
116	47	100.0	8	3	US-09-813-197-7	Sequence 7, Appl1	189	47	100.0	8	4	US-10-116-519-47	Sequence 47, Appl1
117	47	100.0	8	4	US-10-000-628-10	Sequence 10, Appl1	190	47	100.0	8	4	US-10-309-515-4	Sequence 4, Appl1
118	47	100.0	8	4	US-10-036-568-6	Sequence 6, Appl1	191	47	100.0	8	4	US-10-192-294-14	Sequence 14, Appl1
119	47	100.0	8	4	US-10-115-178-14	Sequence 14, Appl1	192	47	100.0	8	4	US-10-295-723-37	Sequence 37, Appl1
120	47	100.0	8	4	US-10-025-167-50	Sequence 50, Appl1	193	47	100.0	8	4	US-10-137-953-16	Sequence 16, Appl1
121	47	100.0	8	4	US-10-003-496-15	Sequence 15, Appl1	194	47	100.0	8	4	US-10-338-395-28	Sequence 28, Appl1
122	47	100.0	8	4	US-10-137-447-5	Sequence 5, Appl1	195	47	100.0	8	4	US-10-195-707B-40	Sequence 40, Appl1
123	47	100.0	8	4	US-10-035-451A-1	Sequence 1, Appl1	196	47	100.0	8	4	US-10-293-086-142	Sequence 142, App
124	47	100.0	8	4	US-10-158-895-5	Sequence 5, Appl1	197	47	100.0	8	4	US-10-173-461-26	Sequence 26, Appl1
125	47	100.0	8	4	US-10-029-009-1	Sequence 1, Appl1	198	47	100.0	8	4	US-10-032-214-256	Sequence 256, App
126	47	100.0	8	4	US-10-029-009-29	Sequence 29, Appl1	199	47	100.0	8	4	US-10-158-825-147	Sequence 147, App
127	47	100.0	8	4	US-10-082-659-15	Sequence 15, Appl1	200	47	100.0	8	4	US-10-187-049-6	Sequence 6, Appl1
128	47	100.0	8	4	US-10-086-135-6	Sequence 6, Appl1	201	47	100.0	8	4	US-10-284-400-18	Sequence 18, Appl1
129	47	100.0	8	4	US-10-208-357-8	Sequence 8, Appl1	202	47	100.0	8	4	US-10-284-089-12	Sequence 12, Appl1
130	47	100.0	8	4	US-10-116-273-40	Sequence 40, Appl1	203	47	100.0	8	4	US-10-028-374-16	Sequence 16, Appl1
131	47	100.0	8	4	US-10-076-248-1	Sequence 1, Appl1	204	47	100.0	8	4	US-10-200-242-25	Sequence 25, Appl1
132	47	100.0	8	4	US-10-216-408-26	Sequence 26, Appl1	205	47	100.0	8	4	US-10-153-244-261	Sequence 261, App
133	47	100.0	8	4	US-10-029-347-27	Sequence 27, Appl1	206	47	100.0	8	4	US-10-265-071-20	Sequence 20, Appl1
134	47	100.0	8	4	US-10-006-069A-225	Sequence 225, App	207	47	100.0	8	4	US-10-256-705-14	Sequence 14, Appl1
135	47	100.0	8	4	US-10-219-248-25	Sequence 25, Appl1	208	47	100.0	8	4	US-10-342-103-7	Sequence 7, Appl1
136	47	100.0	8	4	US-10-133-205-1	Sequence 1, Appl1	209	47	100.0	8	4	US-10-243-072-49	Sequence 49, Appl1
137	47	100.0	8	4	US-10-059-720-50	Sequence 50, Appl1	210	47	100.0	8	4	US-10-291-990-14	Sequence 14, Appl1
138	47	100.0	8	4	US-10-139-662-39	Sequence 39, Appl1	211	47	100.0	8	4	US-10-345-618-9	Sequence 9, Appl1
139	47	100.0	8	4	US-10-077-023-94	Sequence 94, Appl1	212	47	100.0	8	4	US-10-025-966A-70	Sequence 20, Appl1
140	47	100.0	8	4	US-10-075-846-36	Sequence 36, Appl1	213	47	100.0	8	4	US-10-128-587A-74	Sequence 74, Appl1
141	47	100.0	8	4	US-10-040-805-7	Sequence 7, Appl1	214	47	100.0	8	4	US-10-199-869-35	Sequence 35, Appl1
142	47	100.0	8	4	US-10-219-247-25	Sequence 25, Appl1	215	47	100.0	8	4	US-10-268-336-7	Sequence 7, Appl1
143	47	100.0	8	4	US-10-056-884-26	Sequence 26, Appl1	216	47	100.0	8	4	US-10-234-816-69	Sequence 69, Appl1
144	47	100.0	8	4	US-10-080-980-22	Sequence 22, Appl1	217	47	100.0	8	4	US-10-305-555-40	Sequence 40, Appl1
145	47	100.0	8	4	US-10-158-238-5	Sequence 5, Appl1	218	47	100.0	8	4	US-10-010-568-15	Sequence 15, Appl1
146	47	100.0	8	4	US-10-071-838-14	Sequence 14, Appl1	219	47	100.0	8	4	US-10-318-966-14	Sequence 14, Appl1
147	47	100.0	8	4	US-10-191-029-11	Sequence 11, Appl1	220	47	100.0	8	4	US-10-162-497-50	Sequence 50, Appl1
148	47	100.0	8	4	US-10-084-826-14	Sequence 14, Appl1	221	47	100.0	8	4	US-10-327-620-5	Sequence 5, Appl1
149	47	100.0	8	4	US-10-241-476-26	Sequence 26, Appl1	222	47	100.0	8	4	US-10-210-152-251	Sequence 251, App
150	47	100.0	8	4	US-10-270-877-32	Sequence 32, Appl1	223	47	100.0	8	4	US-10-384-743-5	Sequence 5, Appl1
151	47	100.0	8	4	US-10-230-875-5	Sequence 5, Appl1	224	47	100.0	8	4	US-10-234-951A-24	Sequence 24, Appl1
152	47	100.0	8	4	US-10-185-425-12	Sequence 12, Appl1	225	47	100.0	8	4	US-10-372-874-21	Sequence 21, Appl1
153	47	100.0	8	4	US-10-270-837-32	Sequence 32, Appl1	226	47	100.0	8	4	US-10-005-966A-1	Sequence 1, Appl1
154	47	100.0	8	4	US-10-086-156-22	Sequence 22, Appl1	227	47	100.0	8	4	US-10-185-567-24	Sequence 24, Appl1
155	47	100.0	8	4	US-10-151-882-48	Sequence 48, Appl1	228	47	100.0	8	4	US-10-191-252-12	Sequence 12, Appl1
156	47	100.0	8	4	US-10-081-775-22	Sequence 22, Appl1	229	47	100.0	8	4	US-10-192-253-32	Sequence 32, Appl1
157	47	100.0	8	4	US-10-139-683-39	Sequence 39, Appl1	230	47	100.0	8	4	US-10-190-414-21	Sequence 21, Appl1
158	47	100.0	8	4	US-10-092-771-34	Sequence 34, Appl1	231	47	100.0	8	4	US-10-143-618-29	Sequence 29, Appl1
159	47	100.0	8	4	US-10-222-334-73	Sequence 73, Appl1	232	47	100.0	8	4	US-10-166-098-17	Sequence 17, Appl1
160	47	100.0	8	4	US-10-112-788-13	Sequence 13, Appl1	233	47	100.0	8	4	US-10-126-764-4	Sequence 4, Appl1
161	47	100.0	8	4	US-10-090-365-11	Sequence 11, Appl1	234	47	100.0	8	4	US-10-084-706-54	Sequence 54, Appl1
162	47	100.0	8	4	US-10-040-862-10467	Sequence 10467, A	235	47	100.0	8	4	US-10-390-045-4	Sequence 4, Appl1
163	47	100.0	8	4	US-10-278-547-48	Sequence 48, Appl1	236	47	100.0	8	4	US-10-406-209-28	Sequence 28, Appl1
164	47	100.0	8	4	US-10-252-408-28	Sequence 28, Appl1	237	47	100.0	8	4	US-10-408-930-27	Sequence 27, Appl1
165	47	100.0	8	4	US-10-067-443-26	Sequence 26, Appl1	238	47	100.0	8	4	US-10-325-720-44	Sequence 44, Appl1
166	47	100.0	8	4	US-10-177-661-5	Sequence 5, Appl1	239	47	100.0	8	4	US-10-351-189-44	Sequence 44, Appl1
167	47	100.0	8	4	US-10-188-343-4	Sequence 4, Appl1	240	47	100.0	8	4	US-10-424-409-1	Sequence 1, Appl1
168	47	100.0	8	4	US-10-028-392-12	Sequence 12, Appl1	241	47	100.0	8	4	US-10-308-373-5	Sequence 5, Appl1
169	47	100.0	8	4	US-10-164-080-3	Sequence 3, Appl1	242	47	100.0	8	4	US-10-336-608-1	Sequence 1, Appl1
170	47	100.0	8	4	US-10-158-847-147	Sequence 147, App	243	47	100.0	8	4	US-10-414-186-49	Sequence 49, Appl1
171	47	100.0	8	4	US-10-104-943-34	Sequence 34, Appl1	244	47	100.0	8	4	US-10-405-878-7	Sequence 7, Appl1
172	47	100.0	8	4	US-10-174-368A-6	Sequence 6, Appl1	245	47	100.0	8	4	US-10-155-693-36	Sequence 36, Appl1
173	47	100.0	8	4	US-10-100-957A-36	Sequence 36, Appl1	246	47	100.0	8	4	US-10-325-717-77	Sequence 77, Appl1

247	47	100.0	8	4	US-10-082-649-16	Sequence 16, Appl	320	47	100.0	8	4	US-10-280-139-18	Sequence 18, Appl
248	47	100.0	8	4	US-10-188-608-13	Sequence 13, Appl	321	47	100.0	8	4	US-10-019-065A-4	Sequence 4, Appl
249	47	100.0	8	4	US-10-183-770-16	Sequence 16, Appl	322	47	100.0	8	4	US-10-688-100-2	Sequence 2, Appl
250	47	100.0	8	4	US-10-376-406-3	Sequence 3, Appl	323	47	100.0	8	4	US-10-632-694-9	Sequence 9, Appl
251	47	100.0	8	4	US-10-100-217-5	Sequence 5, Appl	324	47	100.0	8	4	US-10-431-096-122	Sequence 122, App
252	47	100.0	8	4	US-10-264-171-7	Sequence 7, Appl	325	47	100.0	8	4	US-10-399-518-135	Sequence 135, App
253	47	100.0	8	4	US-10-271-078-51	Sequence 51, Appl	326	47	100.0	8	4	US-10-399-518-142	Sequence 142, App
254	47	100.0	8	4	US-10-222-026A-39	Sequence 39, Appl	327	47	100.0	8	4	US-10-434-479-4	Sequence 4, Appl
255	47	100.0	8	4	US-10-203-531-9	Sequence 9, Appl	328	47	100.0	8	4	US-10-616-897-24	Sequence 24, Appl
256	47	100.0	8	4	US-10-264-127-7	Sequence 7, Appl	329	47	100.0	8	4	US-10-621-758A-37	Sequence 37, Appl
257	47	100.0	8	4	US-10-062-923-19	Sequence 19, Appl	330	47	100.0	8	4	US-10-343-663A-39	Sequence 39, Appl
258	47	100.0	8	4	US-10-193-477-117	Sequence 117, App	331	47	100.0	8	4	US-10-275-339A-8	Sequence 8, Appl
259	47	100.0	8	4	US-10-295-693-28	Sequence 28, Appl	332	47	100.0	8	4	US-10-659-684-37	Sequence 37, Appl
260	47	100.0	8	4	US-10-427-208-73	Sequence 73, Appl	333	47	100.0	8	4	US-10-363-145A-13	Sequence 13, Appl
261	47	100.0	8	4	US-10-245-227B-9	Sequence 9, Appl	334	47	100.0	8	4	US-10-742-161-3	Sequence 3, Appl
262	47	100.0	8	4	US-10-350-516-30	Sequence 30, Appl	335	47	100.0	8	4	US-10-742-372-3	Sequence 3, Appl
263	47	100.0	8	4	US-10-279-687-9	Sequence 9, Appl	336	47	100.0	8	4	US-10-276-272A-1	Sequence 1, Appl
264	47	100.0	8	4	US-10-438-537-10	Sequence 10, Appl	337	47	100.0	8	4	US-10-763-992-34	Sequence 34, Appl
265	47	100.0	8	4	US-10-351-157-36	Sequence 36, Appl	338	47	100.0	8	4	US-10-158-825-147	Sequence 147, App
266	47	100.0	8	4	US-10-372-003A-50	Sequence 50, Appl	339	47	100.0	8	4	US-10-456-153A-3	Sequence 3, Appl
267	47	100.0	8	4	US-10-275-025-8	Sequence 8, Appl	340	47	100.0	8	4	US-10-663-208A-37	Sequence 37, Appl
268	47	100.0	8	4	US-10-412-897-73	Sequence 73, Appl	341	47	100.0	8	4	US-10-612-410-16	Sequence 16, Appl
269	47	100.0	8	4	US-10-273-180-26	Sequence 26, Appl	342	47	100.0	8	4	US-10-467-243-33	Sequence 33, Appl
270	47	100.0	8	4	US-10-388-215-35	Sequence 35, Appl	343	47	100.0	8	4	US-10-451-947A-10	Sequence 10, Appl
271	47	100.0	8	4	US-10-293-418-3238	Sequence 3238, Ap	344	47	100.0	8	4	US-10-646-301A-37	Sequence 37, Appl
272	47	100.0	8	4	US-10-369-405-28	Sequence 28, Appl	345	47	100.0	8	4	US-10-745-034-29	Sequence 29, Appl
273	47	100.0	8	4	US-10-405-793-251	Sequence 251, App	346	47	100.0	8	4	US-10-769-131-12	Sequence 12, Appl
274	47	100.0	8	4	US-10-375-157-15	Sequence 15, Appl	347	47	100.0	8	4	US-10-772-531-35	Sequence 35, Appl
275	47	100.0	8	4	US-10-126-103-122	Sequence 122, App	348	47	100.0	8	4	US-10-656-441-2	Sequence 2, Appl
276	47	100.0	8	4	US-10-352-554-36	Sequence 36, Appl	349	47	100.0	8	4	US-10-684-332-55	Sequence 55, Appl
277	47	100.0	8	4	US-10-175-689-33	Sequence 33, Appl	350	47	100.0	8	4	US-10-738-454-9	Sequence 9, Appl
278	47	100.0	8	4	US-10-253-471-1547	Sequence 1547, Ap	351	47	100.0	8	4	US-10-154-670-3	Sequence 3, Appl
279	47	100.0	8	4	US-10-253-471-1779	Sequence 1779, Ap	352	47	100.0	8	4	US-10-806-294-15	Sequence 15, Appl
280	47	100.0	8	4	US-10-366-630-5	Sequence 5, Appl	353	47	100.0	8	4	US-10-615-659-61	Sequence 61, Appl
281	47	100.0	8	4	US-10-277-216-33	Sequence 33, Appl	354	47	100.0	8	4	US-10-671-054-2	Sequence 2, Appl
282	47	100.0	8	4	US-10-154-884B-11290	Sequence 11290, A	355	47	100.0	8	4	US-10-688-016-23	Sequence 23, Appl
283	47	100.0	8	4	US-10-200-242-25	Sequence 25, Appl	356	47	100.0	8	4	US-10-736-979-37	Sequence 37, Appl
284	47	100.0	8	4	US-10-602-350-5	Sequence 5, Appl	357	47	100.0	8	4	US-10-472-724-21	Sequence 21, Appl
285	47	100.0	8	4	US-10-204-581-11	Sequence 11, Appl	358	47	100.0	8	4	US-10-156-708-4	Sequence 4, Appl
286	47	100.0	8	4	US-10-609-296-54	Sequence 54, Appl	359	47	100.0	8	4	US-10-635-977-61	Sequence 61, Appl
287	47	100.0	8	4	US-10-339-712-7	Sequence 7, Appl	360	47	100.0	8	4	US-10-472-724-21	Sequence 21, Appl
288	47	100.0	8	4	US-10-339-712-63	Sequence 63, Appl	361	47	100.0	8	4	US-10-472-724-21	Sequence 21, Appl
289	47	100.0	8	4	US-10-390-585-66	Sequence 66, Appl	362	47	100.0	8	4	US-10-764-324-10467	Sequence 10467, A
290	47	100.0	8	4	US-10-436-715-464	Sequence 464, App	363	47	100.0	8	4	US-10-629-313-50	Sequence 50, Appl
291	47	100.0	8	4	US-10-356-289-3	Sequence 3, Appl	364	47	100.0	8	4	US-10-098-935-7	Sequence 7, Appl
292	47	100.0	8	4	US-10-126-022-33	Sequence 33, Appl	365	47	100.0	8	4	US-10-762-588-10	Sequence 10, Appl
293	47	100.0	8	4	US-10-320-104B-3	Sequence 3, Appl	366	47	100.0	8	4	US-10-343-389A-10	Sequence 10, Appl
294	47	100.0	8	4	US-10-395-418-15	Sequence 15, Appl	367	47	100.0	8	4	US-10-744-379-3	Sequence 3, Appl
295	47	100.0	8	4	US-10-275-589-13	Sequence 13, Appl	368	47	100.0	8	4	US-10-821-583-31	Sequence 31, Appl
296	47	100.0	8	4	US-10-253-493-1547	Sequence 1547, Ap	369	47	100.0	8	4	US-10-828-817-1	Sequence 1, Appl
297	47	100.0	8	4	US-10-253-493-1779	Sequence 1779, Ap	370	47	100.0	8	4	US-10-843-189-3	Sequence 3, Appl
298	47	100.0	8	4	US-10-449-831A-162	Sequence 162, App	371	47	100.0	8	4	US-10-843-189-3	Sequence 3, Appl
299	47	100.0	8	4	US-10-420-034A-12	Sequence 12, Appl	372	47	100.0	8	4	US-10-715-998-49	Sequence 49, Appl
300	47	100.0	8	4	US-10-460-524-15	Sequence 15, Appl	373	47	100.0	8	4	US-10-612-742-33	Sequence 33, Appl
301	47	100.0	8	4	US-10-403-847-122	Sequence 122, App	374	47	100.0	8	4	US-10-699-088-93	Sequence 93, Appl
302	47	100.0	8	4	US-10-308-847-122	Sequence 162, App	375	47	100.0	8	4	US-10-474-600-1	Sequence 1, Appl
303	47	100.0	8	4	US-10-308-128-162	Sequence 28, Appl	376	47	100.0	8	4	US-10-842-906-3	Sequence 3, Appl
304	47	100.0	8	4	US-10-223-560-7	Sequence 48, Appl	377	47	100.0	8	4	US-10-627-592-39	Sequence 39, Appl
305	47	100.0	8	4	US-10-664-456-28	Sequence 26, Appl	378	47	100.0	8	4	US-10-768-976-22	Sequence 22, Appl
306	47	100.0	8	4	US-10-646-873-48	Sequence 26, Appl	379	47	100.0	8	4	US-10-103-294A-1	Sequence 1, Appl
307	47	100.0	8	4	US-10-649-873-26	Sequence 2, Appl	380	47	100.0	8	4	US-10-475-538A-48	Sequence 48, Appl
308	47	100.0	8	4	US-10-380-880-2	Sequence 26, Appl	381	47	100.0	8	5	US-10-627-582-48	Sequence 48, Appl
309	47	100.0	8	4	US-10-651-722-26	Sequence 26, Appl	382	47	100.0	8	5	US-10-761-905-24	Sequence 24, Appl
310	47	100.0	8	4	US-10-351-891-93	Sequence 93, Appl	383	47	100.0	8	5	US-10-817-607-96	Sequence 96, Appl
311	47	100.0	8	4	US-10-401-053A-8	Sequence 8, Appl	384	47	100.0	8	5	US-10-871-776-12	Sequence 12, Appl
312	47	100.0	8	4	US-10-652-244-7	Sequence 7, Appl	385	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
313	47	100.0	8	4	US-10-296-718-3	Sequence 3, Appl	386	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
314	47	100.0	8	4	US-10-257-864A-106	Sequence 106, App	387	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
315	47	100.0	8	4	US-10-315-379-20	Sequence 20, Appl	388	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
316	47	100.0	8	4	US-10-252-155-605	Sequence 605, App	389	47	100.0	8	5	US-10-872-161-58	Sequence 58, Appl
317	47	100.0	8	4	US-10-380-614-12	Sequence 12, Appl	390	47	100.0	8	5	US-10-699-113-2	Sequence 23, Appl
318	47	100.0	8	4	US-10-448-525-36	Sequence 36, Appl	391	47	100.0	8	5	US-10-677-593-15	Sequence 15, Appl
319	47	100.0	8	4	US-10-444-958-38	Sequence 38, Appl	392	47	100.0	8	5	US-10-491-277-12	Sequence 12, Appl
	47	100.0	8	4	US-10-668-453-1	Sequence 1, Appl						US-10-801-487-186	Sequence 186, App

393	47	100.0	8	5	US-10-705-745-14	Sequence 14, Appl	466	47	100.0	8	5	US-10-500-671A-18	Sequence 18, Appl
394	47	100.0	8	5	US-10-399-585-134	Sequence 134, App	467	47	100.0	8	5	US-10-972-052-15	Sequence 15, Appl
395	47	100.0	8	5	US-10-399-585-140	Sequence 140, App	468	47	100.0	8	5	US-10-507-421-28	Sequence 28, Appl
396	47	100.0	8	5	US-10-478-058A-20	Sequence 20, Appl	469	47	100.0	8	5	US-10-719-144-22	Sequence 22, Appl
397	47	100.0	8	5	US-10-781-564-10	Sequence 10, Appl	470	47	100.0	8	5	US-10-790-273-3	Sequence 3, Appl
398	47	100.0	8	5	US-10-888-918-11	Sequence 11, Appl	471	47	100.0	8	5	US-10-994-824-94	Sequence 94, Appl
399	47	100.0	8	5	US-10-831-622-101	Sequence 101, App	472	47	100.0	8	5	US-10-994-987-21	Sequence 21, Appl
400	47	100.0	8	5	US-10-745-447-29	Sequence 29, Appl	473	47	100.0	8	5	US-10-868-673-61	Sequence 61, Appl
401	47	100.0	8	5	US-10-857-664-5	Sequence 5, Appl	474	47	100.0	8	5	US-10-981-998-11	Sequence 11, Appl
402	47	100.0	8	5	US-10-801-938-186	Sequence 186, App	475	47	100.0	8	5	US-10-910-507-5	Sequence 5, Appl
403	47	100.0	8	5	US-10-801-509-186	Sequence 186, App	476	47	100.0	8	5	US-10-982-555-35	Sequence 35, Appl
404	47	100.0	8	5	US-10-801-486-186	Sequence 186, App	477	47	100.0	8	5	US-10-520-408-2	Sequence 2, Appl
405	47	100.0	8	5	US-10-645-085A-106	Sequence 106, App	478	47	100.0	8	5	US-10-482-803B-4	Sequence 4, Appl
406	47	100.0	8	5	US-10-837-776-1	Sequence 1, Appl	479	47	100.0	8	5	US-10-997-078-81	Sequence 81, Appl
407	47	100.0	8	5	US-10-787-442-37	Sequence 37, Appl	480	47	100.0	8	5	US-10-756-813-21	Sequence 21, Appl
408	47	100.0	8	5	US-10-882-761-27	Sequence 27, Appl	481	47	100.0	8	5	US-10-800-248-56	Sequence 56, Appl
409	47	100.0	8	5	US-10-812-232-10	Sequence 10, Appl	482	47	100.0	8	5	US-10-971-736-470	Sequence 470, App
410	47	100.0	8	5	US-10-841-798-9	Sequence 9, Appl	483	47	100.0	8	5	US-10-484-273A-4	Sequence 4, Appl
411	47	100.0	8	5	US-10-802-133-7	Sequence 7, Appl	484	47	100.0	8	5	US-10-990-276-7	Sequence 7, Appl
412	47	100.0	8	5	US-10-494-248-4	Sequence 4, Appl	485	47	100.0	8	5	US-10-636-320-7	Sequence 7, Appl
413	47	100.0	8	5	US-10-888-867-11	Sequence 11, Appl	486	47	100.0	8	5	US-10-933-025-20	Sequence 20, Appl
414	47	100.0	8	5	US-10-888-779-11	Sequence 11, Appl	487	47	100.0	8	5	US-10-966-483-52	Sequence 52, Appl
415	47	100.0	8	5	US-10-888-780-11	Sequence 11, Appl	488	47	100.0	8	5	US-10-950-747-18	Sequence 18, Appl
416	47	100.0	8	5	US-10-888-931-11	Sequence 11, Appl	489	47	100.0	8	5	US-10-983-120-20	Sequence 20, Appl
417	47	100.0	8	5	US-10-863-729-12	Sequence 12, Appl	490	47	100.0	8	5	US-10-903-612B-121	Sequence 121, App
418	47	100.0	8	5	US-10-926-217-21	Sequence 21, Appl	491	47	100.0	8	5	US-10-498-665-77	Sequence 77, Appl
419	47	100.0	8	5	US-10-851-637-83	Sequence 83, Appl	492	47	100.0	8	5	US-10-993-568-6	Sequence 6, Appl
420	47	100.0	8	5	US-10-900-926-68	Sequence 68, Appl	493	47	100.0	8	5	US-10-513-263-6	Sequence 6, Appl
421	47	100.0	8	5	US-10-925-448-19	Sequence 19, Appl	494	47	100.0	8	5	US-10-381-094A-3	Sequence 3, Appl
422	47	100.0	8	5	US-10-926-225-12	Sequence 12, Appl	495	47	100.0	8	5	US-10-237-813-43	Sequence 43, Appl
423	47	100.0	8	5	US-10-858-367-18	Sequence 18, Appl	496	47	100.0	8	6	US-11-004-111-47	Sequence 47, Appl
424	47	100.0	8	5	US-10-857-644-27	Sequence 27, Appl	497	47	100.0	8	6	US-11-004-461-14	Sequence 14, Appl
425	47	100.0	8	5	US-10-719-523-7	Sequence 7, Appl	498	47	100.0	8	6	US-11-020-965-7	Sequence 7, Appl
426	47	100.0	8	5	US-10-835-096-16	Sequence 16, Appl	499	47	100.0	8	6	US-11-045-944-11	Sequence 11, Appl
427	47	100.0	8	5	US-10-874-923-66	Sequence 66, Appl	500	47	100.0	8	6	US-11-218-020-17	Sequence 17, Appl
428	47	100.0	8	5	US-10-634-645-10	Sequence 10, Appl							
429	47	100.0	8	5	US-10-841-250-101	Sequence 101, App							
430	47	100.0	8	5	US-10-311-144-2	Sequence 2, Appl							
431	47	100.0	8	5	US-10-769-088-15	Sequence 15, Appl							
432	47	100.0	8	5	US-10-888-805-71	Sequence 71, Appl							
433	47	100.0	8	5	US-10-699-114-93	Sequence 93, Appl							
434	47	100.0	8	5	US-10-864-249-49	Sequence 49, Appl							
435	47	100.0	8	5	US-10-926-386-73	Sequence 73, Appl							
436	47	100.0	8	5	US-10-738-780-22	Sequence 22, Appl							
437	47	100.0	8	5	US-10-865-663-2	Sequence 2, Appl							
438	47	100.0	8	5	US-10-497-003A-17	Sequence 17, Appl							
439	47	100.0	8	5	US-10-658-752-8	Sequence 8, Appl							
440	47	100.0	8	5	US-10-765-063-3	Sequence 3, Appl							
441	47	100.0	8	5	US-10-487-132-10	Sequence 10, Appl							
442	47	100.0	8	5	US-10-968-432-11	Sequence 11, Appl							
443	47	100.0	8	5	US-10-935-290-39	Sequence 39, Appl							
444	47	100.0	8	5	US-10-819-054-19	Sequence 19, Appl							
445	47	100.0	8	5	US-10-949-685-4	Sequence 4, Appl							
446	47	100.0	8	5	US-10-258-182A-7	Sequence 7, Appl							
447	47	100.0	8	5	US-10-801-493-186	Sequence 186, App							
448	47	100.0	8	5	US-10-955-218-21	Sequence 21, Appl							
449	47	100.0	8	5	US-10-917-844-91	Sequence 91, Appl							
450	47	100.0	8	5	US-10-508-309-1	Sequence 1, Appl							
451	47	100.0	8	5	US-10-988-091-32	Sequence 32, Appl							
452	47	100.0	8	5	US-10-931-916-71	Sequence 71, Appl							
453	47	100.0	8	5	US-10-980-669-9	Sequence 9, Appl							
454	47	100.0	8	5	US-10-488-806-9	Sequence 9, Appl							
455	47	100.0	8	5	US-10-918-685A-7	Sequence 7, Appl							
456	47	100.0	8	5	US-10-922-339-39	Sequence 39, Appl							
457	47	100.0	8	5	US-10-029-345A-75	Sequence 75, Appl							
458	47	100.0	8	5	US-10-356-264A-22	Sequence 22, Appl							
459	47	100.0	8	5	US-10-841-819B-22	Sequence 22, Appl							
460	47	100.0	8	5	US-10-964-215-101	Sequence 101, App							
461	47	100.0	8	5	US-10-957-433-4	Sequence 4, Appl							
462	47	100.0	8	5	US-10-991-681-39	Sequence 39, Appl							
463	47	100.0	8	5	US-10-479-901-296	Sequence 296, App							
464	47	100.0	8	5	US-10-900-399-7	Sequence 7, Appl							
465	47	100.0	8	5	US-10-764-212-80	Sequence 80, Appl							

RESULT 1
 US-08-971-317A-9
 ; Sequence 9, Application US/08971317A
 ; Publication No. US20010010925A1
 GENERAL INFORMATION:
 APPLICANT: Wiley, Steven R.
 TITLE OF INVENTION: TNF-DELTA LIGAND AND USBS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971,317A
 FILING DATE: 17-NOV-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Goller, Mimi C
 REGISTRATION NUMBER: 39,046
 REFERENCE/DOCKET NUMBER: 6255.US.01
 TELECOMMUNICATION INFORMATION:

ALIGNMENTS

Sequence 18, Appl	
Sequence 25, Appl	
Sequence 18, Appl	
Sequence 22, Appl	
Sequence 34, Appl	
Sequence 61, Appl	
Sequence 21, Appl	
Sequence 11, Appl	
Sequence 35, Appl	
Sequence 2, Appl	
Sequence 4, Appl	
Sequence 81, Appl	
Sequence 21, Appl	
Sequence 56, Appl	
Sequence 470, App	
Sequence 7, Appl	
Sequence 7, Appl	
Sequence 20, Appl	
Sequence 18, Appl	
Sequence 121, App	
Sequence 77, Appl	
Sequence 6, Appl	
Sequence 3, Appl	
Sequence 43, Appl	
Sequence 47, Appl	
Sequence 14, Appl	
Sequence 7, Appl	
Sequence 11, Appl	
Sequence 17, Appl	

TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-9

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 2
US-08-926-626-12
Sequence 12, Application US/08926626
Publication No. US2002003524A1
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLBITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASSEL, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE PROSTATE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,626
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6158.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-926-626-12
Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 3
US-09-728-401A-14
Sequence 14, Application US/09728401A
Publication No. US20010000075A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NEUROTACTIN AND USES THEREFOR
FILE REFERENCE: MB1096-001CP2CN2M (formerly 07334-190003)
CURRENT APPLICATION NUMBER: US/09/728,401A
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 09/481,485
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 08/991,426
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: US 08/851,160
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/643,798
PRIOR FILING DATE: 1996-05-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-728-401A-14

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 4
US-09-042-643-3
Sequence 3, Application US/09042643
Publication No. US20010008766A1
GENERAL INFORMATION:
APPLICANT: DAUNERT, SYLVIA
APPLICANT: LEWIS, Jennifer C
APPLICANT: HERNANDEZ, Emily
TITLE OF INVENTION: QUANTITATIVE BINDING ASSAYS USING GREEN FLUORESCENT PROTEIN AS A
FILE REFERENCE: 3798-0102P
CURRENT APPLICATION NUMBER: US/09/042,643
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Octapeptide fused to GFP
US-09-042-643-3

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 5
US-09-754-105-3
; Sequence 3, Application US/09754105
; Patent No. US20010009768A1
; GENERAL INFORMATION:
; APPLICANT: Carretti, Douglas
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
; FILE REFERENCE: 28332
; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Flag peptide
; NAME/KEY: Artificial
; LOCATION: (1)..(8)
US-09-754-105-3

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 6
US-09-050-516-48
; Sequence 48, Application US/09050516
; Patent No. US20010010904A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HAYDEN, MARK
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/050,516
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6065.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-050-516-48

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 7
US-09-276-600-10
; Sequence 10, Application US/09276600
; Patent No. US20010010908A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpits
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for
; TITLE OF INVENTION: Detecting Disease of the Prostate
; FILE REFERENCE: 6397.US.01
; CURRENT APPLICATION NUMBER: US/09/276,600
; CURRENT FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-276-600-10

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 8
US-09-771-956-12
; Sequence 12, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brobeck, Robin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001

CURRENT APPLICATION NUMBER: US/09/771,956
CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FLAG EPITOPE
US-09-771-956-12

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 9
US-09-065-383-32
Sequence 32, Application US/09065383
Publication No. US20010055758A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLBITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAEP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,383
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/842,385
FILING DATE: 23-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084-US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-09-065-383-32

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 10
US-09-785-934-3
Sequence 3, Application US/09785934
Patent No. US2002002132A1
GENERAL INFORMATION:
APPLICANT: Plueneke, John
TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 3005
CURRENT APPLICATION NUMBER: US/09/785,934
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 09/579,808
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FLAG Peptide
US-09-785-934-3

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 11
US-09-835-147-10
Sequence 10, Application US/09835147
Patent No. US2002002277A1
GENERAL INFORMATION:
APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-835-147-10
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8

RESULT 12
US-09-760-008A-14
; Sequence 14, Application US/09760008A
; Patent No. US20020004483A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/760,008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-760-008A-14
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8

RESULT 13
US-09-728-911-11
; Sequence 11, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
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; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG Tag amino acid sequence
US-09-728-911-11
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8

RESULT 14
US-09-813-329-65
; Sequence 65, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Molc
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: bacteriophage T7
US-09-813-329-65
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8

RESULT 15
US-09-099-823-26
; Sequence 26, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLLITS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: KRAUSE, JOHN C.
; APPLICANT: SCHREFFEL, CHRISTI
; APPLICANT: STROUBE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
```

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,354
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20020018990A1e
US-09-099-823-26

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 16
US-09-790-264-68
Sequence 68, Application US/09790264
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: McCarthy, Sean A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: 07334-332001
CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/298,511
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 09/065,363
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538

PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: flag epitope
US-09-790-264-68

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 17
US-09-809-517A-8
Sequence 8, Application US/09809517A
Patent No. US2002003473A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US2002003473A1 methods for displaying (poly)peptides/prot
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-8

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 18
US-09-234-717-24
Sequence 24, Application US/09234717A
Patent No. US20020034740A1
GENERAL INFORMATION:
APPLICANT: Patricia Billing-Medel
APPLICANT: Maurice Cohen
APPLICANT: Tracey L. Coldilts
APPLICANT: Paula N. Friedman
APPLICANT: Julian Gordon
APPLICANT: Edward N. Granados
APPLICANT: Steven C. Hodges
APPLICANT: Michael R. Klass
APPLICANT: Jon D. Kratochvill
APPLICANT: John C. Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of
TITLE OF INVENTION: the Breast
FILE REFERENCE: 6450.US.01

```

; CURRENT APPLICATION NUMBER: US/09/234,717A
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-234-717-24

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 19
US-09-850-178-18
; Sequence 18, Application US/09850178
; Patent No. US20020034749A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Russel, John C.
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klase, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Stroupe, Stephen D.
; APPLICANT: Gordon, Juliana
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST
; FILE REFERENCE: 6251.US.P1
; CURRENT APPLICATION NUMBER: US/09/850,178
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 08/972,376
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-850-178-18

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 20
US-09-193-538-22
; Sequence 22, Application US/09193538A
; Patent No. US20020037503A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
```

```

; APPLICANT: Paula N. Friedman
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: Steven C. Hodges
; APPLICANT: Michael R. Klase
; APPLICANT: Jon D. Kratochvil
; APPLICANT: Lisa Roberts-Rapp
; APPLICANT: John C. Russel
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6193.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,538A
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: US 08/971,772
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Affinity purification system recognition site
US-09-193-538-22

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 21
US-09-250-883-22
; Sequence 22, Application US/09250883
; Patent No. US20020042049A1
; GENERAL INFORMATION:
; APPLICANT: Russel, John
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASE OF THE BREAST
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/250,883
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,316
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6131.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
```


SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-250-883-22

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
| | | | |
DB 1 DYKDDDK 8

RESULT 22
US-09-735-368-4
Sequence 4, Application US/09735368
Patent No. US20020042094A1
GENERAL INFORMATION:
APPLICANT: Venezia, Domenick R.
APPLICANT: Taft, David W.
APPLICANT: Whitmore, Theodore E.
TITLE OF INVENTION: RING FINGER PROTEIN ZAPO2
FILE REFERENCE: 98-11
CURRENT APPLICATION NUMBER: US/09/735,368
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 60/171,258
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 8
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Flag peptide sequence
US-09-735-368-4

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
| | | | |
DB 1 DYKDDDK 8

RESULT 23
US-09-096-259-32
Sequence 32, Application US/09096259
Patent No. US20020045164A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park

STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/049,183
FILING DATE: 11-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6113, US, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-096-259-32

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
| | | | |
DB 1 DYKDDDK 8

RESULT 24
US-09-215-652-47
Sequence 47, Application US/09215652
Patent No. US20020045165A1
GENERAL INFORMATION:
APPLICANT: Patricia Billing-Medel
APPLICANT: Maurice Cohen
APPLICANT: Tracey L. Colpits
APPLICANT: Paula N. Friedman
APPLICANT: Julian Gordon
APPLICANT: Edward N. Granados
APPLICANT: Steven C. Hodges
APPLICANT: Michael R. Kلاس
APPLICANT: Jon D. Kratochvil
APPLICANT: Lisa Roberts-Rapp
APPLICANT: John C. Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
FILE REFERENCE: 6192, US, P1
CURRENT APPLICATION NUMBER: US/09/215,652
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: US 08/998,496
EARLIER FILING DATE: 1997-12-26
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 8
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Affinity purification system recognition site
US-09-215-652-47

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 25

US-09-970-308-1
; Sequence 1, Application US/09970308
; Patent No. US20020045193A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L.
; APPLICANT: HERNAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE
; FILE REFERENCE: SGM 6933.2
; CURRENT APPLICATION NUMBER: US/09/970,308
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/415,000
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthesized
US-09-970-308-1

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 26

US-09-309-668A-1
; Sequence 1, Application US/09309668A
; Patent No. US20020045271A1
; GENERAL INFORMATION:
; APPLICANT: Hussain, M. Mahmood
; APPLICANT: Bakillah, Ahmed
; TITLE OF INVENTION: Compounds and Methods for Identifying Compounds that
; TITLE OF INVENTION: Interact with Microsomal Triglyceride Transfer Protein
; TITLE OF INVENTION: Binding Sites on Apolipoprotein B and Modulate Lipid
; FILE REFERENCE: MCP-0006
; CURRENT APPLICATION NUMBER: US/09/309,668A
; CURRENT FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/088,767
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-309-668A-1

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 27

US-09-855-722-25
; Sequence 25, Application US/09855722
; Patent No. US20020049306A1
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic amino acid
US-09-855-722-25

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 28

US-09-817-413-1
; Sequence 1, Application US/09817413
; Publication No. US20020052478A1
; GENERAL INFORMATION:
; APPLICANT: SRINIVASAN, ALGARSAMY
; APPLICANT: KOPROWSKI, HILARY
; TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
; FILE REFERENCE: Chimeric Viral Proteins
; CURRENT APPLICATION NUMBER: US/09/817,413
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/043,380
; PRIOR FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-817-413-1

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
|||||
Db 1 DYKDDDDK 8

RESULT 29

US-09-193-663-9
; Sequence 9, Application US/09193663

Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255 US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-193-663-9

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 30
US-09-887-855-7
; Sequence 7, Application US/09887855
; Patent No. US20020058310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2883-US
; CURRENT APPLICATION NUMBER: US/09/887,855
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antigenic peptide used in fusion proteins
US-09-887-855-7

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 31
US-09-904-245-3
; Sequence 3, Application US/09904245
; Patent No. US20020076409A1
; GENERAL INFORMATION:
; APPLICANT: March, Carl
; APPLICANT: Flueneke, John
; APPLICANT: O'Neal, Larry
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; FILE REFERENCE: 2943-A
; CURRENT APPLICATION NUMBER: US/09/904,245
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/217,888
; PRIOR FILING DATE: 2000-07-12

NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG peptide
US-09-904-245-3

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 32
US-09-245-603A-15
; Sequence 15, Application US/09245603A
; Patent No. US20020081280A1
; GENERAL INFORMATION:
; APPLICANT: Curjel, David T.
; APPLICANT: Krasnykh, Victor N.
; APPLICANT: Dmitriev, Igor
; TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide
; TITLE OF INVENTION: Epitope in the HI Loop of the Fiber Knob
; FILE REFERENCE: D6080
; CURRENT APPLICATION NUMBER: US/09/245,603A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/099,801
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of the FLAG octapeptide.
US-09-245-603A-15

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 33
US-09-837-992-45
; Sequence 45, Application US/09837992
; Patent No. US20020081687A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Schultz, Joshua
; APPLICANT: Shan, Bei
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Sirosterolemia Susceptibility Gene (SSG): Compositions
; FILE REFERENCE: 018781-006020US
; CURRENT APPLICATION NUMBER: US/09/837,992
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,465
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/204,234
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-DYKDDDDK
; US-09-837-992-45

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 34
US-09-923-995-6
; Sequence 6, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG peptide tag
; US-09-923-995-6

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 35
US-09-871-856-7
; Sequence 7, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
```

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: No.
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG-peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
; US-09-871-856-7

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8

RESULT 36
US-09-841-894-40
; Sequence 40, Application US/09841894
; Publication No. US20020086301A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; COHEN, MAURICE
; COLETTIS, TRACEY L.
; FRIEDMAN, PAULA N.
; GORDON, JULIAN
; GRANADOS, EDWARD N.
; HODGES, STEVEN C.
; KLAS, MICHAEL R.
; KRATOCHVIL, JON D.
; ROBERTS-RAP, LISA
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841,894
; FILING DATE: 25-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,710
; FILING DATE: <Unknown>
```

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-841-894-40

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 37
US-09-991-681-32
Sequence 32, Application US/09991681
Publication No. US20020086316A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAIP, LISA
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,681
FILING DATE: 26-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/065,383
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6084.US.PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-991-681-32

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 38
US-09-065-902-15
Sequence 15, Application US/09065902
Publication No. US20020086444A1
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
Kim, Tae-Wan
TITLE OF INVENTION: A Purified 20 KDa Presenilin 2
C-terminal Fragment and Methods of Screening for Compounds
that Inhibit Proteolysis of Presenilin 2
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,902
FILING DATE: 24-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,262
FILING DATE: 24-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.4270001/JAG/S-S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-065-902-15

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

RESULT 39
US-09-865-363-7
; Sequence 7, Application US/09865363
; Publication No. US20020086826A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,363
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: Not Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-865-363-7
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDK 8
Db 1 DYKDDDK 8
RESULT 40
US-09-871-291-7
; Sequence 7, Application US/09871291
; Publication No. US20020086827A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation, Law Department

; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,291
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-871-291-7
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDK 8
Db 1 DYKDDDK 8
RESULT 41
US-09-193-881-28
; Sequence 28, Application US/09193881A
; Publication No. US20020086979A1
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klase
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastrSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Affinity purification system recognition site
US-09-193-881-28

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 42
US-09-875-338-94
Sequence 94, Application US/09875338
Patent No. US20020095024A1
GENERAL INFORMATION:
APPLICANT: MIKESELL, GLEN E.
APPLICANT: CHANG, HAN
APPLICANT: FINGER, JOSHUA N.
APPLICANT: YANG, GUOCHEN
APPLICANT: LU, PIN
APPLICANT: ZHOU, XIA-DI
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
FILE REFERENCE: 3053-4071US2
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 94
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Epitope tag
US-09-875-338-94

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 43
US-09-903-248-7
Sequence 7, Application US/09903248
Patent No. US20020102263A1
GENERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REFERENCE: 21486-032 DIV5
CURRENT APPLICATION NUMBER: US/09/903,248
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-248-7

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 44
US-09-798-584-17
Sequence 17, Application US/09798584
Patent No. US20020102676A1
GENERAL INFORMATION:
APPLICANT: Mu, David
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A No. US20020102676A1e1 Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 17
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-DYKDDDDK
US-09-798-584-17

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 45
US-09-978-339-3
Sequence 3, Application US/0978339
Patent No. US20020103358A1
GENERAL INFORMATION:
APPLICANT: Cerritelli, Douglas P.
TITLE OF INVENTION: No. US20020103358A1e1 Cytokine Designated Lerk-5
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,339
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,948
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: FLAG peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-978-339-3

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 46
US-09-859-604-7
; Sequence 7, Application US/09859604
; Patent No. US20020110559A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M
; APPLICANT: Deutch, Alan H
; APPLICANT: Chaudhari, Hossein A
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 CIP
; CURRENT APPLICATION NUMBER: US/09/859,604
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-859-604-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 47
US-09-903-063-7
; Sequence 7, Application US/09903063
; Patent No. US20020114810A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV3
; CURRENT APPLICATION NUMBER: US/09/903,063
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-063-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 48
US-09-903-216-7
; Sequence 7, Application US/09903216
; Patent No. US20020114811A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV2
; CURRENT APPLICATION NUMBER: US/09/903,216
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-216-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 49
US-09-844-508-14
; Sequence 14, Application US/09844508
; Patent No. US20020115215A1
; GENERAL INFORMATION:
; APPLICANT: WOLFFE, Alan P.
; APPLICANT: COLLINGWOOD, Trevor
; TITLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE
; FILE REFERENCE: 8325-0014 / 514-US1
; CURRENT APPLICATION NUMBER: US/09/844,508
```



```
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,590
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/228,523
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: double-stranded oligonucleotide encoding a FLAG
US-09-844-508-14
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 50
US-09-888-358-17
; Sequence 17, Application US/09888358
; Patent No. US20020119137A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, DAVID
; APPLICANT: ADAMS, SEAN H.
; APPLICANT: YU, KING XIAN
; TITLE OF INVENTION: CGI-69 COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 10716/66
; CURRENT APPLICATION NUMBER: US/09/888,358
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,307
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG tag
US-09-888-358-17
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 51
US-09-903-199-7
; Sequence 7, Application US/09903199
; Patent No. US20020122802A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV4
; CURRENT APPLICATION NUMBER: US/09/903,199
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/436,184
```

```
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-903-199-7
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 52
US-09-745-605-43
; Sequence 43, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
; APPLICANT: Starling, Gary C.
; APPLICANT: Finger, Joshua N.
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
; FILE REFERENCE: DB13NP
; CURRENT APPLICATION NUMBER: US/09/745,605
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/172,025
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 43
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG tag
US-09-745-605-43
```

```
Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```
RESULT 53
US-09-780-933-20
; Sequence 20, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHMAYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
```

;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: 60/225,558
;; PRIOR FILING DATE: 2000-08-16
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 20
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-780-933-20

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 54
US-09-873-106B-14
;; Sequence 14, Application US/09873106B
;; Patent No. US20020127657A1
;; GENERAL INFORMATION:
;; APPLICANT: Reinherz, Ellis L.
;; APPLICANT: Freund, Christian
;; APPLICANT: Li, Jing
;; APPLICANT: Nishizawa, Kazuhisa
;; APPLICANT: Wagner, Gerhard
;; TITLE OF INVENTION: Cloning and Characterization of a CD2
;; FILE REFERENCE: 1062.1021-004
;; CURRENT APPLICATION NUMBER: US/09/873,106B
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: US 60/111,007
;; PRIOR FILING DATE: 1998-12-04
;; PRIOR APPLICATION NUMBER: US 60/115,647
;; PRIOR FILING DATE: 1999-01-13
;; PRIOR FILING DATE: 1999-01-13
;; PRIOR APPLICATION NUMBER: PCT/US99/26993
;; PRIOR FILING DATE: 1999-11-15
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Flag Epitope
US-09-873-106B-14

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 55
US-09-995-593A-13
;; Sequence 13, Application US/09995593A
;; Patent No. US20020128197A1
;; GENERAL INFORMATION:
;; APPLICANT: SAKANO, SEIJI
;; APPLICANT: ITOH, AKIRA
;; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
;; FILE REFERENCE: KP8447DIV
;; CURRENT APPLICATION NUMBER: US/09/995,593A

;; CURRENT FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: 09/068,740
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: JP 7-299611
;; PRIOR FILING DATE: 1995-11-17
;; PRIOR APPLICATION NUMBER: JP 7-311811
;; PRIOR FILING DATE: 1995-11-30
;; PRIOR APPLICATION NUMBER: PCT/JP96/03356
;; PRIOR FILING DATE: 1996-11-15
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 13
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-995-593A-13

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 56
US-09-900-530A-13
;; Sequence 13, Application US/09900530A
;; Patent No. US20020128438A1
;; GENERAL INFORMATION:
;; APPLICANT: Seol, Dae-Wu
;; APPLICANT: Billiar, Timothy R.
;; TITLE OF INVENTION: DNA Cassette for the Production of
;; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
;; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their
;; TITLE OF INVENTION: Combination and Use in Gene Therapy
;; FILE REFERENCE: 5006-1-002
;; CURRENT APPLICATION NUMBER: US/09/900,530A
;; CURRENT FILING DATE: 2002-03-19
;; PRIOR APPLICATION NUMBER: KR 2000-38441
;; PRIOR FILING DATE: 2000-07-06
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: FLAG-tag
US-09-900-530A-13

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 57
US-09-923-246-37
;; Sequence 37, Application US/09923246
;; Patent No. US20020128446A1
;; GENERAL INFORMATION:
;; APPLICANT: No. US20020128446A1ak, Julia E.
;; APPLICANT: Presnell, Scott R.
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 37
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C-terminal FLAG amino acid sequence
US-09-923-246-37

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 58
US-09-973-145-6
Sequence 6, Application US/09973145
Patent No. US20020132248A1
GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth J.
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
FILE REFERENCE: AMBER-06819
CURRENT APPLICATION NUMBER: US/09/973,145
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
US-09-973-145-6

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 59
US-09-825-561A-23

Sequence 23, Application US/09825561A
Patent No. US20020137677A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. US20020137677A1ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: FLAG tag amino acid sequence
US-09-825-561A-23

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 60
US-09-049-695A-21
Sequence 21, Application US/09049695A
Patent No. US20020137904A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA A.
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: HAYDEN, MARK
APPLICANT: KLAS, MICHAEL R.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,695A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,845
FILING DATE: 31-MAR-1997

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6066.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-049-695A-21

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 61
US-09-092-297-21
; Sequence 21, Application US/09092297
; Patent No. US20020142371A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITS, TRACEY L.
; APPLICANT: GORDON, JULIAN
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRAMADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLOSS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAFF, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: YU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE URINARY TRACT
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,297
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/869,579
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6107.US.PI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
```

```
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-092-297-21

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 62
US-09-903-023-7
; Sequence 7, Application US/09903023
; Patent No. US20020146421A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: 21486-032 DIV1
; CURRENT APPLICATION NUMBER: US/09/903,023
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/436,184
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
;
US-09-903-023-7

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 63
US-09-852-391-3
; Sequence 3, Application US/09852391
; Patent No. US20020146819A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John
; APPLICANT: Lyman, Stewart
; APPLICANT: Armstrong, Allison
; APPLICANT: McKenna, Hilary
; TITLE OF INVENTION: Human TSLP DNA and Polypeptides
; FILE REFERENCE: 03260.0087-00304/2881-WO
; CURRENT APPLICATION NUMBER: US/09/852,391
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/108,452
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence: antigenic
OTHER INFORMATION: peptide used in fusion proteins
US-09-952-391-3

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 64
US-09-931-087A-19
Sequence 19, Application US/09931087A
Patent No. US20020147322A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: NSP Molecules
FILE REFERENCE: P123R1E
CURRENT APPLICATION NUMBER: US/09/931,087A
CURRENT FILING DATE: 2001-08-15, 206
PRIOR APPLICATION NUMBER: 09/367,206
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/082,767
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 60/113,296
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 19
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-931-087A-19

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 65
US-09-263-959-985
Sequence 985, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaesters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 985:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-263-959-985

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 66
US-09-969-192-2
Sequence 2, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSER: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION NUMBER:
APPLICATION DATA:
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-455061
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-969-192-2

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8

```
Db          1 DYKDDDDK 8
|||||
RESULT 67
US-09-840-243B-20
; Sequence 20, Application US/09840243B
; Patent No. US20020156258A1
; GENERAL INFORMATION:
; APPLICANT: MASTERNAK, Krzysztof
; APPLICANT: REITH, Walter
; APPLICANT: MACH, Bernard
; TITLE OF INVENTION: New Transcription Factor of MHC Class II Genes, Substances
; TITLE OF INVENTION: Capable of Inhibiting This New Transcription Factor and
; FILE REFERENCE: 010830-117
; CURRENT APPLICATION NUMBER: US/09/840,243B
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 98120085.0
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-840-243B-20

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 DYKDDDDK 8
|||||
Db          1 DYKDDDDK 8

RESULT 68
US-09-766-700A-8
; Sequence 8, Application US/09766700A
; Patent No. US2002015989A1
; GENERAL INFORMATION:
; APPLICANT: Bein, Kietai
; APPLICANT: Simons, Michael
; TITLE OF INVENTION: Peptide Inhibitor of MMP Activity and Angiogenesis
; FILE REFERENCE: BIT-003
; CURRENT APPLICATION NUMBER: US/09/766,700A
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flag tag
US-09-766-700A-8

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 DYKDDDDK 8
|||||
Db          1 DYKDDDDK 8

RESULT 69
US-09-843-245-12
; Sequence 12, Application US/09843245
; Patent No. US20020164672A1
```

```
; GENERAL INFORMATION:
; APPLICANT: McPherson, Peter S.
; APPLICANT: Ramjoun, Antoine Rachid
; TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE
; TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN
; TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KINASE
; FILE REFERENCE: 9555.116US01
; CURRENT APPLICATION NUMBER: US/09/843,245
; CURRENT FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG Epitope
US-09-843-245-12

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 DYKDDDDK 8
|||||
Db          1 DYKDDDDK 8

RESULT 70
US-09-989-350-19
; Sequence 19, Application US/09989350
; Patent No. US20020164716A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Lih-Ling
; APPLICANT: Chen, Jennifer H.
; APPLICANT: Schiavella, Andrea
; APPLICANT: Graham, James
; TITLE OF INVENTION: No. US20020164716A1 TNF receptor death domain ligand proteins a
; TITLE OF INVENTION: Inhibitors of ligand binding(as amended)
; FILE REFERENCE: GFN-5232CP4DV3
; CURRENT APPLICATION NUMBER: US/09/989,350
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/185,258
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: 08/839,032
; PRIOR FILING DATE: 1997-04-23
; PRIOR APPLICATION NUMBER: 08/698,551
; PRIOR FILING DATE: 1996-08-15
; PRIOR APPLICATION NUMBER: 08/602,228
; PRIOR FILING DATE: 1996-02-15
; PRIOR APPLICATION NUMBER: 08/533,901
; PRIOR FILING DATE: 1995-09-26
; PRIOR APPLICATION NUMBER: 08/494,440
; PRIOR FILING DATE: 1995-06-19
; PRIOR APPLICATION NUMBER: 08/327,514
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Flag-tag
US-09-989-350-19

Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 DYKDDDDK 8
|||||
Db          1 DYKDDDDK 8
```

RESULT 71
US-09-858-332-12
; Sequence 12, Application US/09858332
; Patent No. US20020164718A1
; GENERAL INFORMATION:
; APPLICANT: Tchaga, Grigory S.
; APPLICANT: Jokhadze, George
; TITLE OF INVENTION: Metal Ion Affinity Tags and Methods for
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: CLON056CIP
; CURRENT APPLICATION NUMBER: US/09/858,332
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 09/404,017
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,867
; PRIOR FILING DATE: 1998-09-25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-858-332-12

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 72
US-09-877-650-7
; Sequence 7, Application US/09877650
; Patent No. US20020169117A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: FLAG peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-877-650-7

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 73
US-09-981-636-1
; Sequence 1, Application US/09981636
; Publication No. US20020182643A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES
; APPLICANT: NIELSEN, ULRIK
; APPLICANT: KIRPOTIN, DMITRI
; TITLE OF INVENTION: METHODS OF HIGH-THROUGHPUT SCREENING FOR INTERNALIZING ANTIBODIES
; FILE REFERENCE: 407T-897710US
; CURRENT APPLICATION NUMBER: US/09/981,636
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/241,279
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: epitope tag
US-09-981-636-1

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

RESULT 74
US-09-092-296-19
; Sequence 19, Application US/09092296
; Publication No. US20020186114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUBE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Abbott Laboratories
;; STREET: 100 Abbott Park Road
;; CITY: Abbott Park
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/092,296
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/048,810
;; FILING DATE: 05-JUN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 6104.US.01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-092-296-19
;;
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8
;;
RESULT 75
US-09-104-408-36
;; Sequence 36, Application US/09104408
;; Publication No. US20020188115A1
;; GENERAL INFORMATION:
;; APPLICANT: Billings-Medel, Patricia A. et al.
;; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
;; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Abbott Laboratories
;; STREET: 100 Abbott Park Road
;; CITY: Abbott Park
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60064-3500
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/104,408
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 6122.US.01
;; FILING DATE: 25-JUN-1997
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-104-408-36
;;
Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 1 DYKDDDDK 8
;;
RESULT 76
US-09-861-097-15
;; Sequence 15, Application US/09861097
;; Publication No. US20020192218A1
;; GENERAL INFORMATION:
;; APPLICANT: KARIN, MICHAEL
;; DAVIS, ROGER
;; MASAHIKO, HIBI
;; ANNING, LIN
;; DERRARD, BENOIT
;; TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FISH & RICHARDSON P.C.
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/861,097
;; FILING DATE: 18-May-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/220,602
;; FILING DATE: 25-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hallie, Ph.D., Lisa A.,
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 678-5070
;; TELEFAX: (619) 678-5099
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..8
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-861-097-15

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 77

US-09-814-604-5
; Sequence 5, Application US/09814604
; Publication No. US20030003517A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Elliott S.
; APPLICANT: Chandraratna Roshantha A.
; TITLE OF INVENTION: Methods of Detecting Disassociated Nuclear
; TITLE OF INVENTION: Hormone Receptor Ligands
; FILE REFERENCE: P-AR 4528
; CURRENT APPLICATION NUMBER: US/09/814,604
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-814-604-5

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 78

US-09-908-943A-186
; Sequence 186, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heiniksen, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 186
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide sequence
US-09-908-943A-186

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 79

US-09-997-623-47
; Sequence 47, Application US/09997623
; Publication No. US20030018175A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219us410 - protein C
; CURRENT APPLICATION NUMBER: US/09/997,623
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 09/978,917
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-997-623-47

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 80

US-09-995-898A-12
; Sequence 12, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG peptide tag
US-09-995-898A-12

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYKDDDK 8
Db 1 DYKDDDK 8

```
RESULT 81
US-09-978-917A-47
; Sequence 47, Application US/09978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - protein C
; CURRENT APPLICATION NUMBER: US/09/978,917A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-978-917A-47

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 82
US-09-436-184-7
; Sequence 7, Application US/09436184
; Publication No. US20030031670A1
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne M.
; APPLICANT: Ince, Nedim
; APPLICANT: Carlson, Rolf I.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
; FILE REFERENCE: R.1. Hosp. - Malignant Neoplasms
; CURRENT APPLICATION NUMBER: US/09/436,184
; CURRENT FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-09-436-184-7

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 83
US-09-950-634-23
; Sequence 23, Application US/09950634
; Publication No. US20030032775A1
; GENERAL INFORMATION:
; APPLICANT: Molnar-Kimber, Katherine L.
; APPLICANT: Fallis, Amedeo F.
; APPLICANT: Casagiano, Thomas J.
; APPLICANT: Nakanishi, Koji
; APPLICANT: Chen, Yangju
; TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN
```

```
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,634
FILING DATE: 13-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/471,112
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
APPLICATION NUMBER: US 08/312,023
FILING DATE: 26-SEP-1995
APPLICATION NUMBER: US 08/207,975
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Siekman, Michael T.
REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142, 0058-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-950-634-23

Query Match      100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 DYKDDDDK 8
DB      1 DYKDDDDK 8

RESULT 84
US-09-846-033B-225
; Sequence 225, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolfe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis with zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
```

PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 225
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: FLAG peptide
US-09-846-033B-225

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 85
US-09-861-098-15
Sequence 15, Application US/09861098
Publication No. US2003004788A1
GENERAL INFORMATION:
APPLICANT: KARIN, MICHAEL
DAVIS, ROGER
MASAHITO, HIRI
ANNING, LIN
DERJARD, BENOIT
TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,098
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,602
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.,
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/015001 (PD3205)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-861-098-15

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 86
US-09-989-981A-12
Sequence 12, Application US/09989981A
Publication No. US20030049730A1
GENERAL INFORMATION:
APPLICANT: Hobbs, Helen H.
APPLICANT: Shan, Bei
APPLICANT: Barnes, Robert
APPLICANT: Tian, Hui
APPLICANT: Talarik Inc.
TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
FILE REFERENCE: 018781-007320US
CURRENT APPLICATION NUMBER: US/09/989,981A
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/253,645
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: anti-DYKDDDK
US-09-989-981A-12

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 1 DYKDDDK 8

RESULT 87
US-09-993-180-33
Sequence 33, Application US/09993180
Publication No. US2003005445A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM LYMPH
FILE REFERENCE: D0051.NP
CURRENT APPLICATION NUMBER: US/09/993,180
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 60/248,434
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/257,610
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/282,745
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patent In version 3.0
SEQ ID NO 33
LENGTH: 8
TYPE: PRT
ORGANISM: Bacteriophage T7
US-09-993-180-33

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
DB 1 DYKDDDDK 8

RESULT 88

US-09-759-595-7
; Sequence 7, Application US/09759595
; Publication No. US20030059916A1
; GENERAL INFORMATION:
; APPLICANT: Wesche, Holger
; APPLICANT: Li, Shyun
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
; FILE REFERENCE: 018781-003910US
; CURRENT APPLICATION NUMBER: US/09/759,595
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 60/176,395
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope tag
US-09-759-595-7

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
DB 1 DYKDDDDK 8

RESULT 89

US-09-999-220B-9
; Sequence 9, Application US/09999220B
; Publication No. US20030059923A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL ALPHA-SUB
; FILE REFERENCE: D0050NP
; CURRENT APPLICATION NUMBER: US/09/999,220B
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/245,383
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/257,780
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/269,854
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: bacteriophage T7
US-09-999-220B-9

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
DB 1 DYKDDDDK 8

RESULT 90

US-09-880-748-3238
; Sequence 3238, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3238
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: site
; LOCATION: (1)..(8)
; OTHER INFORMATION: Flag Tag
US-09-880-748-3238

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||
DB 1 DYKDDDDK 8

RESULT 91

US-09-904-196B-14
; Sequence 14, Application US/09904196B
; Publication No. US20030064922A1
; GENERAL INFORMATION:
; APPLICANT: NISSEN, TORBEN LADESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/904,196B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/760,008
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176,376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189,506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215,644
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

```

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-904-1968-14
```

```
Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```

RESULT 92
US-09-972-473-19
; Sequence 19, Application US/09972473
; Publication No. US20030068312A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
; FILE REFERENCE: MNI-108CP2
; CURRENT APPLICATION NUMBER: US/09/972,473
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/263,022
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 08/843,704
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: 08/842,898
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: 60/071,589
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 09/009,802
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-972-473-19
```

```
Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```

RESULT 93
US-09-922-226-39
; Sequence 39, Application US/09922226
; Publication No. US20030077664A1
; GENERAL INFORMATION:
; APPLICANT: Zhao, Yi
; APPLICANT: Thacher, Scott M.
; APPLICANT: Xiao, Jia-Hao
; APPLICANT: Kusari, Jyotiimoy
; APPLICANT: Chandraratna, Koshantha A.
; TITLE OF INVENTION: Methods of Screening For Compounds That
; FILE REFERENCE: P-AR 4681
; CURRENT APPLICATION NUMBER: US/09/922,226
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/284,797
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 191
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-922-226-39
```

```
Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

```

RESULT 94
US-09-774-381-21
; Sequence 21, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL EDIIRF, MTR-1, LSP-1, TAB-1, AND PA-I MOLECULES
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: flag epitope
US-09-774-381-21
```

```
Query Match          100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
Db      1 DYKDDDDK 8
```

RESULT 95
US-09-876-790-11
; Sequence 11, Application US/09876790
; Publication No. US20030091532A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/09/876,790
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide used in fusion proteins
US-09-876-790-11

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||
Db 1 DYKDDDDK 8

RESULT 96
US-09-932-613-183
; Sequence 183, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Belzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYK-025.1 PCT; DYK-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 183
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: epitope tag
US-09-932-613-183

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||
Db 1 DYKDDDDK 8

RESULT 97
US-09-782-587B-18
; Sequence 18, Application US/09782587B

; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-09-782-587B-18

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||
Db 1 DYKDDDDK 8

RESULT 98
US-09-892-949-35
; Sequence 35, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Fresnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kulper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FLAG tag peptide sequence
US-09-892-949-35

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
|||||||
Db 1 DYKDDDDK 8

RESULT 99

US-09-994-487-2
; Sequence 2, Application US/09994487
; Publication No. US20030099954A1
; GENERAL INFORMATION:
; APPLICANT: Miltenyi, Stefan
; APPLICANT: Kohler, Mathias
; TITLE OF INVENTION: Apparatus and method for modification of
; TITLE OF INVENTION: magnetically immobilized biomolecules
; FILE REFERENCE: MILT004
; CURRENT APPLICATION NUMBER: US/09/994,487
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-994-487-2

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 100

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; Sequence 5, Application US/09803472
; Publication No. US20030118990A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Alan R.
; APPLICANT: Deng, Gary G.
; APPLICANT: Rubanyi, Gabor M.
; APPLICANT: Schering Aktiengesellschaft
; TITLE OF INVENTION: No. US20030118990A1 Estrogen-Regulated G Protein Gamma Subunit;
; FILE REFERENCE: 015303-000510US
; CURRENT APPLICATION NUMBER: US/09/803,472
; CURRENT FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: US 60/188,460
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 8
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: General
US-09-803-472-5

Query Match 100.0%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DYKDDDDK 8

Search completed: June 29, 2006, 11:55:57
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 11:52:56 ; Search time 19 Seconds
(without alignments)
9.945 Million cell updates/sec

Title: US-10-671-054-2

Perfect score: 47
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Scoring table: BIOSUM62
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Searched: 103426 seqs, 23619683 residues

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	47	100.0	8	7	US-11-252-276-36
6	47	100.0	8	7	US-11-261-630-5
7	47	100.0	8	7	US-11-134-228A-5
8	47	100.0	8	7	US-11-313-356-28
9	47	100.0	8	7	US-11-328-747-16
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12	47	100.0	8	7	US-11-270-796-29
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18	47	100.0	23	7	US-11-251-734-19
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ALIGNMENTS

US-09-728-720A-13
; Sequence 13, Application US/09728720A
; Publication No. US20060104980A1
; GENERAL INFORMATION:
; APPLICANT: Fourn, Steven K.H.
; APPLICANT: Hadlock, Kenneth G.
; TITLE OF INVENTION: Prevention and Treatment of HCV Infection Employing
; TITLE OF INVENTION: Antibodies that Inhibit the Interaction of HCV Virions
; TITLE OF INVENTION: with Their Receptor.
; FILE REFERENCE: 2002850-0009
; CURRENT APPLICATION NUMBER: US/09/728,720A
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Flag Epitope
US-09-728-720A-13

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Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 1 DYKDDDK 8

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; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
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; OTHER INFORMATION: Synthesized in laboratory
US-10-660-893A-3

Query Match
Best Local Similarity 100.0%; Score 47; DB 6; Length 8;
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RESULT 4
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; Publication No. US20060088878A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L
; APPLICANT: HERNAN, RON
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE EPITOPES
; FILE REFERENCE: SGM6933.7
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US-11-252-276-36
; Sequence 36, Application US/11252276
; Publication No. US20060094868A1
; GENERAL INFORMATION:
; APPLICANT: Giuliani, Kenneth A.
; APPLICANT: Bright, Gary
; APPLICANT: Olson, Keith
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-K2-CO
; CURRENT APPLICATION NUMBER: US/11/252,276
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: 09/713,572
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/430,656
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/398,965

```

```
/ PRIOR FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: 09/031,271
/ PRIOR FILING DATE: 1998-02-27
/ PRIOR APPLICATION NUMBER: 08/810,983
/ PRIOR FILING DATE: 1997-02-27
/ PRIOR APPLICATION NUMBER: 60/136,078
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 60/106,308
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 168
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 36
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG epitope
US-11-252-276-36
```

```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 6
US-11-261-630-5
/ Sequence 5, Application US/11261630
/ Publication No. US20060094062A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Herten
/ TITLE OF INVENTION: ULTRA HIGH THROUGHPUT CAPTURE LIFT SCREENING METHODS
/ FILE REFERENCE: AE703US
/ CURRENT APPLICATION NUMBER: US/11/261,630
/ CURRENT FILING DATE: 2005-10-31
/ PRIOR APPLICATION NUMBER: 60/623,240
/ PRIOR FILING DATE: 2004-11-01
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patent In version 3.3
/ SEQ ID NO 5
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: epitope tag
US-11-261-630-5
```

```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 7
US-11-134-228A-5
/ Sequence 5, Application US/11134228A
/ Publication No. US20060105320A1
/ GENERAL INFORMATION:
/ APPLICANT: Lindquist et al.
/ TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
/ FILE REFERENCE: 30554/40155A
/ CURRENT APPLICATION NUMBER: US/11/134,228A
/ CURRENT FILING DATE: 2005-05-20
/ PRIOR APPLICATION NUMBER: 60/573,277
/ PRIOR FILING DATE: 2004-05-20
/ NUMBER OF SEQ ID NOS: 73
```

```
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
US-11-134-228A-5
```

```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 8
US-11-313-356-28
/ Sequence 28, Application US/11313356
/ Publication No. US20060105379A1
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Shujian
/ APPLICANT: Chen, Jian
/ APPLICANT: Feder, John
/ APPLICANT: Lee, Liana
/ APPLICANT: Krystek, Stanley
/ TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED
/ FILE REFERENCE: D0141DIY
/ CURRENT APPLICATION NUMBER: US/11/313,356
/ CURRENT FILING DATE: 2005-12-21
/ PRIOR APPLICATION NUMBER: US 60/286,764
/ PRIOR FILING DATE: 2001-04-26
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: Patent In version 3.2
/ SEQ ID NO 28
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: bacteriophage T7
US-11-313-356-28
```

```
Query Match          100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```
RESULT 9
US-11-328-747-16
/ Sequence 16, Application US/11328747
/ Publication No. US20060105409A1
/ GENERAL INFORMATION:
/ APPLICANT: Isekeni, Sarkiz D.
/ APPLICANT: Huang, Jianing
/ APPLICANT: Sheung, Julie
/ APPLICANT: Pray, Todd R.
/ TITLE OF INVENTION: Ubiquitin Ligase Assay
/ FILE REFERENCE: 021044-007010US
/ CURRENT APPLICATION NUMBER: US/11/328,747
/ CURRENT FILING DATE: 2006-01-09
/ PRIOR APPLICATION NUMBER: US/10/835,096
/ PRIOR FILING DATE: 2004-04-28
/ PRIOR APPLICATION NUMBER: US/09/826,312
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 09/542,497
/ PRIOR FILING DATE: 2000-04-03
/ NUMBER OF SEQ ID NOS: 21
```

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
US-11-328-747-16

Query Match 100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 10
US-11-264-463-2
Sequence 2, Application US/11264463
Publication No. US20060110782A1
GENERAL INFORMATION:
APPLICANT: BERTOZZI, CAROLYN R.
APPLICANT: AGARD, NICHOLAS J.
APPLICANT: PRESCHER, JENNIFER A.
APPLICANT: BASKIN, JEREMY MICHAEL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: BERK-039
CURRENT APPLICATION NUMBER: US/11/264,463
CURRENT FILING DATE: 2005-10-31
PRIOR APPLICATION NUMBER: 60/624,202
PRIOR FILING DATE: 2004-11-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic epitope
US-11-264-463-2

Query Match 100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 11
US-11-128-422-16
Sequence 16, Application US/11128422
Publication No. US20060127985A1
GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/128,422
FILING DATE: 13-May-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918
FILING DATE: 06-May-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: FLAG peptide
US-11-128-422-16

Query Match 100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

RESULT 12
US-11-270-796-29
Sequence 29, Application US/11270796
Publication No. US20060134068A1
GENERAL INFORMATION:
APPLICANT: Dong, Jiani
TITLE OF INVENTION: TREATMENT OF CANCER BY SIMULTANEOUS INHIBITION OF BRAF AND
FILE REFERENCE: 02420/1201581-US1
CURRENT APPLICATION NUMBER: US/11/270,796
CURRENT FILING DATE: 2005-11-08
PRIOR APPLICATION NUMBER: 60/592,592
PRIOR FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.3
SEQ ID NO 29
LENGTH: 8
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: synthetic peptide tag
US-11-270-796-29

Query Match 100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
DB 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

```
RESULT 13
US-11-328-747-17
; Sequence 17, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; PRIOR FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-Cys
US-11-328-747-17
```

```
Query Match 100.0%; Score 47; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 DYKDDDDK 8
Db 1 DYKDDDDK 8

```
RESULT 14
US-11-264-463-3
; Sequence 3, Application US/11264463
; Publication No. US20060110782A1
; GENERAL INFORMATION:
; APPLICANT: BERTOZZI, CAROLYN R.
; APPLICANT: AGARD, NICHOLAS J.
; APPLICANT: PRESCHER, JENNIFER A.
; APPLICANT: BASKIN, JEREMY MICHAEL
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODIFICATION OF BIOMOLECULES
; FILE REFERENCE: BERK-039
; CURRENT APPLICATION NUMBER: US/11/264,463
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: 60/624,202
; PRIOR FILING DATE: 2004-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic epitope
US-11-264-463-3
```

```
Query Match 100.0%; Score 47; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 DYKDDDDK 8

Db 1 DYKDDDDK 8

```
RESULT 15
US-11-251-734-20
; Sequence 20, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVANTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 US NP1
; CURRENT APPLICATION NUMBER: US/11/251,734
; PRIOR FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US 09/933,780
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-251-734-20
```

```
Query Match 100.0%; Score 47; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 DYKDDDDK 8
Db 3 DYKDDDDK 10

```
RESULT 16
US-10-821-930-26
; Sequence 26, Application US/10821930
; Publication No. US20060133994A1
; GENERAL INFORMATION:
; APPLICANT: NERI, Dario
; APPLICANT: TARLI, Lorenzo
; APPLICANT: VITTI, Francesca
; APPLICANT: BIRCHLER, Manfred
; TITLE OF INVENTION: SPECIFIC BINDING MOLECULES FOR SCINTIGRAPHY, CONJUGATES
; TITLE OF INVENTION: CONTAINING THEM AND THERAPEUTIC METHOD FOR TREATMENT OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: SCH-1733P2
; CURRENT APPLICATION NUMBER: US/10/821,930
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/512,082
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 09/300,425
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/075,338
; PRIOR FILING DATE: 1998-05-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide construct
US-10-821-930-26
```


Query Match 100.0%; Score 47; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYKDDDDK 8
Db 7 DYKDDDDK 14

RESULT 17
US-11-251-734-18
; Sequence 18, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 US NP1
; CURRENT APPLICATION NUMBER: US/11/251,734
; PRIOR FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US 09/933,780
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-251-734-18

Query Match 100.0%; Score 47; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 3 DYKDDDDK 10

RESULT 18
US-11-251-734-19
; Sequence 19, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 US NP1
; CURRENT APPLICATION NUMBER: US/11/251,734
; PRIOR FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US 09/933,780
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic peptide
US-11-251-734-19

Query Match 100.0%; Score 47; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 3 DYKDDDDK 10

RESULT 19
US-11-328-747-14
; Sequence 14, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jiansheng
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; PRIOR FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-ubiquitin
US-11-328-747-14

Query Match 100.0%; Score 47; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDDK 8
Db 2 DYKDDDDK 9

RESULT 20
US-11-090-563-14
; Sequence 14, Application US/11090563
; Publication No. US20060115864A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jiansheng
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: Assays for Identifying Ubiquitin Agents and for
; TITLE OF INVENTION: Identifying Agents that Modify the Activity of
; FILE REFERENCE: 021044-007061US
; CURRENT APPLICATION NUMBER: US/11/090,563
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/291,863
; PRIOR FILING DATE: 2001-05-18

```
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/152,156
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:FLAG-ubiquitin
US-11-090-563-14
```

```
Query Match          100.0%; Score 47; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```
RESULT 21
; Sequence 15, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:FLAG-Cys-ubiquitin
US-11-328-747-15
```

```
Query Match          100.0%; Score 47; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```
RESULT 22
US-11-090-563-15
; Sequence 15, Application US/11090563
; Publication No. US20060115864A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Assays for Identifying Ubiquitin Agents and for
; TITLE OF INVENTION: Identifying Agents That Modify the Activity of
; FILE REFERENCE: 021044-007061US
; CURRENT APPLICATION NUMBER: US/11/090,563
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/291,863
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/152,156
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:FLAG-Cys-ubiquitin
US-11-090-563-15
```

```
Query Match          100.0%; Score 47; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db      2 DYKDDDDK 9
```

```
RESULT 23
; Sequence 16, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 86
; TYPE: PRT
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:FLAG-Ala-Cys-ubiquitin
US-11-328-747-18

Query Match 100.0%; Score 47; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 2 DYKDDDK 9

RESULT 24

US-10-971-483-12
Sequence 12, Application US/10971483
Publication No. US2006008934A1
GENERAL INFORMATION:
APPLICANT: Columbia University
APPLICANT: Greene, Lloyd A.
APPLICANT: Angelastro, James M.
TITLE OF INVENTION: METHODS FOR REGULATING THE GROWTH AND/OR
TITLE OF INVENTION: SURVIVAL OF TUMOR CELLS AND STEM CELLS BY MODULATING THE
FILE REFERENCE: 070050.2879 Greene
CURRENT APPLICATION NUMBER: US/10/971,483
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 10/809,312
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: US 60/460,242
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 99
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic tag
US-10-971-483-12

Query Match 100.0%; Score 47; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 2 DYKDDDK 9

RESULT 25

US-11-180-855-3
Sequence 3, Application US/11180855
Publication No. US20060088912A1
GENERAL INFORMATION:
APPLICANT: YAN, GOUYING
APPLICANT: XIE, YUHONG
APPLICANT: PAULSEN, JANET E
APPLICANT: ZHANG, JIMIN
APPLICANT: ROOKEY, DIONNA
APPLICANT: BATES, BRIAN
APPLICANT: LU, ZHIJIAN
APPLICANT: MARK, ROBERT
APPLICANT: CAMPOS, SUSIE J
TITLE OF INVENTION: Compositions and Methods of Purifying Myelin-Associated
FILE REFERENCE: 102729-29
CURRENT APPLICATION NUMBER: US/11/180,855
PRIOR FILING DATE: 2005-07-13
PRIOR APPLICATION NUMBER: US 60/587,893
PRIOR FILING DATE: 2004-07-14

PRIOR APPLICATION NUMBER: US 60/588,239
PRIOR FILING DATE: 2004-07-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-11-180-855-3

Query Match 100.0%; Score 47; DB 7; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 332 DYKDDDK 339

RESULT 26

US-11-180-855-2
Sequence 2, Application US/11180855
Publication No. US20060088912A1
GENERAL INFORMATION:
APPLICANT: YAN, GOUYING
APPLICANT: XIE, YUHONG
APPLICANT: PAULSEN, JANET E
APPLICANT: ZHANG, JIMIN
APPLICANT: ROOKEY, DIONNA
APPLICANT: BATES, BRIAN
APPLICANT: LU, ZHIJIAN
APPLICANT: MARK, ROBERT
APPLICANT: CAMPOS, SUSIE J
TITLE OF INVENTION: Compositions and Methods of Purifying Myelin-Associated
FILE REFERENCE: 102729-29
CURRENT APPLICATION NUMBER: US/11/180,855
PRIOR FILING DATE: 2005-07-13
PRIOR APPLICATION NUMBER: US 60/587,893
PRIOR FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 60/588,239
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 531
TYPE: PRT
ORGANISM: Homo sapiens
US-11-180-855-2

Query Match 100.0%; Score 47; DB 7; Length 531;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDK 8
Db 523 DYKDDDK 530

RESULT 27

US-11-267-837A-6
Sequence 6, Application US/11267837A
Publication No. US20060105952A1
GENERAL INFORMATION:
APPLICANT: Allison, Anthony
TITLE OF INVENTION: Modified Annexin Proteins and Methods for Their Use in Organ
FILE REFERENCE: SURR. 90/CIP2
CURRENT APPLICATION NUMBER: US/11/267,837A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: 60/270,402
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 11/078,231

```

; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/080,370
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/552,428
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/579,589
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/332,582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (335)..(335)
; OTHER INFORMATION: The 'Xaa' at location 335 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: The 'Xaa' at location 352 stands for Lys, Asn, Arg, Ser, Thr,
; OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
; OTHER INFORMATION: Cys, or Phe.
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-267-837A-6
```

```
Query Match          100.0%; Score 47; DB 7; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       2 DYKDDDDK 9
```

```

RESULT 28
US-11-134-228A-6
; Sequence 6, Application US/11134228A
; Publication No. US20060105320A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40155A
; CURRENT APPLICATION NUMBER: US/11/134,228A
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,277
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
US-11-134-228A-6
```

```
Query Match          91.5%; Score 43; DB 7; Length 8;
Best Local Similarity 87.5%; Pred. No. 9.6e+04;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
        |||||
Db       1 DYKDDDDK 8
```

```

RESULT 29
US-10-484-105-4
; Sequence 4, Application US/10484105
; Publication No. US20060127893A1
; GENERAL INFORMATION:
; APPLICANT: Universitat Zurich
; TITLE OF INVENTION: Modification of Human Variable Domains
; FILE REFERENCE: P 2289 US S3
; CURRENT APPLICATION NUMBER: US/10/484,105
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: EP 01 11 6756.6
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-484-105-4
```

```
Query Match          89.4%; Score 42; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDD 7
        |||||
Db       1 DYKDDDD 7
```

```

RESULT 30
US-11-299-013-17
; Sequence 17, Application US/11299013
; Publication No. US20060088878A1
; GENERAL INFORMATION:
; APPLICANT: BRIZZARD, BILLY L
; TITLE OF INVENTION: PURIFICATION OF RECOMBINANT PROTEINS FUSED TO MULTIPLE EPITOPES
; FILE REFERENCE: SGM6933.7
; CURRENT APPLICATION NUMBER: US/11/299,013
; PRIOR FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 09/415,000
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/970,308
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized inventive sequence
US-11-299-013-17
```

```
Query Match          89.4%; Score 42; DB 7; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDD 7
        |||||
Db       16 DYKDDDD 22
```

```

RESULT 31
US-10-953-349-29832
; Sequence 29832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
```

```

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29832
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-29832
```

```
Query Match      83.0%; Score 39; DB 6; Length 91;
Best Local Similarity 75.0%; Pred. No. 5.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
        ||::|||
Db      16 DYEDDDK 23
```

```

RESULT 32
US-10-953-349-29831
; Sequence 29831, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29831
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-29831
```

```
Query Match      83.0%; Score 39; DB 6; Length 92;
Best Local Similarity 75.0%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
        ||::|||
Db      17 DYEDDDK 24
```

```

RESULT 33
US-10-953-349-33141
; Sequence 33141, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33141
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33141
```

```
Query Match      83.0%; Score 39; DB 6; Length 428;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
        ||::|||
Db      16 DYEDDDK 23
```

```

RESULT 34
US-10-953-349-33140
; Sequence 33140, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33140
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33140
```

```
Query Match      83.0%; Score 39; DB 6; Length 429;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
        ||::|||
Db      17 DYEDDDK 24
```

```

RESULT 35
US-10-953-349-33139
; Sequence 33139, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33139
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33139
```

```
Query Match      83.0%; Score 39; DB 6; Length 463;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 DYKDDDK 8
        ||::|||
Db      51 DYEDDDK 58
```

```

RESULT 36
US-10-953-349-6317
; Sequence 6317, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

```
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6317
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6317
```

```
Query Match          80.9%; Score 38; DB 6; Length 275;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
      |||||
Db      192 DYDDDDK 199
```

```
RESULT 37
US-10-953-349-6316
; Sequence 6316, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6316
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6316
```

```
Query Match          80.9%; Score 38; DB 6; Length 294;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
      |||||
Db      211 DYDDDDK 218
```

```
RESULT 38
US-10-953-349-6315
; Sequence 6315, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6315
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6315
```

```
Query Match          80.9%; Score 38; DB 6; Length 315;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
      |||||
Db      232 DYDDDDK 239
```

RESULT 39

```
US-10-449-902-39313
; Sequence 39313, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39313
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39313
```

```
Query Match          78.7%; Score 37; DB 6; Length 164;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDD 7
      |||||
Db      147 DYSDDDD 153
```

```
RESULT 40
US-10-953-349-21221
; Sequence 21221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 21221
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21221
```

```
Query Match          78.7%; Score 37; DB 6; Length 389;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DYKDDDDK 8
      |||||
Db      142 DYDDDDK 149
```

```
RESULT 41
US-10-953-349-21220
; Sequence 21220, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
```

SOFTWARE: PatentIn version 3.3
SEQ ID NO 21220
LENGTH: 433
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21220

Query Match 78.7%; Score 37; DB 6; Length 433;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 186 DYDDDDQ 193

RESULT 42
US-10-449-902-45116
Sequence 45116, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45116
LENGTH: 567
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-45116

Query Match 78.7%; Score 37; DB 6; Length 567;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 44 DYDDDDQ 51

RESULT 43
US-09-756-097B-66
Sequence 66, Application US/09756097B
Publication No. US20060088938A1
GENERAL INFORMATION:
APPLICANT: Mitchell, Lloyd G.
APPLICANT: Garcia-Blanco, Mariano A.
APPLICANT: Puttaraju, Madalah
APPLICANT: Mansfield, Gary S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
FILE REFERENCE: A1304-B-A-C 072874.0138
CURRENT APPLICATION NUMBER: US/09/756, 097B
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/158, 863
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/133, 717
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 09/087, 233
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 08/766, 354
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: 60/008, 317

PRIOR FILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C terminal residues from glutathione -S-
US-09-756-097B-66

Query Match 76.6%; Score 36; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDD 6
DB 1 DYKDD 6

RESULT 44
US-10-449-902-29232
Sequence 29232, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29232
LENGTH: 194
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-29232

Query Match 76.6%; Score 36; DB 6; Length 194;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 171 DYDEDDQ 178

RESULT 45
US-10-449-902-49424
Sequence 49424, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49424
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49424

Query Match 76.6%; Score 36; DB 6; Length 194;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|||
Db 171 DYLDDEDK 178

RESULT 46
US-10-449-902-54492
; Sequence 54492, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54492
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54492

Query Match 76.6%; Score 36; DB 6; Length 411;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|||
Db 139 DYDDDD 145

RESULT 47
US-10-449-902-40889
; Sequence 40889, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40889
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Oryza sativa

US-10-449-902-40889

Query Match 76.6%; Score 36; DB 6; Length 533;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|||
Db 523 DYTDDD 529

RESULT 48
US-11-267-837A-9
; Sequence 9, Application US/11267837A
; Publication No. US20060105952A1
; GENERAL INFORMATION:
; APPLICANT: Allison, Anthony
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Their Use in Organ
; FILE REFERENCE: SURR-90/CIP2
; CURRENT APPLICATION NUMBER: US/11/267, 837A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/270, 402
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 11/078, 231
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 10/080, 370
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/552, 428
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/579, 589
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/332, 582
; PRIOR FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: purification tag
US-11-267-837A-9

Query Match 74.5%; Score 35; DB 7; Length 8;
Best Local Similarity 85.7%; Pred. No. 9.6e+04;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|||
Db 1 DYLDDD 7

RESULT 49
US-10-449-902-34551
; Sequence 34551, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34551

LENGTH: 204
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-34551

Query Match
Best Local Similarity 74.5%; Score 35; DB 6; Length 204;
Matches 6; Conservative 0; Pred. No. 53; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 162 DYDDDD 168

RESULT 50
US-10-449-902-31822
Sequence 31822, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 2002-12-11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31822
LENGTH: 342
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-31822

Query Match
Best Local Similarity 74.5%; Score 35; DB 6; Length 342;
Matches 6; Conservative 0; Pred. No. 92; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 69 DYGDddd 75

RESULT 51
US-10-449-902-40463
Sequence 40463, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 2002-12-11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40463
LENGTH: 342
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-40463

Query Match
Best Local Similarity 74.5%; Score 35; DB 6; Length 342;
Matches 6; Conservative 0; Pred. No. 92; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 69 DYGDddd 75

RESULT 52
US-10-449-902-44996
Sequence 44996, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 2002-12-11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44996
LENGTH: 351
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-44996

Query Match
Best Local Similarity 74.5%; Score 35; DB 6; Length 351;
Matches 6; Conservative 0; Pred. No. 94; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 69 DYGDddd 75

RESULT 53
US-10-449-902-46241
Sequence 46241, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
NUMBER OF SEQ ID NOS: 2002-12-11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46241
LENGTH: 734
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-46241

Query Match
Best Local Similarity 74.5%; Score 35; DB 6; Length 734;
Matches 6; Conservative 0; Pred. No. 2,1e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 713 DYLDLDD 719

RESULT 54
US-10-953-349-18302
; Sequence 18302, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18302
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18302

Query Match 72.3%; Score 34; DB 6; Length 133;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8
Db 108 YKDEDDR 114

RESULT 55
US-10-953-349-39990
; Sequence 39990, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39990
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39990

Query Match 72.3%; Score 34; DB 6; Length 133;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDK 8
Db 108 YKDEDDR 114

RESULT 56
US-10-953-349-6258
; Sequence 6258, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6258
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6258

Query Match 72.3%; Score 34; DB 6; Length 150;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 132 DYDEDD 138

RESULT 57
US-10-953-349-6257
; Sequence 6257, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6257
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6257

Query Match 72.3%; Score 34; DB 6; Length 163;
Best Local Similarity 71.4%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
Db 145 DYDEDD 151

RESULT 58
US-10-449-902-31740
; Sequence 31740, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31740
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31740

Query Match 72.3%; Score 34; DB 6; Length 219;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 123 DEEDDDK 130

RESULT 59
US-10-449-902-40441

; Sequence 40441, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; PRIOR FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 40441

; LENGTH: 219

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-40441

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 219;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 123 DEEDDDK 130

RESULT 60

US-10-953-349-6256

; Sequence 6256, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERXY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6256

; LENGTH: 222

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-6256

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 222;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 204 DYEDDD 210

RESULT 61

US-10-953-349-2040

; Sequence 2040, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERXY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36044

; LENGTH: 301

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-36044

; TITLE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2040

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-2040

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 229;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7

Db 183 DYEDDED 189

RESULT 62

US-10-449-902-41697

; Sequence 41697, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41697

; LENGTH: 294

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-41697

Query Match

Best Local Similarity 72.3%; Score 34; DB 6; Length 294;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8

Db 31 DYKDDSK 38

RESULT 63

US-10-953-349-36044

; Sequence 36044, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERXY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36044

; LENGTH: 301

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-36044

Query Match 72.3%; Score 34; DB 6; Length 301;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|:|:|:
Db 71 DKDDDD 77

RESULT 64
US-10-953-349-2039
; Sequence 2039, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2039
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2039

Query Match 72.3%; Score 34; DB 6; Length 338;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|:|:|:
Db 292 DYEDDED 298

RESULT 65
US-10-953-349-2038
; Sequence 2038, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2038
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-2038

Query Match 72.3%; Score 34; DB 6; Length 340;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|:|:|:
Db 294 DYEDDED 300

RESULT 66
US-10-953-349-5131
; Sequence 5131, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5131
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5131

Query Match 72.3%; Score 34; DB 6; Length 362;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|:|:|:
Db 310 DYEDDDE 316

RESULT 67
US-10-449-902-52372
; Sequence 52372, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: The Institute of Technology Research Advancement Institution.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52372
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52372

Query Match 72.3%; Score 34; DB 6; Length 373;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
|:|:|:|:
Db 26 DAKDDDE 33

RESULT 68
US-10-449-902-43294
; Sequence 43294, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43294
LENGTH: 410
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-43294

Query Match 72.3%; Score 34; DB 6; Length 410;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 261 DFDSDDE 268

RESULT 69
US-10-449-902-42067
Sequence 42067, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42067
LENGTH: 437
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-42067

Query Match 72.3%; Score 34; DB 6; Length 437;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
DB 134 DAKDDDE 141

RESULT 70
US-10-449-902-50266
Sequence 50266, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50266
LENGTH: 497
TYPE: PRT
ORGANISM: Oryza sativa

US-10-449-902-50266

Query Match 72.3%; Score 34; DB 6; Length 497;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 23 DFDQDDD 29

RESULT 71
US-10-449-902-44569
Sequence 44569, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44569
LENGTH: 520
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-44569

Query Match 72.3%; Score 34; DB 6; Length 520;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
DB 23 DFDQDDD 29

RESULT 72
US-10-449-902-45621
Sequence 45621, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45621
LENGTH: 521
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-45621

Query Match 72.3%; Score 34; DB 6; Length 521;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 23 DFQDDDD 29

RESULT 73
US-10-449-902-45113
; Sequence 45113, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45113
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45113

Query Match 72.3%; Score 34; DB 6; Length 684;
Best Local Similarity 71.4%; Pred. No. 2,7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDD 8
|:|||||
Db 294 YEDDDDR 300

RESULT 74
US-10-953-349-21280
; Sequence 21280, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21280
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21280

Query Match 70.2%; Score 33; DB 6; Length 75;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
|:|||||
Db 47 DDKDDDE 54

RESULT 75
US-10-449-902-30504
; Sequence 30504, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30504
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30504

Query Match 70.2%; Score 33; DB 6; Length 145;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|||||
Db 44 DAKDDDD 50

RESULT 76
US-10-449-902-34122
; Sequence 34122, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34122
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-34122

Query Match 70.2%; Score 33; DB 6; Length 171;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 8
|:|||||
Db 41 DYDDDEE 48

RESULT 77
US-10-953-349-27604
; Sequence 27604, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 27604
;; LENGTH: 203
;; TYPE: PRT
;; ORGANISM: Triticum aestivum
US-10-953-349-27604

Query Match 70.2%; Score 33; DB 6; Length 203;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
| | | | |
Db 42 DKKDDDD 48

RESULT 78
US-10-449-902-50940
; Sequence 50940, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50940
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50940

Query Match 70.2%; Score 33; DB 6; Length 221;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
| | | | |
Db 44 DAKDDDD 50

RESULT 79
US-10-449-902-30872
; Sequence 30872, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30872
; LENGTH: 431

;; TYPE: PRT
;; ORGANISM: Oryza sativa
US-10-449-902-30872

Query Match 70.2%; Score 33; DB 6; Length 431;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYKDDDD 7
| | | | |
Db 206 NFKDDDD 212

RESULT 80
US-10-449-902-37911
; Sequence 37911, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37911
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37911

Query Match 70.2%; Score 33; DB 6; Length 508;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYKDDDD 8
| | | | |
Db 495 DDKDDDE 502

RESULT 81
US-10-471-571A-3230
; Sequence 3230, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3230
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(553)
; OTHER INFORMATION: arginyl-tRNA synthetase
US-10-471-571A-3230

Query Match 70.2%; Score 33; DB 6; Length 553;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDX 8

Db 296 DFRDDKDR 303

RESULT 82

US-10-449-902-40941
; Sequence 40941, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40941
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-40941

Query Match 70.2%; Score 33; DB 6; Length 770;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDX 8

Db 738 DFSDNDX 745

RESULT 83
US-10-449-902-31438
; Sequence 31438, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31438
; LENGTH: 876
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31438

Query Match 70.2%; Score 33; DB 6; Length 876;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDX 8

Db 818 YKDEDE 824

RESULT 84

US-10-449-902-56037
; Sequence 56037, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56037
; LENGTH: 936
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56037

Query Match 70.2%; Score 33; DB 6; Length 936;
Best Local Similarity 71.4%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKDDDX 8

Db 878 YKDEDE 884

RESULT 85
US-10-449-902-52762
; Sequence 52762, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52762
; LENGTH: 1179
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52762

Query Match 70.2%; Score 33; DB 6; Length 1179;
Best Local Similarity 62.5%; Pred. No. 6.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDX 8

Db 87 EYDDDD 94

RESULT 86
US-10-449-902-53947
; Sequence 53947, Application US/10449902


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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53947
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53947

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Query Match      70.2% Score 33; DB 6; Length 1180;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DYKDDDD 7
Db      500 NFKDDDD 506

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RESULT 87
US-11-289-102-378
; Sequence 378, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 378
; LENGTH: 1230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-378

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Query Match      70.2% Score 33; DB 7; Length 1230;
Best Local Similarity 71.4%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 DYKDDDD 7
Db      338 EYSDDD 344

```

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RESULT 88
US-11-074-497-41
; Sequence 41, Application US/11074497
; Publication No. US2006012135A1
; GENERAL INFORMATION:
; APPLICANT: Geerts, Hugo
; APPLICANT: Maure, Stefan
; APPLICANT: Cik, Miroslav
; APPLICANT: Meert, Theo
; APPLICANT: Ver Donck, Luc

```

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; TITLE OF INVENTION: NEUTROTROPHIC GROWTH FACTOR
; FILE REFERENCE: 43962-010700
; CURRENT APPLICATION NUMBER: US/11/074,497
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/357,349
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 09/327,668
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 09/248,772
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: GB 9815283.8
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Plasmid NH2-terminal
US-11-074-497-41

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Query Match      68.1% Score 32; DB 7; Length 39;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 DYKDDDK 8
Db      24 DLYDDDK 31

```

```

RESULT 89
US-10-449-902-43449
; Sequence 43449, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43449
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43449

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Query Match      68.1% Score 32; DB 6; Length 74;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      2 YKDDDD 7
Db      55 YKDEDD 60

```

```

RESULT 90
US-10-449-902-33753
; Sequence 33753, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.

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; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33753
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33753

Query Match      68.1%; Score 32; DB 6; Length 80;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DYKDDDD 7
Db      22 YEDDDD 27

RESULT 91
US-10-449-902-36276
; Sequence 36276, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36276
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-36276

Query Match      68.1%; Score 32; DB 6; Length 146;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYKDDDD 7
Db      131 EYDDDD 137

RESULT 92
US-10-953-349-6227
; Sequence 6227, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
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; SEQ ID NO 6227
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6227

Query Match      68.1%; Score 32; DB 6; Length 203;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 DYKDDDDK 8
Db      34 DSDDDDK 41

RESULT 93
US-10-449-902-29282
; Sequence 29282, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29282
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29282

Query Match      68.1%; Score 32; DB 6; Length 205;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYKDDDD 7
Db      44 DYKDDDD 50

RESULT 94
US-10-516-753-74
; Sequence 74, Application US/10516753
; Publication No. US20060123506A1
; GENERAL INFORMATION:
; APPLICANT: Hammoufa, Abdelali
; APPLICANT: Lydiatte, Derek J.
; APPLICANT: Gao, Ming-Jun
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTOR
; FILE REFERENCE: 270.78USMO
; CURRENT APPLICATION NUMBER: US/10/516,753
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA2003/000822
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 74
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Arabidopsis
; FEATURE:
; OTHER INFORMATION: atKCL2
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US-10-516-753-74

Query Match 68.1%; Score 32; DB 6; Length 221;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKDD 6
|:|
|:|
|:|
Db 170 DYEDDD 175

RESULT 95

US-10-953-349-6226
; Sequence 6226, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6226
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6226

Query Match 68.1%; Score 32; DB 6; Length 231;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|:|
|:|
|:|
Db 62 DSDDDDK 69

RESULT 96

US-10-953-349-16219
; Sequence 16219, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16219
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16219

Query Match 68.1%; Score 32; DB 6; Length 234;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|
|:|
|:|
Db 12 DFDDDD 18

RESULT 97

US-10-953-349-16218
; Sequence 16218, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE;
; FILE OF INVENTION: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16218
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16218

Query Match 68.1%; Score 32; DB 6; Length 240;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
|:|
|:|
|:|
Db 18 DFDDDD 24

RESULT 98

US-10-953-349-31660
; Sequence 31660, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE;
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31660
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-953-349-31660

Query Match 68.1%; Score 32; DB 6; Length 252;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYKDDDK 8
|:|
|:|
|:|
Db 139 DYSSDD 146

RESULT 99

US-10-953-349-20549
; Sequence 20549, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20549
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20549

Query Match 68.1%; Score 32; DB 6; Length 255;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKDDDD 7
 Db 121 DFDDDD 127

RESULT 100
 US-10-953-349-31659
 ; Sequence 31659, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 31659
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 ; US-10-953-349-31659

Query Match 68.1%; Score 32; DB 6; Length 260;
 Best Local Similarity 62.5%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DYKDDDK 8
 Db 147 DYSSDDDE 154

Search completed: June 29, 2006, 11:56:19
 Job time : 25 secs